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(54) Title: NUCLEIC ACIDS AND PROTEINS AND METHODS FOR MAKING AND USING THEM

(57) Abstract: The invention provides polypeptides, including enzymes, structural proteins and binding proteins, polynucleotides encoding these polypeptides, and methods of making and using these polynucleotides and polypeptides. Polypeptides, including enzymes and antibodies, and nucleic acids of the invention can be used in industrial, experimental, food and feed processing, nutri-
tional and pharmaceutical applications, e.g., for food and feed supplements, colorants, nutraceuticals, cosmetic and pharmaceutical needs.



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NUCLEIC ACIDS AND PROTEINS AND METHODS FOR MAKING AND USING THEM

REFERENCE TO SEQUENCE LISTING SUBMITTED ON A COMPACT DISC

The content of the following submissions on compact discs are incorporated herein by reference in their entirety: A computer readable form (CRF) of the Sequence Listing (file name: 564462014340 SEQUENCE LISTING.txt, date recorded: March 4, 2005, size: 36,463,033 bytes); a duplicate compact disc copy (COPY 1) of the Sequence Listing (file name: 564462014340 SEQUENCE LISTING.txt, date recorded: March 4, 2005, size: 36,463,033 bytes); and a duplicate compact disc copy (COPY 2) of the Sequence Listing (file name: 564462014340 SEQUENCE LISTING.txt, date recorded: March 4, 2005, size: 36,463,033 bytes).

FIELD OF THE INVENTION

This invention relates to molecular and cellular biology and biochemistry. In one aspect, the invention provides polypeptides, including enzymes, structural proteins and binding proteins (e.g., ligands, receptors), polynucleotides encoding these polypeptides, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, structural proteins and binding proteins, including thermostable and thermotolerant activity, and polynucleotides encoding these enzymes, structural proteins and binding proteins and making and using these polynucleotides and polypeptides. The polypeptides of the invention can be used in a variety of pharmaceutical, agricultural and industrial contexts, including the manufacture of cosmetics and nutraceuticals.

Additionally, the polypeptides of the invention can be used in food processing, brewing, bath additives, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver recovery in the photographic industry, medical treatment, silk degumming, biofilm degradation, biomass conversion to ethanol, biodefense, antimicrobial agents and disinfectants, personal care and cosmetics, biotech reagents, in corn wet milling and pharmaceuticals such as digestive aids and anti-inflammatory (anti-phlogistic) agents.

BACKGROUND

The invention provides isolated and recombinant polypeptides, including enzymes, structural proteins and binding proteins, polynucleotides encoding these polypeptides, and methods of making and using these polynucleotides and polypeptides. The polypeptides of the invention, and the polynucleotides encoding the polypeptides of the invention, encompass many classes of enzymes, structural proteins and binding proteins. In one aspect, the enzymes and proteins of the invention include, e.g. aldolases, alpha-galactosidases, amidases, e.g. secondary amidases, amylases, catalases, carotenoid pathway enzymes, dehalogenases, endoglucanases, epoxide hydrolases, esterases, hydrolases, glucosidases, glycosidases, inteins, isomerases, laccases, lipases, monooxygenases, nitroreductases, nitrilases, P450 enzymes, pectate lyases, phosphatases, phospholipases, phytases, polymerases and xylanases. The invention also provides isolated and recombinant polypeptides, including enzymes, structural proteins and binding proteins, polynucleotides encoding these polypeptides, having the activities described in Table 1, Table 2 or Table 3, below. The enzymes and proteins of the invention have utility in a variety of applications.

SUMMARY

The invention provides isolated or recombinant nucleic acids comprising a nucleic acid sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary nucleic acid of the invention, e.g., including SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000, 2050, 2100, 2200, 2250, 2300, 2350, 2400, 2450, 2500, or more residues, encodes at least one polypeptide having an enzyme, structural or binding activity, and the sequence identities are determined by analysis with

a sequence comparison algorithm or by a visual inspection. In one aspect, the enzymes and proteins of the invention include, e.g. aldolases, alpha-galactosidases, amidases, e.g. secondary amidases, amylases, catalases, carotenoid pathway enzymes, dehalogenases, endoglucanases, epoxide hydrolases, esterases, hydrolases, glucosidases, glycosidases, inteins, isomerases, laccases, lipases, monooxygenases, nitroreductases, nitrilases, P450 enzymes, pectate lyases, phosphatases, phospholipases, phytases, polymerases and xylanases. In another aspect, the isolated and recombinant polypeptides of the invention, including enzymes, structural proteins and binding proteins, and polynucleotides encoding these polypeptides, of the invention have activity as described in Table 1, Table 2 or Table 3, below.

In one aspect, the invention also provides isolated or recombinant nucleic acids with a common novelty in that they are all derived from a common source, e.g., an environmental source, mixed environmental sources or mixed cultures. The invention provides isolated or recombinant nucleic acids isolated from a common source, e.g. an environmental source, mixed environmental sources or mixed cultures comprising a polynucleotide of the invention, e.g., an exemplary sequence of the invention, including SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000, 2050, 2100, 2200, 2250, 2300, 2350, 2400, 2450, 2500, or more residues, encodes at least one polypeptide having an enzyme, structural or binding activity, and the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection. In one aspect, the enzymes and proteins of the invention include, e.g. aldolases, alpha-galactosidases, amidases, e.g. secondary amidases, amylases, catalases, carotenoid pathway enzymes, dehalogenases, endoglucanases, epoxide hydrolases, esterases, hydrolases, glucosidases, glycosidases, inteins, isomerases, laccases, lipases, monooxygenases, nitroreductases, nitrilases, P450 enzymes, pectate lyases, phosphatases, phospholipases, phytases, polymerases and xylanases. In another aspect, the isolated and recombinant polypeptides of the invention, including enzymes, structural proteins and binding proteins, and polynucleotides

encoding these polypeptides, of the invention have activity as described in Table 1, Table 2 or Table 3, below.

In alternative aspects, the isolated or recombinant nucleic acid encodes a polypeptide comprising an exemplary sequence of the invention, e.g., including sequences as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO: 26,898. In one aspect these polypeptides have an enzyme, structural or binding activity. In one aspect, the enzymes and proteins of the invention include, e.g. aldolases, alpha-galactosidases, amidases, e.g. secondary amidases, amylases, catalases, carotenoid pathway enzymes, dehalogenases, endoglucanases, epoxide hydrolases, esterases, hydrolases, glucosidases, glycosidases, inteins, isomerases, laccases, lipases, monooxygenases, nitroreductases, nitrilases, P450 enzymes, pectate lyases, phosphatases, phospholipases, phytases, polymerases and xylanases. In another aspect, the isolated and recombinant polypeptides of the invention, including enzymes, structural proteins and binding proteins, and polynucleotides encoding these polypeptides, of the invention have activity as described in Table 1, Table 2 or Table 3, below.

In alternative aspects, the enzyme, structural or binding activity comprises a recombinase activity, a helicase activity, a DNA replication activity, a DNA recombination activity, an isomerase, a trans-isomerase activity or topoisomerase activity, a methyl transferase activity, an aminotransferase activity, a uracil-5- methyl transferase activity, a cysteinyl tRNA synthetase activity, a hydrolase, an esterase activity, a phosphoesterase activity, an acetylmuramyl pentapeptide phosphotransferase activity, a glycosyltransferase activity, an acetyltransferase activity, an acetylglucosamine phosphate transferase activity, a centromere binding activity, a telomerase activity or a transcriptional regulatory activity, a heat shock protein activity, a protease activity, a proteinase activity, a peptidase activity, a carboxypeptidase activity, an endonuclease activity, an exonuclease activity, a RecB family exonuclease activity, a polymerase activity, a carbamoyl phosphate synthetase activity, a methyl-thioadenine synthetase activity, an oxidoreductase activity, an Fe-S oxidoreductase activity, a flavodoxin reductase activity, a permease activity, a thymidylate activity, a dehydrogenase activity, a pyrophosphorylase activity, a coenzyme metabolism activity, a dinucleotide-utilizing enzyme activity, a molybdopterin or thiamine biosynthesis activity, a beta-lactamase

activity, a ligand binding activity, an ion transport activity, an ion metabolism activity, a tellurite resistance protein activity, an inorganic ion transport activity, a nucleotide transport activity, a nucleotide metabolism activity, an actin or myosin activity, a lipase activity or a lipid acyl hydrolase (LAH) activity, a cell envelop biogenesis activity, an outer membrane synthesis activity, a ribosomal structure synthesis activity, a translational processing activity, a transcriptional initiation activity, a TATA-binding activity, a signal transduction activity, an energy metabolism activity, an ATPase activity, an information storage and/or processing activity, and/or any of the polypeptides activities as set forth in Table 1, Table 2 or Table 3, below.

In one aspect, the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

Another aspect of the invention is an isolated or recombinant nucleic acid including at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000, 2050, 2100, 2200, 2250, 2300, 2350, 2400, 2450, 2500, or more consecutive bases of a nucleic acid sequence of the invention, sequences substantially identical thereto, and the sequences complementary thereto.

In one aspect, the isolated or recombinant nucleic acid encodes a polypeptide having a enzyme, structural or binding activity, that is thermostable. The polypeptide can retain activity under conditions comprising a temperature range of between about 37°C to about 95°C; between about 55°C to about 85°C, between about 70°C to about 95°C, or, between about 90°C to about 95°C.

In another aspect, the isolated or recombinant nucleic acid encodes a polypeptide having an enzyme, structural or binding activity, which is thermotolerant. The polypeptide can retain activity after exposure to a temperature in the range from greater than 37°C to about 95°C or anywhere in the range from greater than 55°C to about 85°C. The polypeptide can retain activity after exposure to a temperature in the range between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more. In one aspect, the polypeptide retains activity after exposure to a temperature in the range from greater than 90°C to about 95°C at about pH 4.5.

The invention provides isolated or recombinant nucleic acids comprising a sequence that hybridizes under stringent conditions to a nucleic acid comprising a sequence of the invention, e.g., an exemplary sequence of the invention, including SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, or fragments or subsequences thereof. In one aspect, the nucleic acid encodes a polypeptide having a enzyme, structural or binding activity. The nucleic acid can be at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200 or more residues in length or the full length of the gene or transcript. In one aspect, the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes.

The invention provides a nucleic acid probe for identifying a nucleic acid encoding a polypeptide having a enzyme, structural or binding activity, wherein the probe comprises at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000 or more, consecutive bases of a sequence comprising a sequence of the invention, or fragments or subsequences thereof, wherein the probe identifies the nucleic acid by binding or hybridization. The probe can comprise an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 consecutive bases of a sequence comprising a sequence of the invention, or fragments or subsequences thereof.

The invention provides a nucleic acid probe for identifying a nucleic acid encoding a polypeptide having a enzyme, structural or binding activity, wherein the probe comprises a nucleic acid comprising a sequence at least about 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000 or more residues having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to a nucleic acid of the invention. In one aspect, the sequence identities are determined by analysis with a sequence comparison

algorithm or by visual inspection. In alternative aspects, the probe can comprise an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 consecutive bases of a nucleic acid sequence of the invention, or a subsequence thereof.

The invention provides an amplification primer pair for amplifying a nucleic acid encoding a polypeptide having a enzyme, structural or binding activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence of the invention, or fragments or subsequences thereof. One or each member of the amplification primer sequence pair can comprise an oligonucleotide comprising at least about 10 to 50, or more, consecutive bases of the sequence, or about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more consecutive bases of the sequence.

The invention provides amplification primer pairs, wherein the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36 or more residues of a nucleic acid of the invention, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36 or more residues of the complementary strand of the first member.

The invention provides polypeptide-, enzyme-, protein-, e.g. structural or binding protein-encoding nucleic acids generated by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. The invention provides polypeptide-, enzyme-, protein-, e.g. structural or binding protein-encoding nucleic acids generated by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. The invention provides methods of making a polypeptide, enzyme, protein, e.g. structural or binding protein, by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. In one aspect, the amplification primer pair amplifies a nucleic acid from a library, e.g., a gene library, such as an environmental library.

The invention provides methods of amplifying a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity, comprising amplification of a template nucleic acid with an amplification primer sequence pair capable of amplifying a nucleic acid sequence of the invention, or fragments or subsequences thereof.

The invention provides expression cassettes comprising a nucleic acid of the invention or a subsequence thereof. In one aspect, the expression cassette can comprise the nucleic acid that is operably linked to a promoter. The promoter can be a viral, bacterial, mammalian or plant promoter. In one aspect, the plant promoter can be a potato, rice, corn, wheat, tobacco or barley promoter. The promoter can be a constitutive promoter. The constitutive promoter can comprise CaMV35S. In another aspect, the promoter can be an inducible promoter. In one aspect, the promoter can be a tissue-specific promoter or an environmentally regulated or a developmentally regulated promoter. Thus, the promoter can be, e.g., a seed-specific, a leaf-specific, a root-specific, a stem-specific or an abscission-induced promoter. In one aspect, the expression cassette can further comprise a plant or plant virus expression vector.

The invention provides cloning vehicles comprising an expression cassette (e.g., a vector) of the invention or a nucleic acid of the invention. The cloning vehicle can be a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome. The viral vector can comprise an adenovirus vector, a retroviral vector or an adeno-associated viral vector. The cloning vehicle can comprise a bacterial artificial chromosome (BAC), a plasmid, a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC), or a mammalian artificial chromosome (MAC).

The invention provides transformed cell comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention, or a cloning vehicle of the invention. In one aspect, the transformed cell can be a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell. In one aspect, the plant cell can be a cereal, a potato, wheat, rice, corn, tobacco or barley cell.

The invention provides transgenic non-human animals comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention. In one aspect, the animal is a mouse, a rat, a pig, a goat or a sheep.

The invention provides transgenic plants comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention. The transgenic plant can be a cereal plant, a corn plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant or a tobacco plant.

The invention provides transgenic seeds comprising a nucleic acid of the invention or an expression cassette (e.g., a vector) of the invention. The transgenic seed

can be a cereal plant, a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a peanut or a tobacco plant seed.

The invention provides an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a nucleic acid of the invention. The invention provides methods of inhibiting the translation of a polypeptide, enzyme, protein, e.g. structural or binding protein message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a nucleic acid of the invention. In one aspect, the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length, e.g., 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more bases in length.

The invention provides methods of inhibiting the translation of a polypeptide, enzyme, protein, e.g. structural or binding protein message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a nucleic acid of the invention. The invention provides double-stranded inhibitory RNA (RNAi, or RNA interference) molecules (including small interfering RNA, or siRNAs, for inhibiting transcription, and microRNAs, or miRNAs, for inhibiting translation) comprising a subsequence of a sequence of the invention. In one aspect, the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or more duplex nucleotides in length. The invention provides methods of inhibiting the expression of a polypeptide, enzyme, protein, peptide, e.g. structural or binding protein in a cell comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (iRNA, including small interfering RNA, or siRNAs, for inhibiting transcription, and microRNAs, or miRNAs, for inhibiting translation), wherein the RNA comprises a subsequence of a sequence of the invention.

The invention provides isolated or recombinant polypeptides encoded by a nucleic acid of the invention. In alternative aspects, the polypeptide can have a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc., and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898 (the exemplary sequences of the invention), or subsequences thereof, including fragments having

enzymatic and/or substrate binding activity. The polypeptide can have an enzyme, structural or binding activity.

In alternative aspects, the enzyme, structural or binding activity comprises a recombinase activity, a helicase activity, a DNA replication activity, a DNA recombination activity, an isomerase, a trans-isomerase activity or topoisomerase activity, a methyl transferase activity, an aminotransferase activity, a uracil-5- methyl transferase activity, a cysteinyl tRNA synthetase activity, a hydrolase, an esterase activity, a phosphoesterase activity, an acetylmuramyl pentapeptide phosphotransferase activity, a glycosyltransferase activity, an acetyltransferase activity, an acetylglucosamine phosphate transferase activity, a centromere binding activity, a telomerase activity or a transcriptional regulatory activity, a heat shock protein activity, a protease activity, a proteinase activity, a peptidase activity, a carboxypeptidase activity, an endonuclease activity, an exonuclease activity, a RecB family exonuclease activity, a polymerase activity, a carbamoyl phosphate synthetase activity, a methyl-thioadenine synthetase activity, an oxidoreductase activity, an Fe-S oxidoreductase activity, a flavodoxin reductase activity, a permease activity, a thymidylate activity, a dehydrogenase activity, a pyrophosphorylase activity, a coenzyme metabolism activity, a dinucleotide-utilizing enzyme activity, a molybdopterin or thiamine biosynthesis activity, a beta-lactamase activity, a ligand binding activity, an ion transport activity, an ion metabolism activity, a tellurite resistance protein activity, an inorganic ion transport activity, a nucleotide transport activity, a nucleotide metabolism activity, an actin or myosin activity, a lipase activity or a lipid acyl hydrolase (LAH) activity, a cell envelop biogenesis activity, an outer membrane synthesis activity, a ribosomal structure synthesis activity, a translational processing activity, a transcriptional initiation activity, a TATA-binding activity, a signal transduction activity, an energy metabolism activity, an ATPase activity, an information storage and/or processing activity, and/or any of the polypeptides activities as set forth in Table 1, Table 2 or Table 3, below.

Exemplary polypeptide or peptide sequences of the invention include SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc., and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898, and subsequences thereof and variants thereof. Exemplary polypeptides also include fragments of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600 or more residues in length, or over the full length of an enzyme. Exemplary

polypeptide or peptide sequences of the invention include sequence encoded by a nucleic acid of the invention. Exemplary polypeptide or peptide sequences of the invention include polypeptides or peptides specifically bound by an antibody of the invention.

In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein, is thermostable. The polypeptide, enzyme, protein, e.g. structural or binding protein can retain activity under conditions comprising a temperature range of between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more. In another aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein can be thermotolerant. The polypeptide, enzyme, protein, e.g. structural or binding protein can retain activity after exposure to a temperature in the range from greater than 37°C to about 95°C, or in the range from greater than 55°C to about 85°C. In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein can retain activity after exposure to a temperature in the range from greater than 90°C to about 95°C at pH 4.5.

Another aspect of the invention provides an isolated or recombinant polypeptide or peptide including at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 or more consecutive bases of a polypeptide or peptide sequence of the invention, sequences substantially identical thereto, and the sequences complementary thereto. The peptide can be, e.g., an immunogenic fragment, a motif (e.g., a binding site), a signal sequence, a prepro sequence or an active site.

The invention provides isolated or recombinant nucleic acids comprising a sequence encoding a polypeptide, enzyme, protein, e.g. structural or binding protein having any of the activities as set forth in Tables 1, 2 or 3, and a signal sequence, wherein the nucleic acid comprises a sequence of the invention. In one aspect, the isolated or recombinant polypeptide can comprise the polypeptide of the invention comprising a heterologous signal sequence or a heterologous preprosequence, such as a heterologous enzyme or non-enzyme signal sequence. The invention provides isolated or recombinant nucleic acids comprising a sequence encoding a polypeptide, enzyme, protein, e.g. structural or binding protein having any of the activities as set forth in Tables 1, 2 or 3, wherein the sequence does not contain a signal sequence and the nucleic acid comprises a sequence of the invention. In one aspect, the invention provides an isolated or

recombinant polypeptide comprising a polypeptide of the invention lacking all or part of a signal sequence.

In one aspect, the invention provides chimeric proteins comprising a first domain comprising a signal sequence of the invention and at least a second domain. The protein can be a fusion protein. The second domain can comprise an enzyme. The enzyme can be a non-enzyme.

The invention provides chimeric polypeptides comprising at least a first domain comprising signal peptide (SP), a prepro sequence and/or a catalytic domain (CD) of the invention and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP), prepro sequence and/or catalytic domain (CD). In one aspect, the heterologous polypeptide or peptide is not an enzyme. The heterologous polypeptide or peptide can be amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP), prepro sequence and/or catalytic domain (CD).

The invention provides isolated or recombinant nucleic acids encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP), a prepro domain and/or a catalytic domain (CD) of the invention and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP), prepro domain and/or catalytic domain (CD).

The invention provides isolated or recombinant signal sequences (e.g., signal peptides) consisting of or comprising a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 29, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43, 1 to 44, 1 to 45, 1 to 46 or 1 to 47, of a polypeptide of the invention, including the exemplary polypeptides of the invention (including SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc., and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898). In one aspect, the invention provides signal sequences comprising the first 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70 or more amino terminal residues of a polypeptide of the invention.

In one aspect, the enzyme, structural or binding activity comprises a specific activity at about 37°C in the range from about 1 to about 1200 units per milligram of protein, or, about 100 to about 1000 units per milligram of protein. In another aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein activity comprises a specific activity from about 100 to about 1000 units per milligram of protein, or, from about 500 to about 750 units per milligram of protein. Alternatively, the enzyme, structural or binding activity comprises a specific activity at 37°C in the range from about 1 to about 750 units per milligram of protein, or, from about 500 to about 1200 units per milligram of protein. In one aspect, the enzyme, structural or binding activity comprises a specific activity at 37°C in the range from about 1 to about 500 units per milligram of protein, or, from about 750 to about 1000 units per milligram of protein. In another aspect, the enzyme, structural or binding activity comprises a specific activity at 37°C in the range from about 1 to about 250 units per milligram of protein. Alternatively, the enzyme, structural or binding activity comprises a specific activity at 37°C in the range from about 1 to about 100 units per milligram of protein.

In another aspect, thermotolerance comprises retention of at least half of the specific activity of the enzyme, structural or binding protein at 37°C after being heated to the elevated temperature. Alternatively, thermotolerance can comprise retention of specific activity at 37°C in the range from about 1 to about 1200 units per milligram of protein, or, from about 500 to about 1000 units per milligram of protein, after being heated to the elevated temperature. In another aspect, thermotolerance can comprise retention of specific activity at 37°C in the range from about 1 to about 500 units per milligram of protein after being heated to the elevated temperature.

The invention provides the isolated or recombinant polypeptide of the invention, wherein the polypeptide comprises at least one glycosylation site. In one aspect, glycosylation can be an N-linked glycosylation. In one aspect, the polypeptide can be glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein can retain activity under conditions comprising about pH 6.5, pH 6, pH 5.5, pH 5, pH 4.5 or pH 4. In another aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein can retain activity under conditions comprising about pH 7, pH 7.5 pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10, pH 10.5 or pH 11. In one aspect, the polypeptide can retain an enzyme, structural or binding activity after exposure to conditions comprising about pH 6.5, pH 6, pH 5.5, pH 5, pH 4.5 or pH 4. In another aspect, the polypeptide can retain

enzyme, structural or binding activity after exposure to conditions comprising about pH 7, pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10, pH 10.5 or pH 11.

In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein of the invention has activity at under alkaline conditions, e.g., the alkaline conditions of the gut, e.g., the small intestine. In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein can retain activity after exposure to the acidic pH of the stomach.

The invention provides protein preparations comprising a polypeptide of the invention, wherein the protein preparation comprises a liquid, a solid or a gel.

The invention provides heterodimers comprising a polypeptide of the invention and a second protein or domain. The second member of the heterodimer can be a different enzyme, a different enzyme or another protein. In one aspect, the second domain can be a polypeptide and the heterodimer can be a fusion protein. In one aspect, the second domain can be an epitope or a tag. In one aspect, the invention provides homodimers comprising a polypeptide of the invention.

The invention provides immobilized polypeptides having enzyme, structural or binding activity, wherein the polypeptide comprises a polypeptide of the invention, a polypeptide encoded by a nucleic acid of the invention, or a polypeptide comprising a polypeptide of the invention and a second domain. In one aspect, the polypeptide can be immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.

The invention provides arrays comprising an immobilized nucleic acid of the invention. The invention provides arrays comprising an antibody of the invention.

The invention provides isolated or recombinant antibodies that specifically bind to a polypeptide of the invention or to a polypeptide encoded by a nucleic acid of the invention. These antibodies of the invention can be a monoclonal or a polyclonal antibody. The invention provides hybridomas comprising an antibody of the invention, e.g., an antibody that specifically binds to a polypeptide of the invention or to a polypeptide encoded by a nucleic acid of the invention. The invention provides nucleic acids encoding these antibodies.

The invention provides method of isolating or identifying a polypeptide having enzyme, structural or binding activity comprising the steps of: (a) providing an antibody of the invention; (b) providing a sample comprising polypeptides; and (c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can

specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having an enzyme, structural or binding activity.

The invention provides methods of making an anti-polypeptide, anti-enzyme, or anti-protein, e.g. anti-structural or anti-binding protein, antibody comprising administering to a non-human animal a nucleic acid of the invention or a polypeptide of the invention or subsequences thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-polypeptide, anti-enzyme, or anti-protein, e.g. anti-structural or anti-binding protein, antibody. The invention provides methods of making an anti-polypeptide, anti-enzyme, or anti-protein, e.g. anti-structural or anti-binding protein, immune comprising administering to a non-human animal a nucleic acid of the invention or a polypeptide of the invention or subsequences thereof in an amount sufficient to generate an immune response.

The invention provides methods of producing a recombinant polypeptide comprising the steps of: (a) providing a nucleic acid of the invention operably linked to a promoter; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide. In one aspect, the method can further comprise transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide in a transformed cell.

The invention provides methods for identifying a polypeptide having enzyme, structural or binding activity comprising the following steps: (a) providing a polypeptide of the invention; or a polypeptide encoded by a nucleic acid of the invention; (b) providing an enzyme, structural or binding activity substrate; and (c) contacting the polypeptide or a fragment or variant thereof of step (a) with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having an enzyme, structural or binding activity.

The invention provides methods for identifying a polypeptide, enzyme, protein, e.g. structural or binding protein, substrate comprising the following steps: (a) providing a polypeptide of the invention; or a polypeptide encoded by a nucleic acid of the invention; (b) providing a test substrate; and (c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction product, wherein a decrease in the amount of the substrate or an

increase in the amount of a reaction product identifies the test substrate as a polypeptide, enzyme, protein, e.g. structural or binding protein, substrate.

The invention provides methods of determining whether a test compound specifically binds to a polypeptide comprising the following steps: (a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid comprises a nucleic acid of the invention, or, providing a polypeptide of the invention; (b) providing a test compound; (c) contacting the polypeptide with the test compound; and (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

The invention provides methods for identifying a modulator of a enzyme, structural or binding activity comprising the following steps: (a) providing a polypeptide of the invention or a polypeptide encoded by a nucleic acid of the invention; (b) providing a test compound; (c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the polypeptide, enzyme, protein, e.g. structural or binding protein, wherein a change in the enzyme, structural or binding activity measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the enzyme, structural or binding activity. In one aspect, the enzyme, structural or binding activity can be measured by providing a polypeptide, enzyme, protein, e.g. structural or binding protein, substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product. A decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of enzyme, structural or binding activity. An increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of enzyme, structural or binding activity.

The invention provides computer systems comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence of the invention (e.g., a polypeptide encoded by a nucleic acid of the invention). In one aspect, the computer system can further comprise a sequence comparison algorithm and a data storage device having at least one reference sequence

stored thereon. In another aspect, the sequence comparison algorithm comprises a computer program that indicates polymorphisms. In one aspect, the computer system can further comprise an identifier that identifies one or more features in said sequence. The invention provides computer readable media having stored thereon a polypeptide sequence or a nucleic acid sequence of the invention. The invention provides methods for identifying a feature in a sequence comprising the steps of: (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence of the invention; and (b) identifying one or more features in the sequence with the computer program. The invention provides methods for comparing a first sequence to a second sequence comprising the steps of: (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence of the invention; and (b) determining differences between the first sequence and the second sequence with the computer program. The step of determining differences between the first sequence and the second sequence can further comprise the step of identifying polymorphisms. In one aspect, the method can further comprise an identifier that identifies one or more features in a sequence. In another aspect, the method can comprise reading the first sequence using a computer program and identifying one or more features in the sequence.

The invention provides methods for isolating or recovering a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, from an environmental sample comprising the steps of: (a) providing an amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, wherein the primer pair is capable of amplifying a nucleic acid of the invention; (b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and, (c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein from an environmental sample. One or each member of the amplification primer sequence pair can comprise an oligonucleotide comprising an amplification primer sequence pair of the invention, e.g., having at least about 10 to 50 consecutive bases of a sequence of the invention.

The invention provides methods for isolating or recovering a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein from an environmental sample comprising the steps of: (a) providing a polynucleotide probe comprising a nucleic acid of the invention or a subsequence thereof; (b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a); (c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and (d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein from an environmental sample. The environmental sample can comprise a water sample, a liquid sample, a soil sample, an air sample or a biological sample. In one aspect, the biological sample can be derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

The invention provides methods of generating a variant of a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity comprising the steps of: (a) providing a template nucleic acid comprising a nucleic acid of the invention; and (b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid. In one aspect, the method can further comprise expressing the variant nucleic acid to generate a variant the polypeptide, enzyme, protein, e.g. structural or binding protein. The modifications, additions or deletions can be introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR) or a combination thereof. In another aspect, the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

In one aspect, the method can be iteratively repeated until a polypeptide, enzyme, protein, e.g. structural or binding protein having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced. In one aspect, the variant the polypeptide, enzyme, protein, e.g. structural or binding protein is thermotolerant, and retains some activity after being exposed to an elevated temperature. In another aspect, the variant the polypeptide, enzyme, protein, e.g. structural or binding protein has increased glycosylation as compared to the polypeptide, enzyme, protein, e.g. structural or binding protein encoded by a template nucleic acid. Alternatively, the variant the polypeptide, enzyme, protein, e.g. structural or binding protein has an enzyme, structural or binding activity under a high temperature, wherein the polypeptide, enzyme, protein, e.g. structural or binding protein encoded by the template nucleic acid is not active under the high temperature. In one aspect, the method can be iteratively repeated until a polypeptide, enzyme, protein, e.g. structural or binding protein coding sequence having an altered codon usage from that of the template nucleic acid is produced. In another aspect, the method can be iteratively repeated until a polypeptide, enzyme, protein, e.g. structural or binding protein gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

The invention provides methods for modifying codons in a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity to increase its expression in a host cell, the method comprising the following steps: (a) providing a nucleic acid of the invention encoding a polypeptide having an enzyme, structural or binding activity; and, (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

The invention provides methods for modifying codons in a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity; the method comprising the following steps: (a) providing a nucleic acid of the invention; and, (b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein.

The invention provides methods for modifying codons in a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity to increase its expression in a host cell, the method comprising the following steps: (a) providing a nucleic acid of the invention encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, polypeptide; and, (b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

The invention provides methods for modifying a codon in a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity to decrease its expression in a host cell, the method comprising the following steps: (a) providing a nucleic acid of the invention; and (b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell. In one aspect, the host cell can be a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

The invention provides methods for producing a library of nucleic acids encoding a plurality of modified polypeptides, enzymes, proteins, e.g. structural or binding proteins, active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps: (a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to a nucleic acid of the invention, and the nucleic acid encodes a polypeptide, enzyme, protein, e.g. structural or binding protein, active site or a polypeptide, enzyme, protein, e.g. structural or binding protein, substrate binding site; (b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and, (c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or

substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified the polypeptide, enzyme, protein, e.g. structural or binding protein, active sites or substrate binding sites. In one aspect, the method comprises mutagenizing the first nucleic acid of step (a) by a method comprising an optimized directed evolution system, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR), error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, and a combination thereof. In another aspect, the method comprises mutagenizing the first nucleic acid of step (a) or variants by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

The invention provides methods for making a small molecule comprising the steps of: (a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises an enzyme encoded by a nucleic acid of the invention; (b) providing a substrate for at least one of the enzymes of step (a); and, (c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions.

The invention provides methods for modifying a small molecule comprising the steps: (a) providing a enzyme encoded by a nucleic acid of the invention; (b) providing a small molecule; and, (c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the enzyme, thereby modifying a small molecule by an enzymatic reaction. In one aspect, the method comprises providing a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the enzyme. In one aspect, the method further comprises a plurality of additional enzymes under conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the

plurality of enzymatic reactions. In one aspect, the method further comprises the step of testing the library to determine if a particular modified small molecule that exhibits a desired activity is present within the library. The step of testing the library can further comprises the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

The invention provides methods for determining a functional fragment of a polypeptide, enzyme, protein, e.g. structural or binding protein, comprising the steps of: (a) providing a polypeptide, enzyme, protein, e.g. structural or binding protein, wherein the enzyme comprises a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention, or a subsequence thereof; and (b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for an enzyme, structural or binding activity, thereby determining a functional fragment of a polypeptide, enzyme, protein, e.g. structural or binding protein. In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein activity is measured by providing a polypeptide, enzyme, protein, e.g. structural or binding protein, substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

The invention provides methods for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis, the method comprising the following steps: (a) making a modified cell by modifying the genetic composition of a cell, wherein the genetic composition is modified by addition to the cell of a nucleic acid of the invention; (b) culturing the modified cell to generate a plurality of modified cells; (c) measuring at least one metabolic parameter of the cell by monitoring the cell culture of step (b) in real time; and, (d) analyzing the data of step (c) to determine if the measured parameter differs from a comparable measurement in an unmodified cell under similar conditions, thereby identifying an engineered phenotype in the cell using real-time metabolic flux analysis. In one aspect, the genetic composition of the cell can be modified by a method comprising deletion of a sequence or modification of a sequence in the cell, or, knocking out the expression of a gene. In one aspect, the method can further comprise selecting a cell comprising a newly engineered phenotype. In another aspect,

the method can comprise culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.

The invention provides methods of increasing thermotolerance or thermostability of a polypeptide, enzyme, protein, e.g. structural or binding protein, polypeptide, the method comprising glycosylating a polypeptide, enzyme, protein, e.g. structural or binding protein, wherein the polypeptide, enzyme, protein, e.g. structural or binding protein comprises at least thirty contiguous amino acids of a polypeptide of the invention; or a polypeptide encoded by a nucleic acid sequence of the invention, thereby increasing thermotolerance or thermostability of the polypeptide, enzyme, protein, e.g. structural or binding protein. In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein specific activity can be thermostable or thermotolerant at a temperature in the range from greater than about 37°C to about 95°C.

The invention provides methods for overexpressing a recombinant polypeptide, enzyme, protein, e.g. structural or binding protein, in a cell comprising expressing a vector comprising a nucleic acid comprising a nucleic acid of the invention or a nucleic acid sequence of the invention, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection, wherein overexpression is effected by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

The invention provides methods of making a transgenic plant comprising the following steps: (a) introducing a heterologous nucleic acid sequence into the cell, wherein the heterologous nucleic sequence comprises a nucleic acid sequence of the invention, thereby producing a transformed plant cell; and (b) producing a transgenic plant from the transformed cell. In one aspect, the step (a) can further comprise introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts. In another aspect, the step (a) can further comprise introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment. Alternatively, the step (a) can further comprise introducing the heterologous nucleic acid sequence into the plant cell DNA using an *Agrobacterium tumefaciens* host. In one aspect, the plant cell can be a potato, corn, rice, wheat, tobacco, or barley cell.

The invention provides methods of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps: (a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the

heterologous nucleic sequence comprises a nucleic acid of the invention; (b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell. The invention provides methods of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps: (a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence of the invention; (b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

The invention provides feeds or foods comprising a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention. In one aspect, the invention provides a food, feed, a liquid, e.g., a beverage (such as a fruit juice or a beer), a bread or a dough or a bread product, or a beverage precursor (e.g., a wort), comprising a polypeptide of the invention. The invention provides food or nutritional supplements for an animal comprising a polypeptide of the invention, e.g., a polypeptide encoded by the nucleic acid of the invention.

In one aspect, the polypeptide in the food or nutritional supplement can be glycosylated. The invention provides edible enzyme delivery matrices comprising a polypeptide of the invention, e.g., a polypeptide encoded by the nucleic acid of the invention. In one aspect, the delivery matrix comprises a pellet. In one aspect, the polypeptide can be glycosylated. In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein activity is thermotolerant. In another aspect, the polypeptide, enzyme, protein, e.g. structural or binding protein activity is thermostable.

The invention provides a food, a feed or a nutritional supplement comprising a polypeptide of the invention. The invention provides methods for utilizing a polypeptide, enzyme, protein, e.g. structural or binding protein, as a nutritional supplement in an animal diet, the method comprising: preparing a nutritional supplement containing a polypeptide, enzyme, protein, e.g. structural or binding protein, comprising at least thirty contiguous amino acids of a polypeptide of the invention; and administering the nutritional supplement to an animal. The animal can be a human, a ruminant or a monogastric animal. The polypeptide, enzyme, protein, e.g. structural or binding protein can be prepared by expression of a polynucleotide encoding the polypeptide, enzyme, protein, e.g. structural or binding protein in an organism selected from the group consisting of a bacterium, a yeast, a plant, an insect, a fungus and an animal. The

organism can be selected from the group consisting of an *S. pombe*, *S. cerevisiae*, *Pichia pastoris*, *E. coli*, *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

The invention provides edible enzyme delivery matrix comprising thermostable recombinant polypeptide, enzyme, protein, e.g. structural or binding protein of the invention. The invention provides methods for delivering a polypeptide, enzyme, protein, e.g. structural or binding protein, supplement to an animal, the method comprising: preparing an edible enzyme delivery matrix in the form of pellets comprising a granulate edible carrier and thermostable recombinant polypeptide, enzyme, protein, e.g. structural or binding protein, wherein the pellets readily disperse the polypeptide, enzyme, protein, e.g. structural or binding protein contained therein into aqueous media, and administering the edible enzyme delivery matrix to the animal. The recombinant polypeptide, enzyme, protein, e.g. structural or binding protein can comprise a polypeptide of the invention. The polypeptide, enzyme, protein, e.g. structural or binding protein can be glycosylated to provide thermostability at pelletizing conditions. The delivery matrix can be formed by pelletizing a mixture comprising a grain germ and a polypeptide, enzyme, protein, e.g. structural or binding protein. The pelletizing conditions can include application of steam. The pelletizing conditions can comprise application of a temperature in excess of about 80°C for about 5 minutes and the enzyme retains a specific activity of at least 350 to about 900 units per milligram of enzyme.

In one aspect, invention provides a pharmaceutical composition comprising a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention, or a polypeptide encoded by a nucleic acid of the invention. In one aspect, the pharmaceutical composition acts as a digestive aid.

The details of one or more aspects of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

All publications, patents, patent applications, GenBank sequences and ATCC deposits, cited herein are hereby expressly incorporated by reference for all purposes.

BRIEF DESCRIPTION OF DRAWINGS

The following drawings are illustrative of aspects of the invention and are not meant to limit the scope of the invention as encompassed by the claims.

Figure 1 is a block diagram of a computer system.

Figure 2 is a flow diagram illustrating one aspect of a process for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database.

Figure 3 is a flow diagram illustrating one aspect of a process in a computer for determining whether two sequences are homologous.

Figure 4 is a flow diagram illustrating one aspect of an identifier process 300 for detecting the presence of a feature in a sequence.

Like reference symbols in the various drawings indicate like elements.

DETAILED DESCRIPTION

The invention provides isolated and recombinant polypeptides, including enzymes, structural proteins and binding proteins, polynucleotides encoding these polypeptides, and methods of making and using these polynucleotides and polypeptides. The polypeptides of the invention, and the polynucleotides encoding the polypeptides of the invention, encompass many classes of enzymes, structural proteins and binding proteins. In one aspect, the enzymes and proteins of the invention comprise, e.g. aldolases, alpha-galactosidases, amidases, e.g. secondary amidases, amylases, catalases, carotenoid pathway enzymes, dehalogenases, endoglucanases, epoxide hydrolases, esterases, hydrolases, glucosidases, glycosidases, inteins, isomerases, laccases, lipases, monooxygenases, nitroreductases, nitrilases, P450 enzymes, pectate lyases, phosphatases, phospholipases, phytases, polymerases and xylanases, which are more specifically described below. The invention also provides isolated and recombinant polypeptides, including enzymes, structural proteins and binding proteins, polynucleotides encoding these polypeptides, having the activities described in Table 1, Table 2 or Table 3, below.

Aldolases

In one aspect, the invention provides aldolases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an aldolase activity, including thermostable and thermotolerant aldolase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides. In one aspect, the aldolase activity comprises catalysis of the formation of a carbon-carbon bond. In one aspect, the aldolase activity comprises an aldol condensation. The aldol condensation can have an aldol donor substrate comprising an acetaldehyde and an aldol acceptor substrate comprising an aldehyde. The aldol condensation can yield a

product of a single chirality. In one aspect, the aldolase activity is enantioselective. The aldolase activity can comprise a 2-deoxyribose-5-phosphate aldolase (DERA) activity. The aldolase activity can comprise catalysis of the condensation of acetaldehyde as donor and a 2(R)-hydroxy-3-(hydroxy or mercapto)-propionaldehyde derivative to form a 2-deoxysugar. The aldolase activity can comprise catalysis of the condensation of acetaldehyde as donor and a 2-substituted acetaldehyde acceptor to form a 2,4,6-trideoxyhexose via a 4-substituted-3-hydroxybutanal intermediate. The aldolase activity can comprise catalysis of the generation of chiral aldehydes using two acetaldehydes as substrates. The aldolase activity can comprises enantioselective assembling of chiral β,δ -dihydroxyheptanoic acid side chains. The aldolase activity can comprise enantioselective assembling of the core of [R-(R*,R*)]-2-(4-fluorophenyl)-b,d-dihydroxy-5-(1-methylethyl)-3-phenyl-4-(phenylamino)-carbonyl]-1H-pyrrole-1-heptanoic acid (Atorvastatin, or LIPITOR™), rosuvastatin (CRESTOR™) and/or fluvastatin (LESCOL™). The aldolase activity can comprise, with an oxidation step, synthesis of a 3R,5S-6-chloro-2,4,6-trideoxy-erythro-hexonolactone.

Alpha-galactosidases

In one aspect, the invention provides alpha-galactosidases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an alpha-galactosidase activity, including thermostable and thermotolerant alpha-galactosidase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

An alpha galactosidase hydrolyses the non-reducing terminal alpha 1-3,4,6 linked galactose from poly- and oligosaccharides. These saccharides are commonly found in legumes and are difficult to digest. As such, alpha-galactosidases can be used as a digestive aid to break down raffinose, stachyose, and verbascose, found in such foods as beans and other gassy foods.

Amidases

In one aspect, the invention provides amidases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an amidase activity, including thermostable and thermotolerant amidase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the amidases of the invention are used in the removal of arginine, phenylalanine or methionine from the N-terminal end of peptides in peptide or peptidomimetic synthesis. In one aspect, the enzyme of the invention, e.g. an amidase, is selective for the L, or "natural" enantiomer of the amino acid derivatives and is therefore useful for the production of optically active compounds. These reactions can be performed in the presence of the chemically more reactive ester functionality, a step which is very difficult to achieve with nonenzymatic methods. The enzyme is also able to tolerate high temperatures (at least 70° C), and high concentrations of organic solvents (>40% DMSO), both of which cause a disruption of secondary structure in peptides, which enables cleavage of otherwise resistant bonds.

Secondary amidases

In one aspect, the invention provides secondary amidases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a secondary amidase activity, including thermostable and thermotolerant secondary amidase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Secondary amidases include a variety of useful enzymes including peptidases, proteases, and hydantoinases. This class of enzymes can be used in a range of commercial applications. For example, secondary amidases can be used to: 1) increase flavor in food, in particular cheese (known as enzyme ripened cheese); 2) promote bacterial and fungal killing; 3) modify and de-protect fine chemical intermediates 4) synthesize peptide bonds; 5) and carry out chiral resolutions. Particularly, there is a need in the art for an enzyme capable of hydrolyzing Cephalosporin C.

Amylases

In one aspect, the invention provides amylases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an amylase activity, including thermostable and thermotolerant amylase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the polypeptides of the invention can be used as amylases, for example, alpha amylases or glucoamylases, to catalyze the hydrolysis of starch into sugars. In one aspect, the invention is directed to polypeptides having thermostable

amylase activity, such as alpha amylases or glucoamylase activity, e.g., a 1,4-alpha-D-glucan glucohydrolase activity. In one aspect, the polypeptides of the invention can be used as amylases, for example, alpha amylases or glucoamylases, to catalyze the hydrolysis of starch into sugars, such as glucose. The invention is also directed to nucleic acid constructs, vectors, and host cells comprising the nucleic acid sequences of the invention as well as recombinant methods for producing the polypeptides of the invention. The invention is also directed to the use of amylases of the invention in starch conversion processes, including production of high fructose corn syrup (HFCS), ethanol, dextrose, and dextrose syrups.

Commercially, glucoamylases are used to further hydrolyze cornstarch, which has already been partially hydrolyzed with an alpha-amylase. The glucose produced in this reaction may then be converted to a mixture of glucose and fructose by a glucose isomerase enzyme. This mixture, or one enriched with fructose, is the high fructose corn syrup commercialized throughout the world. In general, starch to fructose processing consists of four steps: liquefaction of granular starch, saccharification of the liquefied starch into dextrose, purification, and isomerization to fructose. The object of a starch liquefaction process is to convert a concentrated suspension of starch polymer granules into a solution of soluble shorter chain length dextrans of low viscosity.

The amylases of the invention can be used in automatic dish wash (ADW) products and laundry detergent. In ADW products, the amylase will function at pH 10-11 and at 45-60°C in the presence of calcium chelators and oxidative conditions. For laundry, activity at pH 9-10 and 40°C in the appropriate detergent matrix will be required. Amylases are also useful in textile desizing, brewing processes, starch modification in the paper and pulp industry and other processes described in the art.

Amylases can be used commercially in the initial stages (liquefaction) of starch processing; in wet corn milling; in alcohol production; as cleaning agents in detergent matrices; in the textile industry for starch desizing; in baking applications; in the beverage industry; in oilfields in drilling processes; in inking of recycled paper and in animal feed. Amylases are also useful in textile desizing, brewing processes, starch modification in the paper and pulp industry and other processes.

Carotenoid pathway enzymes

The invention provides novel enzymes, and the polynucleotides encoding them, involved in carotenoid (such as lycopenes and luteins), astaxanthin and/or isoprenoid synthesis. The invention also provides novel genes in the carotenoid, astaxanthin and

isoprenoid biosynthetic pathways comprising at least one enzyme of the invention. For example, alternative aspects, the invention provides one or more nucleic acid coding sequences (CDSs, or ORFs) encoding all, or at least one, enzyme(s) involved in a desired biosynthetic pathway for carotenoids, astaxanthins and/or isoprenoids. The nucleic acid coding sequence(s) can be expressed through an expression plasmid, vector, engineered virus or any episomal expression system, or, can be integrated into the genome of the host cell. In one aspect, the enzyme(s) involved in the biosynthetic pathway system comprise a novel combination of enzymes. In another aspect, the enzyme(s) involved in the biosynthetic pathway system comprise at least one novel enzyme of the invention – where nucleic acids used in the system encode a novel enzyme of the invention.

Carotenoids are natural pigments which have antioxidant and anti-carcinogenic activity. They are free radical scavengers, and as such, strong antioxidants. Carotenoids have a conjugated backbone structure and are very rigid molecules, having a backbone consisting of 9 to 11 alternating single/double bonds and have very similar electro-optical properties as polyacetylene. Astaxanthins are abundant naturally occurring carotenoids. They contain an internal unit similar to beta-carotene but have two terminal carbonyl and hydroxyl functionalities. These compounds are useful for food and feed supplements, colorants, nutraceuticals, cosmetic and pharmaceutical needs. Isoprenoids are compounds biosynthesized from or containing isoprene (unsaturated branched chain five-carbon hydrocarbon) units, including terpenes, carotenoids, fat soluble vitamins, ubiquinone, rubber, and some steroids. Biosynthetic pathways for carotenoids, astaxanthins and isoprenoids are known; most of these published pathways are derived from one organism or a combination of genes from a few species.

Catalases

In one aspect, the invention provides catalases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a catalase activity, including thermostable and thermotolerant catalase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In processes where hydrogen peroxide is a by-product, catalases of the invention can be used to destroy or detect hydrogen peroxide, e.g., in production of glyoxylic acid and in glucose sensors. Also, in processes where hydrogen peroxide is used as a bleaching or antibacterial agent, catalases of the invention can be used to destroy residual hydrogen peroxide, e.g. in contact lens cleaning, in bleaching steps in pulp and paper

production, and in the pasteurization of dairy products. Further, such catalases of the invention can be used as catalysts for oxidation reactions, e.g. epoxidation and hydroxylation.

Dehalogenases

In one aspect, the invention provides dehalogenases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a dehalogenase activity, including thermostable and thermotolerant dehalogenase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Environmental pollutants consist of a large quantity and variety of chemicals; many of these are toxic, environmental hazards that were designated in 1979 as priority pollutants by the U.S. Environmental Protection Agency. Microbial and enzymatic biodegradation is one method for the elimination of these pollutants. Accordingly, methods have been designed to treat commercial wastes and to bioremediate polluted environments via microbial and related enzymatic processes. Unfortunately, many chemical pollutants are either resistant to microbial degradation or are toxic to potential microbial-degraders when present in high concentrations and certain combinations.

Dehalogenases, e.g. haloalkane dehalogenases, of the invention can cleave carbon-halogen bonds in haloalkanes and halocarboxylic acids by hydrolysis, thus converting them to their corresponding alcohols. This reaction can be used for detoxification involving haloalkanes, such as ethylchloride, methylchloride, and 1,2-dichloroethane (e.g., detoxification of toxic composition, e.g., pesticides, poisons, chemical warfare agents and the like comprising haloalkanes).

The present invention provides a number of dehalogenase enzymes useful in bioremediation having improved enzymatic characteristics. The polynucleotides and polynucleotide products of the invention are useful in, for example, groundwater treatment involving transformed host cells containing a polynucleotide or polypeptide of the invention (e.g., the bacteria *Xanthobacter autotrophicus*) and the haloalkane 1,2-dichloroethane as well as removal of polychlorinated biphenyls (PCB's) from soil sediment.

The haloalkane dehalogenase of the invention are useful in carbon-halide reduction efforts. The enzymes of the invention initiate the degradation of haloalkanes.

Alternatively, host cells containing a dehalogenase polynucleotide or polypeptide of the invention can feed on the haloalkanes and produce the detoxifying enzyme.

Endoglucanases

In one aspect, the invention provides endoglucanases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an endoglucanase activity, including thermostable and thermotolerant endoglucanase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the enzymes of the invention have a glucanase, e.g., an endoglucanase, activity, e.g., catalyzing hydrolysis of internal endo- β -1,4- and/or β -1,3-glucanase linkages. In one aspect, the endoglucanase activity (e.g., endo-1,4-beta-D-glucan 4-glucano hydrolase activity) comprises hydrolysis of 1,4- and/or β -1,3- beta-D-glycosidic linkages in cellulose, cellulose derivatives (e.g., carboxy methyl cellulose and hydroxy ethyl cellulose) lichenin, beta-1,4 bonds in mixed beta-1,3 glucans, such as cereal beta-D-glucans or xyloglucans and other plant material containing cellulosic parts.

Endoglucanases of the invention (e.g., endo-beta-1,4-glucanases, EC 3.2.1.4; endo-beta-1,3(1)-glucanases, EC 3.2.1.6; endo-beta-1,3-glucanases, EC 3.2.1.39) can hydrolyze internal β -1,4- and/or β -1,3- glucosidic linkages in cellulose and glucan to produce smaller molecular weight glucose and glucose oligomers. Glucans are polysaccharides formed from 1,4- β - and/or 1,3-glycoside-linked D-glucopyranose. Endoglucanases of the invention can be used in the food industry, for baking and fruit and vegetable processing, breakdown of agricultural waste, in the manufacture of animal feed, in pulp and paper production, textile manufacture and household and industrial cleaning agents. Endoglucanases are produced by fungi and bacteria.

Beta-glucans are major non-starch polysaccharides of cereals. The glucan content can vary significantly depending on variety and growth conditions. The physicochemical properties of this polysaccharide are such that it gives rise to viscous solutions or even gels under oxidative conditions. In addition glucans have high water-binding capacity. All of these characteristics present problems for several industries including brewing, baking, animal nutrition. In brewing applications, the presence of glucan results in wort filterability and haze formation issues. In baking applications (especially for cookies and crackers), glucans can create sticky doughs that are difficult to machine and reduce biscuit size. In addition, this carbohydrate is implicated in rapid rehydration of the baked

product resulting in loss of crispiness and reduced shelf-life. For monogastric animal feed applications with cereal diets, beta-glucan is a contributing factor to viscosity of gut contents and thereby adversely affects the digestibility of the feed and animal growth rate. For ruminant animals, these beta-glucans represent substantial components of fiber intake and more complete digestion of glucans would facilitate higher feed conversion efficiencies. It is desirable for animal feed endoglucanases to be active in the animal stomach.

Endoglucanases of the invention can be used in the digestion of cellulose, a beta-1,4-linked glucan found in all plant material. Cellulose is the most abundant polysaccharide in nature. Enzymes of the invention that digest cellulose have utility in the pulp and paper industry, in textile manufacture and in household and industrial cleaning agents.

Epoxide hydrolases

In one aspect, the invention provides epoxide hydrolases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an epoxide hydrolase activity, including thermostable and thermotolerant epoxide hydrolase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides. The polypeptides of the invention can be used as epoxide hydrolases to catalyze the hydrolysis of epoxides and arene oxides to their corresponding diols.

Epoxide hydrolases catalyze the hydrolysis of epoxides and arene oxides to their corresponding diols. Epoxide hydrolases from microbial sources are highly versatile biocatalysts for the asymmetric hydrolysis of epoxides on a preparative scale. Besides kinetic resolution, which furnishes the corresponding vicinal diol and remaining non-hydrolyzed epoxide in nonracemic form, enantioconvergent processes are possible. These are highly attractive as they lead to the formation of a single enantiomeric diol from a racemic oxirane.

Microsomal epoxide hydrolases are biotransformation enzymes that catalyze the conversion of a broad array of xenobiotic epoxide substrates to more polar diol metabolites, see, e.g., Omiecinski (2000) *Toxicol. Lett.* 112-113:365-370. Microsomal epoxide hydrolases catalyze the addition of water to epoxides in a two-step reaction involving initial attack of an active site carboxylate on the oxirane to give an ester

intermediate followed by hydrolysis of the ester. Soluble epoxide hydrolase play a role in the biosynthesis of inflammation mediators.

Epoxide hydrolases of the invention can be used in the detoxification of epoxides or in the biosynthesis of hormones. Additionally, epoxide hydrolases of the invention can efficiently process several substrates, leading to enantiomerically enriched-epoxides (the unreacted enantiomer) and/or to the corresponding vicinal diols.

Esterases

In one aspect, the invention provides esterases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an esterase activity, including thermostable and thermotolerant esterase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Many esterases are known and have been discovered in a broad variety of organisms, including bacteria, yeast and higher animals and plants. A principal example of esterases are the lipases, which are used in the hydrolysis of lipids, acidolysis (replacement of an esterified fatty acid with a free fatty acid) reactions, transesterification (exchange of fatty acids between triglycerides) reactions, and in ester synthesis. The major industrial applications for lipases include: the detergent industry, where they are employed to decompose fatty materials in laundry stains into easily removable hydrophilic substances; the food and beverage industry where they are used in the manufacture of cheese, the ripening and flavoring of cheese, as antistaling agents for bakery products, and in the production of margarine and other spreads with natural butter flavors; in waste systems; and in the pharmaceutical industry where they are used as digestive aids.

Alternatively, esterases of the invention can be used in detergent compositions. In one aspect, the esterase can be a nonsurface-active esterase. In another aspect, the esterase can be a surface-active esterase. The esterase can be formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel form, a paste or a slurry form.

In another aspect, the invention provides fabrics or clothing comprising an esterase of the invention. In another aspect, esterases of the invention are used to treat a lipid-containing fabric.

In another aspect, the invention provides foods and drinks comprising an esterase of the invention. The invention also provides cheeses comprising an esterase of the

invention. Additionally, the invention provides methods for the manufacture of cheese comprising the following steps: (a) providing a polypeptide having an esterase activity, wherein the polypeptide comprises a polypeptide of the invention, or, a polypeptide encoded by a nucleic acid of the invention; (b) providing a cheese precursor; and (c) contacting the polypeptide of step (a) with the precursor of step (b) under condition wherein the esterase can catalyze cheese manufacturing processes. In one aspect, the method can comprise the process of ripening and flavoring of cheese.

In another aspect, the invention provides margarines and spreads comprising an enzyme of the invention. The invention provides methods for production of margarine or other spreads with natural butter flavors comprising the following steps: (a) providing a polypeptide having an esterase activity, wherein the polypeptide comprises a polypeptide of the invention, or, a polypeptide encoded by a nucleic acid of the invention; (b) providing a margarine or a spread precursor; and (c) contacting the polypeptide of step (a) with the precursor of step (b) under condition wherein the esterase can catalyze processes involved in margarine or spread production.

The invention provides methods for treating solid or liquid waste products comprising the following steps: (a) providing a polypeptide having an esterase activity, wherein the polypeptide comprises a polypeptide of the invention, or, a polypeptide encoded by a nucleic acid of the invention; (b) providing a solid or a liquid waste; and (c) contacting the polypeptide of step (a) and the waste of step (b) under conditions wherein the polypeptide can treat the waste. The invention provides solid or liquid waste products comprising a polypeptide of the invention.

The invention provides methods for aiding digestion in a mammal comprising (a) providing a polypeptide having an esterase activity, wherein the polypeptide comprises a polypeptide of the invention, or, a polypeptide encoded by a nucleic acid of the invention; (b) providing a composition comprising a substrate for the polypeptide of step (a); (c) feeding or administering to the mammal the polypeptide of step (a) with a feed or food comprising a substrate for the polypeptide of step (a), thereby helping digestion in the mammal. In one aspect, the mammal is a human.

The invention provides pharmaceutical compositions comprising a polypeptide and/or a nucleic acid of the invention, e.g., a pharmaceutical composition for use as a digestive aid in a mammal comprising a polypeptide having an esterase activity, wherein the polypeptide comprises a polypeptide of the invention, or, a polypeptide encoded by a

nucleic acid of the invention. In one aspect, the mammal comprises a human. The enzymes of the invention are used in the manufacture of medicaments.

The invention provides bakery products comprising a polypeptide of the invention. The invention provides antistaling agents for bakery products comprising a polypeptide having an esterase activity, wherein the polypeptide comprises a polypeptide of the invention, or, a polypeptide encoded by a nucleic acid of the invention.

The invention provides methods for hydrolyzing, breaking up or disrupting a ester-comprising composition comprising the following steps: (a) providing a polypeptide of the invention having an esterase activity, or a polypeptide encoded by a nucleic acid of the invention; (b) providing a composition comprising a protein; and (c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the esterase hydrolyzes, breaks up or disrupts the ester-comprising composition.

Alternatively, the invention provides methods for liquefying or removing ester-comprising compositions comprising the following steps: (a) providing a polypeptide of the invention having an esterase activity, or a polypeptide encoded by a nucleic acid of the invention; (b) providing a composition comprising a protein; and (c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein esterase removes or liquefies the ester-comprising compositions.

Hydrolases

In one aspect, the invention provides hydrolases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a hydrolase activity, e.g., an esterase, acylase, lipase, phospholipase or protease activity, including thermostable and thermotolerant hydrolase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides. The hydrolase activities of the polypeptides and peptides of the invention include esterase activity, lipase activity (hydrolysis of lipids), acidolysis reactions (to replace an esterified fatty acid with a free fatty acid), transesterification reactions (exchange of fatty acids between triglycerides), ester synthesis, ester interchange reactions, phospholipase activity (e.g., phospholipase A, B, C and D activity, patatin activity, lipid acyl hydrolase (LAH) activity) and protease activity (hydrolysis of peptide bonds). The polypeptides of the invention can be used in a variety of pharmaceutical, agricultural and industrial contexts, including the manufacture of cosmetics and nutraceuticals.

In one aspect, the polypeptides of the invention are used in the biocatalytic synthesis of structured lipids (lipids that contain a defined set of fatty acids distributed in a defined manner on the glycerol backbone), including cocoa butter alternatives (CBA), lipids containing poly-unsaturated fatty acids (PUFAs), diacylglycerides, e.g., 1,3-diacylglycerides (DAGs), monoglycerides, e.g., 2-monoglycerides (MAGs) and triacylglycerides (TAGs). In one aspect, the polypeptides of the invention are used to modify oils, such as fish, animal and vegetable oils, and lipids, such as poly-unsaturated fatty acids. The hydrolases of the invention having lipase activity can modify oils by hydrolysis, alcoholysis, esterification, transesterification and/or interesterification. The methods of the invention can use lipases with defined regio-specificity or defined chemoselectivity in biocatalytic synthetic reactions. In another aspect, the polypeptides of the invention are used to synthesize enantiomerically pure chiral products.

Additionally, the polypeptides of the invention can be used in food processing, brewing, bath additives, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver recovery in the photographic industry, medical treatment, silk degumming, biofilm degradation, biomass conversion to ethanol, biodefense, antimicrobial agents and disinfectants, personal care and cosmetics, biotech reagents, in increasing starch yield from corn wet milling and pharmaceuticals such as digestive aids and anti-inflammatory (anti-phlogistic) agents.

The major industrial applications for hydrolases, e.g., esterases, lipases, phospholipases and proteases, include the detergent industry, where they are employed to decompose fatty materials in laundry stains into easily removable hydrophilic substances; the food and beverage industry where they are used in the manufacture of cheese, the ripening and flavoring of cheese, as antistaling agents for bakery products, and in the production of margarine and other spreads with natural butter flavors; in waste systems; and in the pharmaceutical industry where they are used as digestive aids.

Oils and fats are an important renewable raw material for the chemical industry. They are available in large quantities from the processing of oilseeds from plants like rice bran oil, rapeseed (canola), sunflower, olive, palm or soy. Other sources of valuable oils and fats include fish, restaurant waste, and rendered animal fats. These fats and oils are a mixture of triglycerides or lipids, i.e. fatty acids (FAs) esterified on a glycerol scaffold. Each oil or fat contains a wide variety of different lipid structures, defined by the FA content and their regiochemical distribution on the glycerol backbone. These properties of

the individual lipids determine the physical properties of the pure triglyceride. Hence, the triglyceride content of a fat or oil to a large extent determines the physical, chemical and biological properties of the oil. The value of lipids increases greatly as a function of their purity. High purity can be achieved by fractional chromatography or distillation, separating the desired triglyceride from the mixed background of the fat or oil source. However, this is costly and yields are often limited by the low levels at which the triglyceride occurs naturally. In addition, the purity of the product is often compromised by the presence of many structurally and physically or chemically similar triglycerides in the oil.

An alternative to purifying triglycerides or other lipids from a natural source is to synthesize the lipids. The products of such processes are called structured lipids because they contain a defined set of fatty acids distributed in a defined manner on the glycerol backbone. The value of lipids also increases greatly by controlling the fatty acid content and distribution within the lipid. Lipases can be used to affect such control.

Phospholipases are enzymes that hydrolyze the ester bonds of phospholipids. Corresponding to their importance in the metabolism of phospholipids, these enzymes are widespread among prokaryotes and eukaryotes. The phospholipases affect the metabolism, construction and reorganization of biological membranes and are involved in signal cascades. Several types of phospholipases are known which differ in their specificity according to the position of the bond attacked in the phospholipid molecule. Phospholipase A1 (PLA1) removes the 1-position fatty acid to produce free fatty acid and 1-lyso-2-acylphospholipid. Phospholipase A2 (PLA2) removes the 2-position fatty acid to produce free fatty acid and 1-acyl-2-lysophospholipid. PLA1 and PLA2 enzymes can be intra- or extra-cellular, membrane-bound or soluble. Intracellular PLA2 is found in almost every mammalian cell. Phospholipase C (PLC) removes the phosphate moiety to produce 1,2 diacylglycerol and phospho base. Phospholipase D (PLD) produces 1,2-diacylglycerophosphate and base group. PLC and PLD are important in cell function and signaling. Patatins are another type of phospholipase thought to work as a PLA.

In general, enzymes, including hydrolases such as esterases, lipases and proteases, are active over a narrow range of environmental conditions (temperature, pH, etc.), and many are highly specific for particular substrates. The narrow range of activity for a given enzyme limits its applicability and creates a need for a selection of enzymes that (a) have similar activities but are active under different conditions or (b) have different substrates. For instance, an enzyme capable of catalyzing a reaction at 50°C may be so

inefficient at 35°C, that its use at the lower temperature will not be feasible. For this reason, laundry detergents generally contain a selection of proteolytic enzymes (e.g., polypeptides of the invention), allowing the detergent to be used over a broad range of wash temperature and pH. In view of the specificity of enzymes and the growing use of hydrolases in industry, research, and medicine, there is an ongoing need in the art for new enzymes and new enzyme inhibitors.

Glucosidases

In one aspect, the invention provides glucosidases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a glucosidase activity, including thermostable and thermotolerant glucosidase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Alpha-glucosidases of the invention can catalyze the hydrolysis of starches into sugars. Alpha-glucosidases can hydrolyze terminal non-reducing 1,4 or 1,6 linked α -D-glucose residues in starch, with release of α -D-glucose.

Alpha-glucosidases of the invention can be used commercially in the stages liquefaction and saccharification of starch processing; in wet corn milling; in alcohol production; as cleaning agents in detergent matrices; in the textile industry for starch desizing; in baking applications; in the beverage industry; in oilfields in drilling processes; in inking of recycled paper and in animal feed. Alpha-glucosidases of the invention are also useful in textile desizing, brewing processes, starch modification in the paper and pulp industry and other processes.

Glycosidases

In one aspect, the invention provides glycosidases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a glycosidase activity, including thermostable and thermotolerant glycosidase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides. Glycosidase enzymes of the invention can have more specific activity as glucosidases, α -galactosidases, β -galactosidases, β -mannosidases, β -mannanases, endoglucanases, and pullulanases.

α -galactosidases of the invention can catalyze the hydrolysis of galactose groups on a polysaccharide backbone or hydrolyze the cleavage of di- or oligosaccharides comprising galactose. β -mannanases of the invention can catalyze the hydrolysis of mannose groups internally on a polysaccharide backbone or hydrolyze the cleavage of di- or oligosaccharides comprising mannose groups. β -mannosidases of the invention can hydrolyze non-reducing, terminal mannose residues on a mannose-containing polysaccharide and the cleavage of di- or oligosaccharides comprising mannose groups.

Guar gum is a branched galactomannan polysaccharide composed of β -1, 4 linked mannose backbone with α -1, 6 linked galactose sidechains. The enzymes required for the degradation of guar are β -mannanase, β -mannosidase and α -galactosidase. β -mannanase hydrolyses the mannose backbone internally and β -mannosidase hydrolyses non-reducing, terminal mannose residues. α -galactosidase hydrolyses α -linked galactose groups.

Galactomannan polysaccharides and the enzymes of the invention that degrade them have a variety of applications. Guar is commonly used as a thickening agent in food and is utilized in hydraulic fracturing in oil and gas recovery. Consequently, galactomannanases are industrially relevant for the degradation and modification of guar. Furthermore, a need exists for thermostable galactomannanases that are active in extreme conditions associated with oil drilling and well stimulation.

There are other applications for these enzymes in various industries, such as in the beet sugar industry. 20-30% of the domestic U.S. sucrose consumption is sucrose from sugar beets. Raw beet sugar can contain a small amount of raffinose when the sugar beets are stored before processing and rotting begins to set in. Raffinose inhibits the crystallization of sucrose and also constitutes a hidden quantity of sucrose. Thus, there is merit to eliminating raffinose from raw beet sugar. α -Galactosidase has also been used as a digestive aid to break down raffinose, stachyose, and verbascose in such foods as beans and other gassy foods.

β -Galactosidases of the invention can be used for the production of lactose-free dietary milk products. Additionally, β -galactosidases of the invention can be used for the enzymatic synthesis of oligosaccharides via transglycosylation reactions.

Pullulanase is well known as a debranching enzyme of pullulan and starch. The enzyme of the invention can hydrolyze α -1, 6-glucosidic linkages on these polymers. Starch degradation for the production of sweeteners (glucose or maltose) is a very

important industrial application of this enzyme. The degradation of starch is developed in two stages. The first stage involves the liquefaction of the substrate with α -amylase, and the second stage, or saccharification stage, is performed by β -amylase with pullulanase added as a debranching enzyme, to obtain better yields.

Endoglucanases of the invention can be used in a variety of industrial applications. For instance, the endoglucanases of the invention can hydrolyze the internal β -1, 4-glycosidic bonds in cellulose, which may be used for the conversion of plant biomass into fuels and chemicals. Endoglucanases of the invention also have applications in detergent formulations, the textile industry, in animal feed, in waste treatment, oil drilling and well stimulation, and in the fruit juice and brewing industry for the clarification and extraction of juices.

Inteins

In one aspect, the invention provides inteins, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In another aspect, the invention provides a chimeric protein comprising at least three domains, wherein the first domain comprises at least one enzyme domain or a binding protein domain, the second domain comprises at least one intein domain and a third domain comprising a detectable moiety domain, at least one intein domain is positioned between at least one enzyme or binding protein and at least one detectable moiety domain, and the intein domain has at least one cleavage or splicing activity.

In one aspect, the detectable moiety domain comprises a detectable peptide or polypeptide. The detectable peptide or a polypeptide can be a fluorescent peptide or polypeptide. The detectable peptide or a polypeptide can be a bioluminescent or a chemiluminescent peptide or polypeptide. In one aspect, the bioluminescent or chemiluminescent polypeptide comprises a green fluorescent protein (GFP), an aequorin, an obelin, a mnemiopsin or a berovin. In one aspect, the detectable moiety domain comprises an enzyme that generates a detectable signal. The enzyme that generates a detectable signal can comprise an alpha-galactosidase, an antibiotic (e.g., chloramphenicol acetyltransferase) or a kinase. The detectable moiety domain can comprise a radioactive isotope.

In one aspect, the chimeric protein is a recombinant fusion protein. In one aspect, the intein domain splicing activity results in cleavage of the enzyme domain from the intein domain and detectable domain. The intein domain splicing activity can result in cleavage of the enzyme domain from the intein domain and detectable domain and

cleavage of the detectable domain from the intein domain. In one aspect, the intein domain splicing activity results in cleavage of the detectable domain from the intein domain. In one aspect, the intein domain has only splicing activity. The intein domain can have only cleaving activity.

In one aspect, at least one domain is separated from another domain by a linker. The linker can be a flexible linker. The intein domain can be separated from the detectable moiety domain and the enzyme domain by a linker.

Isomerases

In one aspect, the invention provides isomerases, e.g. xylose isomerases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having an isomerase activity, e.g. xylose isomerase activity, including thermostable and thermotolerant isomerase activity, e.g. xylose isomerase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the invention provides xylose isomerase enzymes, polynucleotides encoding the enzymes, methods of making and using these polynucleotides and polypeptides. The polypeptides of the invention can be used in a variety of agricultural and industrial contexts. For example, the polypeptides of the invention can be used for converting glucose to fructose or for manufacturing high content fructose syrups in large quantities. Other examples include use of the polypeptides of the invention in confectionary, brewing, alcohol and soft drinks production, and in diabetic foods and sweeteners.

Laccases

In one aspect, the invention provides laccases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a laccase activity, including thermostable and thermotolerant laccase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the invention provides methods of depolymerizing lignin, e.g., in a pulp or paper manufacturing process, using a polypeptide of the invention. In another aspect, the invention provides methods for oxidizing products that can be mediators of laccase-catalyzed oxidation reactions, e.g., 2,2-azinobis-(3-ethylbenzthiazoline-6-

sulfonate) (ABTS), 1- hydroxybenzotriazole (HBT), 2,2,6,6-tetramethylpiperidin-1-yloxy (TEMPO), dimethoxyphenol, dihydroxyfumaric acid (DHF) and the like.

Laccases are a subclass of the multicopper oxidase super family of enzymes, which includes ascorbate oxidases and the mammalian protein, ceruloplasmin. Laccases are one of the oldest known enzymes and were first implicated in the oxidation of urushiol and laccol. In one aspect, reactions catalyzed by laccases of the invention comprises the oxidation of phenolic substrates. The major target application has been in the delignification of wood fibers during the preparation of pulp.

Lipases

In one aspect, the invention provides lipases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a lipase activity, including thermostable and thermotolerant lipase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the lipases of the invention can be used in a variety of pharmaceutical, agricultural and industrial contexts, including the manufacture of cosmetics and nutraceuticals. In one aspect, the lipases of the invention are used in the biocatalytic synthesis of structured lipids (lipids that contain a defined set of fatty acids distributed in a defined manner on the glycerol backbone), including cocoa butter alternatives (CBA), lipids containing poly-unsaturated fatty acids (PUFAs), diacylglycerides, e.g., 1,3-diacyl glycerides (DAGs), monoglycerides, e.g., 2-monoglycerides (MAGs) and triacylglycerides (TAGs). In one aspect, the polypeptides of the invention are used to modify oils, such as fish, animal and vegetable oils, and lipids, such as poly-unsaturated fatty acids. The lipases of the invention can modify oils by hydrolysis, alcoholysis, esterification, transesterification and/or interesterification. The methods of the invention use lipases with defined regio-specificity or defined chemoselectivity in biocatalytic synthetic reactions. In another aspect, the polypeptides of the invention are used to synthesize enantiomerically pure chiral products.

The invention provides lipase enzymes, polynucleotides encoding the enzymes, methods of making and using these polynucleotides and polypeptides. The polypeptides of the invention can be used in a variety of pharmaceutical, agricultural and industrial contexts, including the manufacture of cosmetics and nutraceuticals. In one aspect, the polypeptides of the invention are used in the biocatalytic synthesis of structured lipids (lipids that contain a defined set of fatty acids distributed in a defined

manner on the glycerol backbone), including cocoa butter alternatives, poly-unsaturated fatty acids (PUFAs), 1,3-diacyl glycerides (DAGs), 2-monoglycerides (MAGs) and triacylglycerides (TAGs), such as 1,3-dipalmitoyl-2-oleoylglycerol (POP), 1,3-distearoyl-2-oleoylglycerol (SOS), 1-palmitoyl-2-oleoyl-3-stearoylglycerol (POS) or 1-oleoyl-2,3-dimyristoylglycerol (OMM), long chain polyunsaturated fatty acids such as arachidonic acid, docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA).

In one aspect, the invention provides synthesis (using lipases of the invention) of a triglyceride mixture composed of POS (Palmitic-Oleic-Stearic), POP (Palmitic-Oleic-Palmitic) and SOS (Stearic-Oleic-Stearic) from glycerol. This synthesis uses free fatty acids versus fatty acid esters. In one aspect, this reaction can be performed in one pot with sequential addition of fatty acids using crude glycerol and free fatty acids and fatty acid esters. In one aspect, stearate and palmitate are mixed together to generate mixtures of DAGs. In one aspect, the diacylglycerides are subsequently acylated with oleate to give components of cocoa butter equivalents. In alternative aspects, the proportions of POS, POP and SOS can be varied according to: stearate to palmitate ratio; selectivity of enzyme for palmitate versus stearate; or enzyme enantioselectivity (could alter levels of POS/SOP). One-pot synthesis of cocoa butter equivalents or other cocoa butter alternatives is possible using this aspect of the invention.

In one aspect, lipases that exhibit regioselectivity and/or chemoselectivity are used in the structure synthesis of lipids or in the processing of lipids. Thus, the methods of the invention use lipases with defined regio-specificity or defined chemoselectivity (e.g., a fatty acid specificity) in a biocatalytic synthetic reaction. For example, the methods of the invention can use lipases with SN1, SN2 and/or SN3 regio-specificity, or combinations thereof. In one aspect, the methods of the invention use lipases that exhibit regioselectivity for the 2-position of a triacylglyceride (TAG). This SN2 regioselectivity can be used in the synthesis of a variety of structured lipids, e.g., triacylglycerides (TAGs), including 1,3-DAGs and components of cocoa butter.

The methods and compositions (lipases) of the invention can be used in the biocatalytic synthesis of structured lipids, and the production of nutraceuticals (e.g., polyunsaturated fatty acids and oils), various foods and food additives (e.g., emulsifiers, fat replacers, margarines and spreads), cosmetics (e.g., emulsifiers, creams), pharmaceuticals and drug delivery agents (e.g., liposomes, tablets, formulations), and animal feed additives (e.g., polyunsaturated fatty acids, such as linoleic acids) comprising

lipids made by the structured synthesis methods of the invention or processed by the methods of the invention

In one aspect, lipases of the invention can act on fluorogenic fatty acid (FA) esters, e.g., umbelliferyl FA esters. In one aspect, profiles of FA specificities of lipases made or modified by the methods of the invention can be obtained by measuring their relative activities on a series of umbelliferyl FA esters, such as palmitate, stearate, oleate, laurate, PUFA, butyrate.

The methods and compositions (lipases) of the invention can be used to synthesize enantiomerically pure chiral products. In one aspect, the methods and compositions (lipases) of the invention can be used to prepare a D-amino acid and corresponding esters from a racemic mix. For example, D-aspartic acid can be prepared from racemic aspartic acid. In one aspect, optically active D-homophenylalanine and/or its esters are prepared. The enantioselectively synthesized D-homophenylalanine can be starting material for many drugs, such as Enalapril, Lisinopril, and Quinapril, used in the treatment of hypertension and congestive heart failure. The D-aspartic acid and its derivatives made by the methods and compositions of the invention can be used in pharmaceuticals, e.g., for the inhibition of argininosuccinate synthetase to prevent or treat sepsis or cytokine-induced systemic hypotension or as immunosuppressive agents. The D-aspartic acid and its derivatives made by the methods and compositions of the invention can be used as taste modifying compositions for foods, e.g., as sweeteners (e.g., ALITAME™). For example, the methods and compositions (lipases) of the invention can be used to synthesize an optical isomer S(+) of 2-(6-methoxy-2-naphthyl) propionic acid from a racemic (R,S) ester of 2-(6-methoxy-2-naphthyl) propionic acid.

In one aspect, the methods and compositions (lipases) of the invention can be used to for stereoselectively hydrolyzing racemic mixtures of esters of 2-substituted acids, e.g., 2-aryloxy substituted acids, such as R-2-(4-hydroxyphenoxy)propionic acid, 2-arylpropionic acid, ketoprofen to synthesize enantiomerically pure chiral products.

The methods and compositions (lipases) of the invention can be used to hydrolyze oils, such as fish, animal and vegetable oils, and lipids, such as poly-unsaturated fatty acids. In one aspect, the polypeptides of the invention are used process fatty acids (such as poly-unsaturated fatty acids), e.g., fish oil fatty acids, for use in or as a feed additive. Addition of poly-unsaturated fatty acids PUFAs to feed for dairy cattle has been demonstrated to result in improved fertility and milk yields. Fish oil contains a high level of PUFAs and therefore is a potentially inexpensive source for PUFAs as a starting

material for the methods of the invention. The biocatalytic methods of the invention can process fish oil under mild conditions, thus avoiding harsh conditions utilized in some processes. Harsh conditions may promote unwanted isomerization, polymerization and oxidation of the PUFAs. In one aspect, the methods of the invention comprise lipase-catalyzed total hydrolysis of fish-oil or selective hydrolysis of PUFAs from fish oil to provide a mild alternative that would leave the high-value PUFAs intact. In one aspect, the methods further comprise hydrolysis of lipids by chemical or physical splitting of the fat.

In one aspect, the lipases and methods of the invention are used for the total hydrolysis of fish oil. Lipases can be screened for their ability to catalyze the total hydrolysis of fish oil under different conditions using. In alternative aspects, a single or multiple lipases are used to catalyze the total splitting of the fish oil. Several lipases of the invention may need to be used, owing to the presence of the PUFAs. In one aspect, a PUFA-specific lipase of the invention is combined with a general lipase to achieve the desired effect.

The methods and compositions (lipases) of the invention can be used to catalyze the partial or total hydrolysis of other oils, e.g. olive oils, that do not contain PUFAs.

The methods and compositions (lipases) of the invention can be used to catalyze the hydrolysis of PUFA glycerol esters. These methods can be used to make feed additives. In one aspect, lipases of the invention catalyze the release of PUFAs from simple esters and fish oil. Standard assays and analytical methods can be utilized.

The methods and compositions (lipases) of the invention can be used to selectively hydrolyze saturated esters over unsaturated esters into acids or alcohols. The methods and compositions (lipases) of the invention can be used to treat latexes for a variety of purposes, e.g., to treat latexes used in hair fixative compositions to remove unpleasant odors. The methods and compositions (lipases) of the invention can be used in the treatment of a lipase deficiency in an animal, e.g., a mammal, such as a human. The methods and compositions (lipases) of the invention can be used to prepare lubricants, such as hydraulic oils. The methods and compositions (lipases) of the invention can be used in making and using detergents. The methods and compositions (lipases) of the invention can be used in processes for the chemical finishing of fabrics, fibers or yarns. In one aspect, the methods and compositions (lipases) of the invention can be used for obtaining flame retardancy in a fabric using, e.g., a halogen-substituted

carboxylic acid or an ester thereof, i.e. a fluorinated, chlorinated or bromated carboxylic acid or an ester thereof.

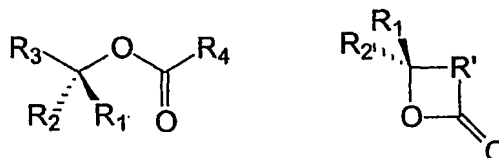
Monooxygenases

In one aspect, the invention provides monooxygenases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a monooxygenase activity, including thermostable and thermotolerant monooxygenase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

In one aspect, the monooxygenases of the invention have commercial utility as biocatalysts for use in the synthesis of aromatic and aliphatic esters and their derivatives, such as acids and alcohols. In one aspect, the monooxygenases of the invention are used in the catalysis of sulfoxidation reactions. In one aspect, the invention provides Baeyer-Villiger monooxygenases, polynucleotides encoding the Baeyer-Villiger monooxygenases, and methods of using these Baeyer-Villiger monooxygenases and polynucleotides. In one aspect, the invention provides methods of producing chiral synthetic intermediates using Baeyer-Villiger monooxygenases.

In one aspect, the monooxygenase activity comprises catalysis of sulfoxidation reactions. The monooxygenase activity can comprise an asymmetric sulfoxidation reaction. The monooxygenase activity can be enantiospecific. In one aspect, it can generate a substantially chiral product.

In one aspect, the monooxygenase activity comprises generation of an ester or a lactone having at least one of the following structures:



wherein: R_1 , R_2 , R_3 and R_4 are each independently selected from -H, substituted or unsubstituted alkyl, alkenyl, alkynyl, aryl, heteroaryl, cycloalkyl, and heterocyclic; wherein the substituted groups are substituted with one or more of lower alkyl, hydroxy, alkoxy, mercapto, cycloalkyl, heterocyclic, aryl, heteroaryl, aryloxy, and halogen, or two or more of R_1 , R_2 , R_3 and R_4 may together form cyclic moieties, and, R' is selected from substituted or unsubstituted alkylene, alkenylene, alkynylene, arylene, heteroarylene, cycloalkylene, and heterocyclic; wherein the substitutions are substituted

with one or more of lower alkyl, hydroxy, alkoxy, mercapto, cycloalkyl, heterocyclic, aryl, heteroaryl, aryloxy, and halogen.

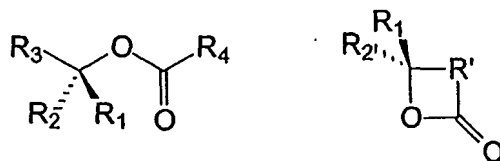
In one aspect, the monooxygenase activity comprises oxidation of a cycloalkanone to produce a chiral lactone. The cycloalkanone can comprise a cyclobutanone, a cyclopentanone, a cyclohexanone, a 2-methylcyclopentanone, a 2-methylcyclohexanone, a cyclohex-2-ene-1-one, a 2-(cyclohex-1-enyl)cyclohexanone, a 1,2-cyclohexanedione, a 1,3-cyclohexanedione or a 1,4-cyclohexanedione.

In one aspect, the monooxygenase activity comprises a chlorophenol 4-monooxygenase activity or a xylene monooxygenase activity.

The invention provides a pharmaceutical composition comprising a polypeptide of the invention.

The invention provides a method for converting a ketone to its corresponding ester comprising contacting the ketone with a polypeptide of the invention under conditions wherein the polypeptide catalyzes the conversion of the ketone to its corresponding ester. In one aspect, the polypeptide has an monooxygenase activity that is enantiospecific to generate a substantially chiral product. In one aspect, the ester is an aromatic or an aliphatic ester.

The invention provides a method for converting a cycloaliphatic ketone to its corresponding lactone comprising contacting the cycloaliphatic ketone with a polypeptide of the invention under conditions wherein the polypeptide catalyzes the conversion of the cycloaliphatic ketone to its corresponding lactone. In one aspect, the polypeptide has an monooxygenase activity that is enantiospecific to generate a substantially chiral product. In one aspect, the ester or lactone has at least one of the following structures:



wherein: R_1 , R_2 , R_3 and R_4 are each independently selected from -H, substituted or unsubstituted alkyl, alkenyl, alkynyl, aryl, heteroaryl, cycloalkyl, and heterocyclic; wherein the substituted groups are substituted with one or more of lower alkyl, hydroxy, alkoxy, mercapto, cycloalkyl, heterocyclic, aryl, heteroaryl, aryloxy, and halogen, or two or more of R_1 , R_2 , R_3 and R_4 may together form cyclic moieties, and, R' is selected from substituted or unsubstituted alkylene, alkenylene, alkynylene, arylene,

heteroarylene, cycloalkylene, and heterocyclic; wherein the substitutions are substituted with one or more of lower alkyl, hydroxy, alkoxy, mercapto, cycloalkyl, heterocyclic, aryl, heteroaryl, aryloxy, and halogen.

Nitroreductases

In one aspect, the invention provides nitroreductases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a nitroreductase activity, including thermostable and thermotolerant nitroreductase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Nitroreductases can catalyze the six-electron reduction of nitro compounds to the corresponding amines. Amines have a variety of applications as synthons and advanced pharmaceutical intermediates. There are markets for both aromatic amines and chiral aliphatic amines.

Nitroreductases of the invention fall in to two main classes. These are the oxygen-sensitive and oxygen-insensitive nitroreductases. The oxygen-sensitive enzyme can catalyze nitroreduction only under anaerobic conditions. A nitro anion radical is formed by a one-electron transfer and is immediately reoxidized in the presence of oxygen thus generating a futile cycle whereby reducing equivalents are consumed without nitroreduction. On the other hand the oxygen-insensitive nitroreductases catalyze nitroreduction in a series of two electron transfers, first via the nitroso and then the hydroxylamine intermediates before forming the amine.

Nitrilases

In one aspect, the invention provides nitrilases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a nitrilase activity, including thermostable and thermotolerant nitrilase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Nitrilases of the invention can be used for hydrolyzing a nitrile to a carboxylic acid. In one embodiment, the conditions of the reaction comprise aqueous conditions. In another embodiment, the conditions comprise a pH of about 8.0 and/or a temperature from about 37° C to about 45° C. Nitrilases of the invention can also be used for hydrolyzing a cyanohydrin moiety or an aminonitrile moiety of a molecule.

Alternatively, the nitrilases of the invention can be used for making a chiral α -hydroxy acid molecule, a chiral amino acid molecule, a chiral β -hydroxy acid molecule, or a chiral gamma-hydroxy acid molecule. In one embodiment, the chiral molecule is an (*R*)-enantiomer. In another embodiment, the chiral molecule is an (*S*)-enantiomer. In one embodiment of the invention, one particular enzyme can have R-specificity for one particular substrate and the same enzyme can have S-specificity for a different particular substrate.

In one aspect, nitrilases of the invention can be used for making a composition or an intermediate thereof, wherein the nitrilase of the invention hydrolyzes a cyanohydrin or a aminonitrile moiety. In one embodiment, the composition or intermediate thereof comprises (*S*)-2-amino-4-phenyl butanoic acid. In a further embodiment, the composition or intermediate thereof comprises an L-amino acid. In a further embodiment, the composition comprises a food additive or a pharmaceutical drug.

In another aspect, nitrilases of the invention can be used for making an (*R*)-ethyl 4-cyano-3-hydroxybutyric acid, wherein the nitrilase of the invention acts upon a hydroxyglutaryl nitrile and selectively produces an (*R*)-enantiomer, so as to make (*R*)-ethyl 4-cyano-3-hydroxybutyric acid. In one embodiment, the *ee* is at least 95% or at least 99%. In another embodiment, the hydroxyglutaryl nitrile comprises 1,3-di-cyano-2-hydroxy-propane or 3-hydroxyglutaronitrile.

In another aspect, nitrilases of the invention can be used for making an (*S*)-ethyl 4-cyano-3-hydroxybutyric acid, wherein the nitrilase of the invention acts upon a hydroxyglutaryl nitrile and selectively produces an (*S*)-enantiomer, so as to make (*S*)-ethyl 4-cyano-3-hydroxybutyric acid.

In another aspect, the nitrilases of the invention can be used for making a (*R*)-mandelic acid, wherein the nitrilase of the invention acts upon a mandelonitrile to produce a (*R*)-mandelic acid. In one embodiment, the (*R*)-mandelic acid comprises (*R*)-2-chloromandelic acid. In another embodiment, the (*R*)-mandelic acid comprises an aromatic ring substitution in the *ortho*-, *meta*-, or *para*- positions; a 1-naphthyl derivative of (*R*)-mandelic acid, a pyridyl derivative of (*R*)-mandelic acid or a thienyl derivative of (*R*)-mandelic acid or a combination thereof.

In another aspect, the nitrilases of the invention can be used for making a (*S*)-mandelic acid, wherein the nitrilase of the invention acts upon a mandelonitrile to produce a (*S*)-mandelic acid. In one embodiment, the (*S*)-mandelic acid comprises (*S*)-methyl benzyl cyanide and the mandelonitrile comprises (*S*)-methoxy-benzyl cyanide. In

one embodiment, the (*S*)-mandelic acid comprises an aromatic ring substitution in the *ortho*-, *meta*-, or *para*- positions; a 1-naphthyl derivative of (*S*)-mandelic acid, a pyridyl derivative of (*S*)-mandelic acid or a thienyl derivative of (*S*)-mandelic acid or a combination thereof.

In yet another aspect, the nitrilases of the invention can be used for making a (*S*)-phenyl lactic acid derivative or a (*R*)-phenyllactic acid derivative, wherein the nitrilase of the invention acts upon a phenyllactonitrile and selectively produces an (*S*)-enantiomer or an (*R*)-enantiomer, thereby producing an (*S*)-phenyl lactic acid derivative or an (*R*)-phenyl lactic acid derivative.

P450 enzymes

In one aspect, the invention provides P450 enzymes, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a P450 enzymatic activity, including thermostable and thermotolerant P450 enzymatic activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

P450s are oxidative enzymes that are widespread in nature and polypeptides of the invention having P450 activity can be used in processes such as detoxifying xenobiotics, catabolism of unusual carbon sources and biosynthesis of secondary metabolites (e.g., detoxification of toxic composition, e.g., pesticides, poisons, chemical warfare agents and the like). These oxygenases activate molecular oxygen using an iron-heme center and utilize a redox electron shuttle to support the epoxidation reaction.

In one aspect, the P450 activity comprises a monooxygenation reaction. In one aspect, the P450 activity comprises catalysis of incorporation of oxygen into a substrate. In one aspect, the P450 activity can further comprise hydroxylation of aliphatic or aromatic carbons. In another aspect, the P450 activity can comprise epoxidation. Alternatively, the P450 activity can comprise N-, O-, or S-dealkylation. In one aspect, the P450 activity can comprise dehalogenation. In another aspect the P450 activity can comprise oxidative deamination. Alternatively, the P450 activity can comprise N-oxidation or N-hydroxylation. In one aspect, the P450 activity can comprise sulfoxide formation.

In one aspect, the epoxidase activity further comprises an alkene substrate. The epoxidase activity can further comprise production of a chiral product. In one aspect, the epoxidase activity can be enantioselective.

Pectate lyases

In one aspect, the invention provides pectate lyases, e.g. pectinases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a pectate lyase, e.g. a pectinase activity, including thermostable and thermotolerant pectate lyase, e.g. a pectinase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

The pectate lyases, e.g. pectinases, of the invention can be used to catalyze the beta-elimination or hydrolysis of pectin and/or polygalacturonic acid, such as 1,4-linked alpha-D-galacturonic acid. They can be used in variety of industrial applications, e.g., to treat plant cell walls, such as those in cotton or other natural fibers. In another exemplary industrial application, the polypeptides of the invention can be used in textile scouring.

In one aspect, pectate lyase activity comprises catalysis of beta-elimination (trans-elimination) or hydrolysis of pectin or polygalacturonic acid (pectate). The pectate lyase activity can comprise the breakup or dissolution of plant cell walls. The pectate lyase activity can comprise beta-elimination (trans-elimination) or hydrolysis of 1,4-linked alpha-D-galacturonic acid. The pectate lyase activity can comprise catalysis of beta-elimination (trans-elimination) or hydrolysis of methyl-esterified galacturonic acid. The pectate lyase activity can be exo-acting or endo-acting. In one aspect, the pectate lyase activity is endo-acting and acts at random sites within a polymer chain to give a mixture of oligomers. In one aspect, the pectate lyase activity is exo-acting and acts from one end of a polymer chain and produces monomers or dimers. The pectate lyase activity can catalyze the random cleavage of alpha-1,4-glycosidic linkages in pectic acid (polygalacturonic acid) by trans-elimination or hydrolysis. The pectate lyase activity can comprise activity the same or similar to pectate lyase (EC 4.2.2.2), poly(1,4-alpha-D-galacturonide) lyase, polygalacturonate lyase (EC 4.2.2.2), pectin lyase (EC 4.2.2.10), polygalacturonase (EC 3.2.1.15), exo-polygalacturonase (EC 3.2.1.67), exo-polygalacturonate lyase (EC 4.2.2.9) or exo-poly-alpha-galacturonosidase (EC 3.2.1.82). The pectate lyase activity can comprise beta-elimination (trans-elimination) or hydrolysis of galactan to galactose or galactooligomers. The pectate lyase activity can comprise beta-elimination (trans-elimination) or hydrolysis of a plant fiber. The plant fiber can comprise cotton fiber, hemp fiber or flax fiber.

The pectate lyases, e.g. pectinases, of the invention can be used for hydrolyzing, breaking up or disrupting a pectin- or pectate (polygalacturonic acid)-comprising

composition, for liquefying or removing a pectin or pectate (polygalacturonic acid) from a composition. Alternatively, the pectate lyases, e.g. pectinases, of the invention can be used in detergent compositions. In one aspect, the pectate lyase is a nonsurface-active pectate lyase or a surface-active pectate lyase. The pectate lyase can be formulated in a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel form, a paste or a slurry form.

In one aspect, the pectate lyases, e.g. pectinases, of the invention can be used for washing an object. In another aspect, textiles or fabrics comprise a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention, wherein the polypeptide has pectate lyase, e.g. pectinase activity. Additionally, the pectate lyases, e.g. pectinases, of the invention can be used for fiber, thread, textile or fabric scouring. In one aspect, the pectate lyase is an alkaline active and thermostable pectate lyase. The desizing and scouring treatments can be combined in a single bath. The method can further comprise addition of an alkaline and thermostable amylase. The desizing or scouring treatments can comprise conditions of between about pH 8.5 to pH 10.0 and temperatures of at about 40°C. The method can further comprise addition of a bleaching step. The desizing, scouring and bleaching treatments can be done simultaneously or sequentially in a single-bath container. The bleaching treatment can comprise hydrogen peroxide or at least one peroxy compound that can generate hydrogen peroxide when dissolved in water, or combinations thereof, and at least one bleach activator. The fiber, thread, textile or fabric can comprise a cellulosic material. The cellulosic material can comprise a crude fiber, a yarn, a woven or knit textile, a cotton, a linen, a flax, a ramie, a rayon, a hemp, a jute or a blend of natural or synthetic fibers.

Alternatively, the pectate lyases, e.g. pectinases, of the invention can be used in feeds or foods. For example, the pectate lyases, e.g. pectinases, of the invention can be used to improve the extraction of oil from an oil-rich plant material. In one aspect, the oil-rich plant material comprises an oil-rich seed. The oil can be a soybean oil, an olive oil, a rapeseed (canola) oil or a sunflower oil.

In another aspect, the pectate lyases, e.g. pectinases, of the invention can be used for preparing a fruit or vegetable juice, syrup, puree or extract. In yet another aspect, the pectate lyases, e.g. pectinases, of the invention can be used for treating a paper or a paper or wood pulp. Alternatively, the invention provides papers or paper products or paper pulps comprising a pectate lyase of the invention, or a polypeptide encoded by a nucleic acid of the invention.

In yet another aspect, the invention provides pharmaceutical compositions comprising a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention, wherein the polypeptide has pectate lyase, e.g. pectinase activity. The pharmaceutical composition can act as a digestive aid.

Alternatively, the invention provides oral care products comprising a polypeptide of the invention, or a polypeptide encoded by a nucleic acid of the invention, wherein the polypeptide has pectate lyase, e.g. pectinase activity. The oral care product can comprise a toothpaste, a dental cream, a gel or a tooth powder, an odontic, a mouth wash, a pre- or post brushing rinse formulation, a chewing gum, a lozenge or a candy.

Phosphatases

In one aspect, the invention provides phosphatases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a phosphatase activity, including thermostable and thermotolerant phosphatase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Phosphatases are a group of enzymes that remove phosphate groups from organophosphate ester compounds. There are numerous phosphatases, including alkaline phosphatases, phosphodiesterases and phytases.

Alkaline phosphatases are widely distributed enzymes and are composed of a group of enzymes which hydrolyze organic phosphate ester bonds at alkaline pH.

Phosphodiesterases are capable of hydrolyzing nucleic acids by hydrolyzing the phosphodiester bridges of DNA and RNA. The classification of phosphodiesterases depends upon which side of the phosphodiester bridge is attacked. The 3' enzymes specifically hydrolyze the ester linkage between the 3' carbon and the phosphoric group whereas the 5' enzymes hydrolyze the ester linkage between the phosphoric group and the 5' carbon of the phosphodiester bridge. The best known of the class 3' enzymes is a phosphodiesterase from the venom of the rattlesnake or from a rattle's viper, which hydrolyses all the 3' bonds in either RNA or DNA liberating nearly all the nucleotide units as nucleotide 5' phosphates. This enzyme requires a free 3' hydroxyl group on the terminal nucleotide residue and proceeds stepwise from that end of the polynucleotide chain. This enzyme and all other nucleases which attack only at the ends of the polynucleotide chains are called exonucleases. The 5' enzymes are represented by a phosphodiesterase from bovine spleen, also an exonuclease, which hydrolyses all the

5' linkages of both DNA and RNA and thus liberates only nucleoside 3' phosphates. It begins its attack at the end of the chain having a free 3' hydroxyl group.

Phytase enzymes remove phosphate from phytic acid (inositol hexaphosphoric acid), a compound found in plants such as corn, wheat and rice. The enzyme has commercial use for the treatment of animal feed, making the inositol of the phytic acid available for animal nutrition. Phytases are used to improve the utilization of natural phosphorus in animal feed. Use of phytase as a feed additive enables the animal to metabolize a larger degree of its cereal feed's natural mineral content thereby reducing or altogether eliminating the need for synthetic phosphorus additives. More important than the reduced need for phosphorus additives is the corresponding reduction of phosphorus in pig and chicken waste. Many European countries severely limit the amount of manure that can be spread per acre due to concerns regarding phosphorus contamination of ground water.

Alkaline phosphatases hydrolyze monophosphate esters, releasing an organic phosphate and the cognate alcohol compound. It is non-specific with respect to the alcohol moiety and it is this feature which accounts for the many uses of this enzyme.

Phospholipases

In one aspect, the invention provides phospholipases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a phospholipase activity, including thermostable and thermotolerant phospholipase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Phospholipases are enzymes that hydrolyze the ester bonds of phospholipids. Corresponding to their importance in the metabolism of phospholipids, these enzymes are widespread among prokaryotes and eukaryotes. The phospholipases affect the metabolism, construction and reorganization of biological membranes and are involved in signal cascades. Several types of phospholipases are known which differ in their specificity according to the position of the bond attacked in the phospholipid molecule. Phospholipase A1 (PLA1) removes the 1-position fatty acid to produce free fatty acid and 1-lyso-2-acylphospholipid. Phospholipase A2 (PLA2) removes the 2-position fatty acid to produce free fatty acid and 1-acyl-2-lysophospholipid. PLA1 and PLA2 enzymes can be intra- or extra-cellular, membrane-bound or soluble. Intracellular PLA2 is found in almost every mammalian cell. Phospholipase C (PLC) removes the phosphate moiety to

produce 1,2 diacylglycerol and phospho base. Phospholipase D (PLD) produces 1,2-diacylglycerophosphate and base group. PLC and PLD are important in cell function and signaling. PLD had been the dominant phospholipase in biocatalysis. Patatins are another type of phospholipase, thought to work as a PLA.

The invention provides methods for cleaving a glycerolphosphate ester linkage comprising the following steps: (a) providing a polypeptide having a phospholipase activity, wherein the polypeptide comprises an amino acid sequence of the invention, or the polypeptide is encoded by a nucleic acid of the invention; (b) providing a composition comprising a glycerolphosphate ester linkage; and, (c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the polypeptide cleaves the glycerolphosphate ester linkage. In one aspect, the conditions comprise between about pH 5 to about 5.5, or, between about pH 4.5 to about 5.0. In one aspect, the conditions comprise a temperature of between about 40°C and about 70°C. In one aspect, the composition comprises a vegetable oil. In one aspect, the composition comprises an oilseed phospholipid. In one aspect, the cleavage reaction can generate a water extractable phosphorylated base and a diglyceride.

Phospholipases of the invention can be used in oil degumming, wherein the phospholipase is used under conditions wherein the phospholipase can cleave ester linkages in an oil, thereby degumming the oil. In one aspect, the oil is a vegetable oil. In another aspect, the vegetable oil comprises oilseed. The vegetable oil can comprise palm oil, rapeseed oil, corn oil, soybean oil, canola oil, sesame oil, peanut oil or sunflower oil. In one aspect, the method further comprises addition of a phospholipase of the invention, another phospholipase, another enzyme, or a combination thereof.

In another aspect of the invention, phospholipases of the invention can be used for converting a non-hydratable phospholipid to a hydratable form or for caustic refining of a phospholipid-containing composition. In the latter use, the polypeptide of the invention can be added before caustic refining and the composition comprising the phospholipid can comprise a plant and the polypeptide can be expressed transgenically in the plant, the polypeptide having a phospholipase activity can be added during crushing of a seed or other plant part, or, the polypeptide having a phospholipase activity is added following crushing or prior to refining. The polypeptide can be added during caustic refining and varying levels of acid and caustic can be added depending on levels of phosphorous and levels of free fatty acids. The polypeptide can be added after caustic refining: in an

intense mixer or retention mixer prior to separation; following a heating step; in a centrifuge; in a soapstock; in a washwater; or, during bleaching or deodorizing steps.

In yet another aspect, the phospholipases of the invention can be used for purification of a phytosterol or a triterpene. The phytosterol or a triterpene can comprise a plant sterol. The plant sterol can be derived from a vegetable oil. The vegetable oil can comprise a coconut oil, canola oil, cocoa butter oil, corn oil, cottonseed oil, linseed oil, olive oil, palm oil, peanut oil, oil derived from a rice bran, safflower oil, sesame oil, soybean oil or a sunflower oil. The method can comprise use of nonpolar solvents to quantitatively extract free phytosterols and phytosteryl fatty-acid esters. The phytosterol or a triterpene can comprise a β -sitosterol, a campesterol, a stigmasterol, a stigmastanol, a β -sitostanol, a sitostanol, a desmosterol, a chalinasterol, a poriferasterol, a clionasterol or a brassicasterol.

In one embodiment, the phospholipases of the invention can be used for refining a crude oil. The polypeptide can have a phospholipase activity is in a water solution that is added to the composition. The water level can be between about 0.5 to 5%. The process time can be less than about 2 hours, less than about 60 minutes, less than about 30 minutes, less than 15 minutes, or less than 5 minutes. The hydrolysis conditions can comprise a temperature of between about 25°C-70°C. The hydrolysis conditions can comprise use of caustics. The hydrolysis conditions can comprise a pH of between about pH 3 and pH 10, between about pH 4 and pH 9, or between about pH 5 and pH 8. The hydrolysis conditions can comprise addition of emulsifiers and/or mixing after the contacting of step (c). The methods can comprise addition of an emulsion-breaker and/or heat to promote separation of an aqueous phase. The methods can comprise degumming before the contacting step to collect lecithin by centrifugation and then adding a PLC, a PLC and/or a PLA to remove non-hydratable phospholipids. The methods can comprise water degumming of crude oil to less than 10 ppm for edible oils and subsequent physical refining to less than about 50 ppm for biodiesel oils. The methods can comprise addition of acid to promote hydration of non-hydratable phospholipids.

Phytases

In one aspect, the invention provides phytases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a phytase activity, including thermostable and thermotolerant phytase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Conversion of phytate to inositol and inorganic phosphorous can be catalyzed by phytase enzymes. Phytases such as phytase #EC 3.1.3.8 are capable of catalyzing the hydrolysis of myo-inositol hexaphosphate to D-myo-inositol 1,2,4,5,6-pentaphosphate and orthophosphate. Other phytases hydrolyze inositol pentaphosphate to tetra-, tri-, and lower phosphates. Acid phosphatases are enzymes that catalytically hydrolyze a wide variety of phosphate esters. For example, #EC 3.1.3.2 enzymes catalyze the hydrolysis of orthophosphoric monoesters to orthophosphate products.

Phytases of the invention can be used in producing phytase as a feed additive, e.g. for monogastric animals, fish, poultry, ruminants and other non-ruminants. Phytases of the invention can also be used for producing animal feed from certain industrial processes, e.g., wheat and corn waste products. In one aspect, the wet milling process of corn produces glutens sold as animal feeds. The addition of phytase improves the nutritional value of the feed product.

Phytases of the invention may also be used in dietary aids or in pharmaceutical compositions, for reducing pollution and increasing nutrient availability in an environment or environmental sample by degrading environmental phytic acid, for liberating minerals from phytates in plant materials either *in vitro*, i.e., in feed treatment processes, or *in vivo*, i.e., by administering the enzymes to animals.

Polymerases

In one aspect, the invention provides polymerases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a polymerase activity, including thermostable and thermotolerant polymerase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

The polymerase enzymes of the invention can have different polymerase activities at various high temperatures. In one aspect, the polymerase activity comprises addition of deoxynucleotides at the 3' hydroxyl end of a polynucleotide. The invention also provides kits, e.g., diagnostic kits, and methods for performing various amplification reactions, e.g., polymerase chain reactions, transcription amplifications, ligase chain reactions, self-sustained sequence replication or Q Beta replicase amplifications.

In one aspect, the polymerase activity comprises addition of nucleotides at the 3' hydroxyl end of a nucleic acid. The polymerase activity can comprise a 5'→3' polymerase activity, a 3'→5' exonuclease activity or a 5'→3' exonuclease activity or all

or a combination thereof. In one aspect, the polymerase activity comprises only a 5'→3' polymerase activity, but not a 3'→5' exonuclease activity or a 5'→3' exonuclease activity. In another aspect, the polymerase activity can comprise a 5'→3' polymerase activity and a 3'→5' exonuclease activity, but not a 5'→3' exonuclease activity. Alternatively, the polymerase activity can comprise a 5'→3' polymerase activity and a 5'→3' exonuclease activity, but not a 3'→5' exonuclease activity. The polymerase activity can comprise addition of dUTP or dITP. The polymerase activity can comprise addition of a modified or a non-natural nucleotide to a polynucleotide, such as an analog of guanine, cytosine, thymine, adenine or uracil, e.g., a 2-aminopurine, an inosine or a 5-methylcytosine.

In one aspect, the polymerase activity can comprise strand displacement properties. In one aspect, the polymerase activity comprises reverse transcriptase activity.

Proteases

In one aspect, the invention provides proteases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a protease activity, including thermostable and thermotolerant protease activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Proteases of the invention can be carbonyl hydrolases which act to cleave peptide bonds of proteins or peptides. Proteolytic enzymes are ubiquitous in occurrence, found in all living organisms, and are essential for cell growth and differentiation. The extracellular proteases are of commercial value and find multiple applications in various industrial sectors. Industrial applications of proteases include food processing, brewing, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver recovery in the photographic industry, medical treatment, silk degumming, biofilm degradation, biomass conversion to ethanol, biodefense, antimicrobial agents and disinfectants, personal care and cosmetics, biotech reagents and in increasing starch yield from corn wet milling. Additionally, proteases are important components of laundry detergents and other products. Within biological research, proteases are used in purification processes to degrade unwanted proteins. It is often desirable to employ proteases of low specificity or mixtures of more specific proteases to obtain the necessary degree of degradation.

Proteases are classified according to their catalytic mechanisms. The International Union of Biochemistry and Molecular Biology (IUBMB) recognizes four mechanistic

classes: (1) the serine proteases; (2) the cysteine proteases; (3) the aspartic proteases; and (4) the metalloproteases. In addition, the IUBMB recognizes a class of endopeptidases (oligopeptidases) of unknown catalytic mechanism. The serine proteases have alkaline pH optima, the metalloproteases are optimally active around neutrality, and the cysteine and aspartic enzymes have acidic pH optima. Serine proteases class comprises two distinct families: the chymotrypsin family, which includes the mammalian enzymes such as chymotrypsin, trypsin, elastase, or kallikrein, and the subtilisin family, which include the bacterial enzymes such as subtilisin. Serine proteases are used for a variety of industrial purposes, such as laundry detergents to aid in the removal of proteinaceous stains. In the food processing industry, serine proteases are used to produce protein-rich concentrates from fish and livestock, and in the preparation of dairy products.

The proteases of the invention can be used in a variety of diagnostic, therapeutic, and industrial contexts. The proteases of the invention can be used as, e.g., an additive for a detergent, for processing foods and for chemical synthesis utilizing a reverse reaction. Additionally, the proteases of the invention can be used in food processing, brewing, bath additives, alcohol production, peptide synthesis, enantioselectivity, hide preparation in the leather industry, waste management and animal degradation, silver recovery in the photographic industry, medical treatment, silk degumming, biofilm degradation, biomass conversion to ethanol, biodefense, antimicrobial agents and disinfectants, personal care and cosmetics, biotech reagents, in increasing starch yield from corn wet milling and pharmaceuticals such as digestive aids and anti-inflammatory (anti-phlogistic) agents.

Xylanases

In one aspect, the invention provides xylanases, polynucleotides encoding them, and methods of making and using these polynucleotides and polypeptides. In one aspect, the invention is directed to polypeptides, e.g., enzymes, having a xylanase activity, including thermostable and thermotolerant xylanase activity, and polynucleotides encoding these enzymes, and making and using these polynucleotides and polypeptides.

Xylanases (e.g., endo-1,4-beta-xylanase, EC 3.2.1.8) of the invention can hydrolyze internal β -1,4-xylosidic linkages in xylan to produce smaller molecular weight xylose and xylo-oligomers. Xylans are polysaccharides formed from 1,4- β -glycoside-linked D-xylopyranoses. Xylanases of the invention are of considerable commercial value, being used in the food industry, for baking and fruit and vegetable processing,

breakdown of agricultural waste, in the manufacture of animal feed and in pulp and paper production.

Arabinoxylanase are major non-starch polysaccharides of cereals representing 2.5 – 7.1% w/w depending on variety and growth conditions. The physicochemical properties of this polysaccharide are such that it gives rise to viscous solutions or even gels under oxidative conditions. In addition, arabinoxylans have high water-binding capacity and may have a role in protein foam stability. All of these characteristics present problems for several industries including brewing, baking, animal nutrition and paper manufacturing. In brewing applications, the presence of xylan results in wort filterability and haze formation issues. In baking applications (especially for cookies and crackers), these arabinoxylans create sticky doughs that are difficult to machine and reduce biscuit size. In addition, this carbohydrate is implicated in rapid rehydration of the baked product resulting in loss of crispiness and reduced shelf-life. For monogastric animal feed applications with cereal diets, arabinoxylan is a major contributing factor to viscosity of gut contents and thereby adversely affects the digestibility of the feed and animal growth rate. For ruminant animals, these polysaccharides represent substantial components of fiber intake and more complete digestion of arabinoxylans would facilitate higher feed conversion efficiencies.

Xylanases are currently used as additives (dough conditioners) in dough processing for the hydrolysis of water soluble arabinoxylan. In baking applications (especially for cookies and crackers), arabinoxylan creates sticky doughs that are difficult to machine and reduce biscuit size. In addition, this carbohydrate is implicated in rapid rehydration of the baked product resulting in loss of crispiness and reduced shelf-life.

The enhancement of xylan digestion in animal feed may improve the availability and digestibility of valuable carbohydrate and protein feed nutrients. For monogastric animal feed applications with cereal diets, arabinoxylan is a major contributing factor to viscosity of gut contents and thereby adversely affects the digestibility of the feed and animal growth rate. For ruminant animals, these polysaccharides represent substantial components of fiber intake and more complete digestion would facilitate higher feed conversion efficiencies. It is desirable for animal feed xylanases to be active in the animal stomach. This requires a feed enzyme to have high activity at 37 °C and at low pH for monogastrics (pH 2-4) and near neutral pH for ruminants (pH 6.5-7). The enzyme should also possess resistance to animal gut xylanases and stability at the higher temperatures involved in feed pelleting. As such, there is a need in the art for xylanase

feed additives for monogastric feed with high specific activity, activity at 35-40°C and pH 2-4, half life greater than 30 minutes in SGF and a half-life > 5 minutes at 85°C in formulated state. For ruminant feed, there is a need for xylanase feed additives that have a high specific activity, activity at 35-40°C and pH 6.5-7.0, half life greater than 30 minutes in SRF and stability as a concentrated dry powder.

In one aspect, the xylanases of the invention are also used in improving the quality and quantity of milk protein production in lactating cows, increasing the amount of soluble saccharides in the stomach and small intestine of pigs, improving late egg production efficiency and egg yields in hens. Additionally, xylanases of the inventions can be used in biobleaching and treatment of chemical pulps, biobleaching and treatment of wood or paper pulps, in reducing lignin in wood and modifying wood, as feed additives and/or supplements or in manufacturing cellulose solutions. Detergent compositions comprising xylanases of the invention are used for fruit, vegetables and/or mud and clay compounds.

In another aspect, xylanases of the invention can be used in compositions for the treatments and/or prophylaxis of coccidiosis. In yet another aspect, xylanases of the invention can be used in the production of water soluble dietary fiber, in improving the filterability, separation and production of starch, the beverage industry in improving filterability of wort or beer, in reducing viscosity of plant material, or in increasing viscosity or gel strength of food products such as jam, marmalade, jelly, juice, paste, soup, salsa, etc. Xylanases of the invention may also be used in hydrolysis of hemicellulose for which it is selective, particularly in the presence of cellulose. In addition, xylanases of the invention can also be used in the production of ethanol, in transformation of a microbe that produces ethanol, in production of oenological tannins and enzymatic composition, in stimulating the natural defenses of plants, in production of sugars from hemicellulose substrates, in the cleaning of fruit, vegetables, mud or clay containing soils, in cleaning beer filtration membranes, and in killing or inhibiting microbial cells.

Table 1, below, lists the various EC (Enzyme Commission) Numbers along with the corresponding mode of action for each enzyme class, subclass and sub-subclass. Enzyme nomenclature is based upon the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB). Table 2, below, lists the various EC Numbers along with the corresponding name given to each enzyme class, subclass and sub-subclass. Tables 1 and 2 list exemplary enzymatic

activities of polypeptides of the invention, as can be determined by sequence identity (e.g., homology); and in one embodiment a sequence of the invention comprises an enzyme having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity (homology) to an enzyme encoded by an exemplary sequence of the invention, including all odd numbered SEQ ID NO:1 to SEQ ID NO:26,897, or an exemplary polypeptide of the invention, including all even numbered SEQ ID NO:2 to SEQ ID NO:26,898, and with an exemplary function as listed in Table 1 or Table 2.

Table 3, below, contains the exemplary SEQ ID NO:s of the invention, and the closest hit (BLAST) information for the polynucleotides and polypeptides of the invention. This information includes the closest hit organism, accession number, definition of the closest hit, EC number, percentage amino acid identity and the percent nucleotide identity, along with the Evalue for the closest hits. The information contained in Table 3 identifies exemplary activities of polypeptides of the invention, based on sequence identity (homology). In one embodiment a sequence of the invention comprises an enzyme with at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity (homology) to an enzyme as listed in Table 3.

Table 1: EC (Enzyme Commission) Numbers with the corresponding mode of action for each enzyme class, subclass and sub-subclass

1. -.- Oxidoreductases.	1. 6. 3.- With a oxygen as acceptor.
1. 1. -.- Acting on the CH-OH group of donors.	1. 6. 4.- With a disulfide as acceptor.
1. 1. 1.- With NAD(+) or NADP(+) as acceptor.	1. 6. 5.- With a quinone or similar compound as acceptor.
1. 1. 2.- With a cytochrome as acceptor.	1. 6. 6.- With a nitrogenous group as acceptor.
1. 1. 3.- With oxygen as acceptor.	1. 6. 8.- With a flavin as acceptor.
1. 1. 4.- With a disulfide as acceptor.	1. 6.99.- With other acceptors.
1. 1. 5.- With a quinone or similar compound as acceptor.	1. 7. -.- Acting on other nitrogenous compounds as donors.
1. 1.99.- With other acceptors.	1. 7. 1.- With NAD(+) or NADP(+) as acceptor.
1. 2. -.- Acting on the aldehyde or oxo group of donors.	1. 7. 2.- With a cytochrome as acceptor.
1. 2. 1.- With NAD(+) or NADP(+) as acceptor.	1. 7. 3.- With oxygen as acceptor.
1. 2. 2.- With a cytochrome as acceptor.	1. 7. 7.- With an iron-sulfur protein as acceptor.
1. 2. 3.- With oxygen as acceptor.	1. 7.99.- With other acceptors.
1. 2. 4.- With a disulfide as acceptor.	1. 8. -.- Acting on a sulfur group of donors.

1. 2. 7.- With an iron-sulfur protein as acceptor.	1. 8. 1.- With NAD(+) or NADP(+) as acceptor.
1. 2.99.- With other acceptors.	1. 8. 2.- With a cytochrome as acceptor.
1. 3. -.- Acting on the CH-CH group of donors.	1. 8. 3.- With oxygen as acceptor.
1. 3. 1.- With NAD(+) or NADP(+) as acceptor.	1. 8. 4.- With a disulfide as acceptor.
1. 3. 2.- With a cytochrome as acceptor.	1. 8. 5.- With a quinone or similar compound as acceptor.
1. 3. 3.- With oxygen as acceptor.	1. 8. 7.- With an iron-sulfur protein as acceptor.
1. 3. 5.- With a quinone or related compound as acceptor.	1. 8.98.- With other, known, acceptors.
1. 3. 7.- With an iron-sulfur protein as acceptor.	1. 8.99.- With other acceptors.
1. 3.99.- With other acceptors.	1. 9. -.- Acting on a heme group of donors.
1. 4. -.- Acting on the CH-NH(2) group of donors.	1. 9. 3.- With oxygen as acceptor.
1. 4. 1.- With NAD(+) or NADP(+) as acceptor.	1. 9. 6.- With a nitrogenous group as acceptor.
1. 4. 2.- With a cytochrome as acceptor.	1. 9.99.- With other acceptors.
1. 4. 3.- With oxygen as acceptor.	1.10. -.- Acting on diphenols and related substances as donors.
1. 4. 4.- With a disulfide as acceptor.	1.10. 1.- With NAD(+) or NADP(+) as acceptor.
1. 4. 7.- With an iron-sulfur protein as acceptor.	1.10. 2.- With a cytochrome as acceptor.
1. 4.99.- With other acceptors.	1.10. 3.- With oxygen as acceptor.
1. 5. -.- Acting on the CH-NH group of donors.	1.10.99.- With other acceptors.
1. 5. 1.- With NAD(+) or NADP(+) as acceptor.	1.11. -.- Acting on a peroxide as acceptor (peroxidases).
1. 5. 3.- With oxygen as acceptor.	1.12. -.- Acting on hydrogen as donor.
1. 5. 4.- With a disulfide as acceptor.	1.12. 1.- With NAD(+) or NADP(+) as acceptor.
1. 5. 5.- With a quinone or similar compound as acceptor.	1.12. 2.- With a cytochrome as acceptor.
1. 5. 8.- With a flavin as acceptor.	1.12. 5.- With a quinone or similar compound as acceptor.
1. 5.99.- With other acceptors.	1.12. 7.- With an iron-sulfur protein as acceptor.
1. 6. -.- Acting on NADH or NADPH.	1.12.98.- With other known acceptors.
1. 6. 1.- With NAD(+) or NADP(+) as acceptor.	1.12.99.- With other acceptors.
1. 6. 2.- With a heme protein as acceptor.	1.13. -.- Acting on single donors with incorporation of molecular oxygen.

1.13.11.- With incorporation of two atoms of oxygen.	1.19. 6.- With dinitrogen as acceptor.
1.13.12.- With incorporation of one atom of oxygen.	1.20. -.- Acting on phosphorus or arsenic in donors.
1.14. -.- Acting on paired donors, with incorporation or reduction of molecular oxygen	1.20. 1.- Acting on phosphorus or arsenic in donors, with NAD(P)(+) as acceptor
1.14.11.- With 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	1.20. 4.- Acting on phosphorus or arsenic in donors, with disulfide as acceptor
1.14.12.- With NADH or NADPH as one donor, and incorporation of two atoms of oxygen into one donor	1.20.98.- Acting on phosphorus or arsenic in donors, with other, known acceptors
1.14.13.- With NADH or NADPH as one donor, and incorporation of one atom of oxygen	1.20.99.- Acting on phosphorus or arsenic in donors, with other acceptors
1.14.14.- With reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	1.21. -.- Acting on x-H and y-H to form an x-y bond.
1.14.15.- With a reduced iron-sulfur protein as one donor, and incorporation of one atom of oxygen	1.21. 3.- With oxygen as acceptor.
1.14.16.- With reduced pteridine as one donor, and incorporation of one atom of oxygen	1.21. 4.- With a disulfide as acceptor.

1.14.17.- With reduced ascorbate as one donor, and incorporation of one atom of oxygen	1.21.99.- With other acceptors.
1.14.18.- With another compound as one donor, and incorporation of one incorporation of one atom of oxygen	1.97. -.- Other oxidoreductases.
1.14.19.- With oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water	2. -.- Transferases.
1.14.20.- With 2-oxoglutarate as one donor, and the other dehydrogenated.	2. 1. -.- Transferring one-carbon groups.
1.14.21.- With NADH or NADPH as one donor, and the other dehydrogenated.	2. 1. 1.- Methyltransferases.
1.15. -.- Acting on superoxide as acceptor.	2. 1. 2.- Hydroxymethyl-, formyl- and related transferases.
1.16. -.- Oxidizing metal ions.	2. 1. 3.- Carboxyl- and carbamoyltransferases.
1.16. 1.- With NAD(+) or NADP(+) as acceptor.	2. 1. 4.- Amidinotransferases.
1.16. 3.- With oxygen as acceptor.	2. 2. -.- Transferring aldehyde or ketone residues.
1.16. 8.- With flavin as acceptor.	2. 2. 1.- Transketolases and transaldolases.
1.17. -.- Acting on CH or CH(2) groups.	2. 3. -.- Acyltransferases.
1.17. 1.- With NAD(+) or NADP(+) as acceptor.	2. 3. 1.- Transferring groups other than amino-acyl groups.
1.17. 3.- With oxygen as acceptor.	2. 3. 2.- Aminoacyltransferases.
1.17. 4.- With a disulfide as acceptor.	2. 3. 3.- Acyl groups converted into alkyl on transfer.
1.17. 5.- With a quinone or similar compound as acceptor	2. 4. -.- Glycosyltransferases.
1.17.99.- With other acceptors.	2. 4. 1.- Hexosyltransferases.
1.18. -.- Acting on iron-sulfur proteins as donors.	2. 4. 2.- Pentosyltransferases.
1.18. 1.- With NAD(+) or NADP(+) as acceptor.	2. 4.99.- Transferring other glycosyl groups.
1.18. 6.- With dinitrogen as acceptor.	2. 5. -.- Transferring alkyl or aryl groups, other than methyl groups.
1.18.96.- With other, known, acceptors.	2. 6. -.- Transferring nitrogenous groups.
1.18.99.- With H(+) as acceptor.	2. 6. 1.- Transaminases (aminotransferases).
1.19. -.- Acting on reduced flavodoxin as donor.	2. 6. 3.- Oximinotransferases.

2. 6.99.- Transferring other nitrogenous groups.	3. 1.22.- Endodeoxyribonucleases producing other than 5'-phosphomonoesters.
2. 7. -.- Transferring phosphorous-containing groups.	3. 1.25.- Site-specific endodeoxyribonucleases specific for altered bases.
2. 7. 1.- Phosphotransferases with an alcohol group as acceptor.	3. 1.26.- Endoribonucleases producing 5'-phosphomonoesters.
2. 7. 2.- Phosphotransferases with a carboxyl group as acceptor.	3. 1.27.- Endoribonucleases producing other than 5'-phosphomonoesters.
2. 7. 3.- Phosphotransferases with a nitrogenous group as acceptor.	3. 1.30.- Endoribonucleases active with either ribo- or deoxyribonucleic and producing 5'-phosphomonoesters
2. 7. 4.- Phosphotransferases with a phosphate group as acceptor.	3. 1.31.- Endoribonucleases active with either ribo- or deoxyribonucleic and producing 3'-phosphomonoesters
2. 7. 6.- Diphosphotransferases.	3. 2. -.- Glycosylases.
2. 7. 7.- Nucleotidyltransferases.	3. 2. 1.- Glycosidases, i.e. enzymes hydrolyzing O- and S-glycosyl compounds
2. 7. 8.- Transferases for other substituted phosphate groups.	3. 2. 2.- Hydrolyzing N-glycosyl compounds.

2. 7. 9.- Phosphotransferases with paired acceptors.	3. 3. -.- Acting on ether bonds.
2. 8. -.- Transferring sulfur-containing groups.	3. 3. 1.- Thioether and trialkylsulfonium hydrolases.
2. 8. 1.- Sulfurtransferases.	3. 3. 2.- Ether hydrolases.
2. 8. 2.- Sulfotransferases.	3. 4. -.- Acting on peptide bonds (peptide hydrolases).
2. 8. 3.- CoA-transferases.	3. 4.11.- Aminopeptidases.
2. 8. 4.- Transferring alkylthio groups.	3. 4.13.- Dipeptidases.
2. 9. -.- Transferring selenium-containing groups.	3. 4.14.- Dipeptidyl-peptidases and tripeptidyl-peptidases.
2. 9. 1.- Selenotransferases.	3. 4.15.- Peptidyl-dipeptidases.
3. -.- Hydrolases.	3. 4.16.- Serine-type carboxypeptidases.
3. 1. -.- Acting on ester bonds.	3. 4.17.- Metallocoarboxypeptidases.
3. 1. 1.- Carboxylic ester hydrolases.	3. 4.18.- Cysteine-type carboxypeptidases.
3. 1. 2.- Thiolester hydrolases.	3. 4.19.- Omega peptidases.
3. 1. 3.- Phosphoric monoester hydrolases.	3. 4.21.- Serine endopeptidases.
3. 1. 4.- Phosphoric diester hydrolases.	3. 4.22.- Cysteine endopeptidases.
3. 1. 5.- Triphosphoric monoester hydrolases.	3. 4.23.- Aspartic endopeptidases.
3. 1. 6.- Sulfuric ester hydrolases.	3. 4.24.- Metalloendopeptidases.
3. 1. 7.- Diphosphoric monoester hydrolases.	3. 4.25.- Threonine endopeptidases.
3. 1. 8.- Phosphoric triester hydrolases.	3. 4.99.- Endopeptidases of unknown catalytic mechanism.
3. 1.11.- Exodeoxyribonucleases producing 5'-phosphomonoesters.	3. 5. -.- Acting on carbon-nitrogen bonds, other than peptide bonds.
3. 1.13.- Exoribonucleases producing 5'-phosphomonoesters.	3. 5. 1.- In linear amides.
3. 1.14.- Exoribonucleases producing 3'-phosphomonoesters.	3. 5. 2.- In cyclic amides.
3. 1.15.- Exonucleases active with either ribo- or deoxyribonucleic acid and producing 5'-phosphomonoesters	3. 5. 3.- In linear amidines.
3. 1.16.- Exonucleases active with either ribo- or deoxyribonucleic acid producing 3'-phosphomonoesters	3. 5. 4.- In cyclic amidines.
3. 1.21.- Endodeoxyribonucleases producing 5'-phosphomonoesters.	3. 5. 5.- In nitriles.

3. 5.99.- In other compounds.	5. 3. -.- Intramolecular oxidoreductases.
3. 6. -.- Acting on acid anhydrides.	5. 3. 1.- Interconverting aldoses and ketoses.
3. 6. 1.- In phosphorous-containing anhydrides.	5. 3. 2.- Interconverting keto- and enol- groups.
3. 6. 2.- In sulfonyl-containing anhydrides.	5. 3. 3.- Transposing C=C bonds.
3. 6. 3.- Acting on acid anhydrides; catalyzing transmembrane movement of substances	5. 3. 4.- Transposing S-S bonds.
3. 6. 4.- Acting on acid anhydrides; involved in cellular and subcellular movement	5. 3.99.- Other intramolecular oxidoreductases.
3. 6. 5.- Acting on GTP; involved in cellular and subcellular movement.	5. 4. -.- Intramolecular transferases (mutases).
3. 7. -.- Acting on carbon-carbon bonds.	5. 4. 1.- Transferring acyl groups.
3. 7. 1.- In ketonic substances.	5. 4. 2.- Phosphotransferases (phosphomutases).
3. 8. -.- Acting on halide bonds.	5. 4. 3.- Transferring amino groups.
3. 8. 1.- In C-halide compounds.	5. 4. 4.- Transferring hydroxy groups.
3. 9. -.- Acting on phosphorus-nitrogen bonds.	5. 4.99.- Transferring other groups.
3.10. -.- Acting on sulfur-nitrogen bonds.	5. 5. -.- Intramolecular lyases.
3.11. -.- Acting on carbon-phosphorus bonds.	5.99. -.- Other isomerases.
3.12. -.- Acting on sulfur-sulfur bonds.	6. -.- Ligases.

3.13. -- Acting on carbon-sulfur bonds.	6. 1. -- Forming carbon-oxygen bonds.
4. -- -- Lyases.	6. 1. 1.- Ligases forming aminoacyl-tRNA and related compounds.
4. 1. -- Carbon-carbon lyases.	6. 2. -- Forming carbon-sulfur bonds.
4. 1. 1.- Carboxy-lyases.	6. 2. 1.- Acid--thiol ligases.
4. 1. 2.- Aldehyde-lyases.	6. 3. -- Forming carbon-nitrogen bonds.
4. 1. 3.- Oxo-acid-lyases.	6. 3. 1.- Acid--ammonia (or amide) ligases (amide synthases).
4. 1.99.- Other carbon-carbon lyases.	6. 3. 2.- Acid--D-amino-acid ligases (peptide synthases).
4. 2. -- Carbon-oxygen lyases.	6. 3. 3.- Cyclo-ligases.
4. 2. 1.- Hydro-lyases.	6. 3. 4.- Other carbon--nitrogen ligases.
4. 2. 2.- Acting on polysaccharides.	6. 3. 5.- Carbon--nitrogen ligases with glutamine as amido-N-donor.
4. 2. 3.- Acting on phosphates.	6. 4. -- Forming carbon-carbon bonds.
4. 2.99.- Other carbon-oxygen lyases.	6. 5. -- Forming phosphoric ester bonds.
4. 3. -- Carbon-nitrogen lyases.	6. 6. -- Forming nitrogen-metal bonds.
4. 3. 1.- Ammonia-lyases.	6. 6. 1.- Forming nitrogen-metal bonds.
4. 3. 2.- Lyases acting on amides, amidines, etc.	
4. 3. 3.- Amine-lyases.	
4. 3.99.- Other carbon-nitrogen-lyases.	
4. 4. -- Carbon-sulfur lyases.	
4. 5. -- Carbon-halide lyases.	
4. 6. -- Phosphorus-oxygen lyases.	
4.99. -- Other lyases.	
5. -- -- Isomerases.	
5. 1. -- Racemases and epimerases.	
5. 1. 1.- Acting on amino acids and derivatives.	
5. 1. 2.- Acting on hydroxy acids and derivatives.	
5. 1. 3.- Acting on carbohydrates and derivatives.	
5. 1.99.- Acting on other compounds.	
5. 2. -- Cis-trans-isomerases.	

Table 2: EC Numbers with the corresponding name given to each enzyme class, subclass and sub-subclass.

ENZYME: 1. -- --	1.1.1.41 Isocitrate dehydrogenase (NAD+).
1.1.1.1 Alcohol dehydrogenase.	1.1.1.42 Isocitrate dehydrogenase (NADP+).
1.1.1.2 Alcohol dehydrogenase (NADP+).	1.1.1.43 Phosphogluconate 2-dehydrogenase.
1.1.1.3 Homoserine dehydrogenase.	1.1.1.44 Phosphogluconate dehydrogenase (decarboxylating).
1.1.1.4 (R,R)-butanediol dehydrogenase.	1.1.1.45 L-gulonate 3-dehydrogenase.
1.1.1.5 Acetoin dehydrogenase.	1.1.1.46 L-arabinose 1-dehydrogenase.
1.1.1.6 Glycerol dehydrogenase.	1.1.1.47 Glucose 1-dehydrogenase.
1.1.1.7 Propanediol-phosphate dehydrogenase.	1.1.1.48 Galactose 1-dehydrogenase.
1.1.1.8 Glycerol-3-phosphate dehydrogenase (NAD+).	1.1.1.49 Glucose-6-phosphate 1-dehydrogenase.
1.1.1.9 D-xylulose reductase.	1.1.1.50 3-alpha-hydroxysteroid dehydrogenase (B-specific).
1.1.1.10 L-xylulose reductase.	1.1.1.51 3(or 17)beta-hydroxysteroid dehydrogenase.
1.1.1.11 D-arabinitol 4-dehydrogenase.	1.1.1.52 3-alpha-hydroxycholanate dehydrogenase.
1.1.1.12 L-arabinitol 4-dehydrogenase.	1.1.1.53 3-alpha(or 20-beta)-hydroxysteroid dehydrogenase.
1.1.1.13 L-arabinitol 2-dehydrogenase.	1.1.1.54 Allyl-alcohol dehydrogenase.

1.1.1.14	L-iditol 2-dehydrogenase.	1.1.1.55	L-acetaldehyde reductase (NADPH).
1.1.1.15	D-iditol 2-dehydrogenase.	1.1.1.56	Ribitol 2-dehydrogenase.
1.1.1.16	Galactitol 2-dehydrogenase.	1.1.1.57	Fructuronate reductase.
1.1.1.17	Mannitol-1-phosphate 5-dehydrogenase.	1.1.1.58	Tagaturonate reductase.
1.1.1.18	Inositol 2-dehydrogenase.	1.1.1.59	3-hydroxypropionate dehydrogenase.
1.1.1.19	L-glucuronate reductase.	1.1.1.60	2-hydroxy-3-oxopropionate reductase.
1.1.1.20	Glucuronolactone reductase.	1.1.1.61	4-hydroxybutyrate dehydrogenase.
1.1.1.21	Aldehyde reductase.	1.1.1.62	Estradiol 17-beta-dehydrogenase.
1.1.1.22	UDP-glucose 6-dehydrogenase.	1.1.1.63	Testosterone 17-beta-dehydrogenase.
1.1.1.23	Histidinol dehydrogenase.	1.1.1.64	Testosterone 17-beta-dehydrogenase (NADP+).
1.1.1.24	Quinate dehydrogenase.	1.1.1.65	Pyridoxine 4-dehydrogenase.
1.1.1.25	Shikimate dehydrogenase.	1.1.1.66	Omega-hydroxydecanoate dehydrogenase.
1.1.1.26	Glyoxylate reductase.	1.1.1.67	Mannitol 2-dehydrogenase.
1.1.1.27	L-lactate dehydrogenase.	1.1.1.69	Gluconate 5-dehydrogenase.
1.1.1.28	D-lactate dehydrogenase.	1.1.1.71	Alcohol dehydrogenase (NAD(P)+).
1.1.1.29	Glycerate dehydrogenase.	1.1.1.72	Glycerol dehydrogenase (NADP+).
1.1.1.30	3-hydroxybutyrate dehydrogenase.	1.1.1.73	Octanol dehydrogenase.
1.1.1.31	3-hydroxyisobutyrate dehydrogenase.	1.1.1.75	(R)-aminopropanol dehydrogenase.
1.1.1.32	Mevaldate reductase.	1.1.1.76	(S,S)-butanediol dehydrogenase.
1.1.1.33	Mevaldate reductase (NADPH).	1.1.1.77	Lactaldehyde reductase.
1.1.1.34	Hydroxymethylglutaryl-CoA reductase (NADPH).	1.1.1.78	D-lactaldehyde dehydrogenase.
1.1.1.35	3-hydroxyacyl-CoA dehydrogenase.	1.1.1.79	Glyoxylate reductase (NADP+).
1.1.1.36	Acetoacetyl-CoA reductase.	1.1.1.80	Isopropanol dehydrogenase (NADP+).
1.1.1.37	Malate dehydrogenase.	1.1.1.81	Hydroxypyruvate reductase.
1.1.1.38	Malate dehydrogenase (oxaloacetate-decarboxylating).	1.1.1.82	Malate dehydrogenase (NADP+).
1.1.1.39	Malate dehydrogenase (decarboxylating).	1.1.1.83	D-malate dehydrogenase (decarboxylating).
1.1.1.40	Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+).	1.1.1.84	Dimethylmalate dehydrogenase.

1.1.1.85	3-isopropylmalate dehydrogenase.	1.1.1.127	2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase.
1.1.1.86	Ketol-acid reductoisomerase.	1.1.1.128	L-idonate 2-dehydrogenase.
1.1.1.87	Homoisocitrate dehydrogenase.	1.1.1.129	L-threonate 3-dehydrogenase.
1.1.1.88	Hydroxymethylglutaryl-CoA reductase.	1.1.1.130	3-dehydro-L-gulonate 2-dehydrogenase.
1.1.1.90	Aryl-alcohol dehydrogenase.	1.1.1.131	Mannuronate reductase.
1.1.1.91	Aryl-alcohol dehydrogenase (NADP+).	1.1.1.132	GDP-mannose 6-dehydrogenase.
1.1.1.92	Oxalglycolate reductase (decarboxylating).	1.1.1.133	dTDP-4-dehydrorhamnose reductase.
1.1.1.93	Tartrate dehydrogenase.	1.1.1.134	dTDP-6-deoxy-L-talose 4-dehydrogenase.
1.1.1.94	Glycerol-3-phosphate dehydrogenase (NAD(P)+).	1.1.1.135	GDP-6-deoxy-D-talose 4-dehydrogenase.
1.1.1.95	Phosphoglycerate dehydrogenase.	1.1.1.136	UDP-N-acetylglucosamine 6-dehydrogenase.
1.1.1.96	Diiodophenylpyruvate reductase.	1.1.1.137	Ribitol-5-phosphate 2-dehydrogenase.
1.1.1.97	3-hydroxybenzyl-alcohol dehydrogenase.	1.1.1.138	Mannitol 2-dehydrogenase (NADP+).
1.1.1.98	(R)-2-hydroxy-fatty-acid dehydrogenase.	1.1.1.140	Sorbitol-6-phosphate 2-dehydrogenase.

1.1.1.99 (S)-2-hydroxy-fatty-acid dehydrogenase.	1.1.1.141 15-hydroxyprostaglandin dehydrogenase (NAD+).
1.1.1.100 3-oxoacyl-[acyl-carrier-protein] reductase.	1.1.1.142 D-pinitol dehydrogenase.
1.1.1.101 Acylglycerone-phosphate reductase.	1.1.1.143 Sequoyitol dehydrogenase.
1.1.1.102 3-dehydrosphinganine reductase.	1.1.1.144 Perillyl-alcohol dehydrogenase.
1.1.1.103 L-threonine 3-dehydrogenase.	1.1.1.145 3-beta-hydroxy-delta(5)-steroid dehydrogenase.
1.1.1.104 4-oxoproline reductase.	1.1.1.146 11-beta-hydroxysteroid dehydrogenase.
1.1.1.105 Retinol dehydrogenase.	1.1.1.147 16-alpha-hydroxysteroid dehydrogenase.
1.1.1.106 Pantoate 4-dehydrogenase.	1.1.1.148 Estradiol 17-alpha-dehydrogenase.
1.1.1.107 Pyridoxal 4-dehydrogenase.	1.1.1.149 20-alpha-hydroxysteroid dehydrogenase.
1.1.1.108 Carnitine 3-dehydrogenase.	1.1.1.150 21-hydroxysteroid dehydrogenase (NAD+).
1.1.1.110 Indolelactate dehydrogenase.	1.1.1.152 3-alpha-hydroxy-5-beta-androstane-17-one 3-alpha-dehydrogenase.
1.1.1.111 3-(imidazol-5-yl)lactate dehydrogenase.	1.1.1.153 Sepiapterin reductase.
1.1.1.112 Indanol dehydrogenase.	1.1.1.154 Ureidoglycolate dehydrogenase.
1.1.1.113 L-xylose 1-dehydrogenase.	1.1.1.155 Homoisocitrate dehydrogenase.
1.1.1.114 Apiose 1-reductase.	1.1.1.156 Glycerol 2-dehydrogenase (NADP+).
1.1.1.115 Ribose 1-dehydrogenase (NADP+).	1.1.1.157 3-hydroxybutyryl-CoA dehydrogenase.
1.1.1.116 D-arabinose 1-dehydrogenase.	1.1.1.158 UDP-N-acetylmuramate dehydrogenase.
1.1.1.117 D-arabinose 1-dehydrogenase (NAD(P)+).	1.1.1.159 7-alpha-hydroxysteroid dehydrogenase.
1.1.1.118 Glucose 1-dehydrogenase (NAD+).	1.1.1.160 Dihydrobunolol dehydrogenase.
1.1.1.119 Glucose 1-dehydrogenase (NADP+).	1.1.1.161 Cholestanetetraol 26-dehydrogenase.
1.1.1.120 Galactose 1-dehydrogenase (NADP+).	1.1.1.162 Erythrulose reductase.
1.1.1.121 Aldose 1-dehydrogenase.	1.1.1.163 Cyclopentanol dehydrogenase.
1.1.1.122 D-threo-aldose 1-dehydrogenase.	1.1.1.164 Hexadecanol dehydrogenase.
1.1.1.123 Sorbose 5-dehydrogenase (NADP+).	1.1.1.165 2-alkyn-1-ol dehydrogenase.
1.1.1.124 Fructose 5-dehydrogenase (NADP+).	1.1.1.166 Hydroxycyclohexanecarboxylate dehydrogenase.
1.1.1.125 2-deoxy-D-gluconate 3-dehydrogenase.	1.1.1.167 Hydroxymalonate dehydrogenase.
1.1.1.126 2-dehydro-3-deoxy-D-gluconate 6-dehydrogenase.	1.1.1.168 2-dehydropantolactone reductase (A-specific).

1.1.1.169 2-dehydropantoate 2-reductase.	1.1.1.207 (-)-menthol dehydrogenase.
1.1.1.170 Sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating).	1.1.1.208 (+)-neomenthol dehydrogenase.
1.1.1.172 2-oxoadipate reductase.	1.1.1.209 3(or 17)-alpha-hydroxysteroid dehydrogenase.
1.1.1.173 L-rhamnose 1-dehydrogenase.	1.1.1.210 3-beta(or 20-alpha)-hydroxysteroid dehydrogenase.
1.1.1.174 Cyclohexane-1,2-diol dehydrogenase.	1.1.1.211 Long-chain-3-hydroxyacyl-CoA dehydrogenase.
1.1.1.175 D-xylose 1-dehydrogenase.	1.1.1.212 3-oxoacyl-[acyl-carrier-protein] reductase (NADH).
1.1.1.176 12-alpha-hydroxysteroid dehydrogenase.	1.1.1.213 3-alpha-hydroxysteroid dehydrogenase (A-specific).
1.1.1.177 Glycerol-3-phosphate 1-dehydrogenase (NADP+).	1.1.1.214 2-dehydropantolactone reductase (B-specific).
1.1.1.178 3-hydroxy-2-methylbutyryl-CoA dehydrogenase.	1.1.1.215 Gluconate 2-dehydrogenase.
1.1.1.179 D-xylose 1-dehydrogenase (NADP+).	1.1.1.216 Farnesol dehydrogenase.

1.1.1.181 Cholest-5-ene-3-beta,7-alpha-diol 3-beta-dehydrogenase.	1.1.1.217 Benzyl-2-methyl-hydroxybutyrate dehydrogenase.
1.1.1.183 Geraniol dehydrogenase.	1.1.1.218 Morphine 6-dehydrogenase.
1.1.1.184 Carbonyl reductase (NADPH).	1.1.1.219 Dihydrokaempferol 4-reductase.
1.1.1.185 L-glycol dehydrogenase.	1.1.1.220 6-pyruvoyltetrahydropterin 2'-reductase.
1.1.1.186 dTDP-galactose 6-dehydrogenase.	1.1.1.221 Vomifoliol 4'-dehydrogenase.
1.1.1.187 GDP-4-dehydro-D-rhamnose reductase.	1.1.1.222 (R)-4-hydroxyphenyllactate dehydrogenase.
1.1.1.188 Prostaglandin-F synthase.	1.1.1.223 Isopiperitenol dehydrogenase.
1.1.1.189 Prostaglandin-E(2) 9-reductase.	1.1.1.224 Mannose-6-phosphate 6-reductase.
1.1.1.190 Indole-3-acetaldehyde reductase (NADH).	1.1.1.225 Chlordecone reductase.
1.1.1.191 Indole-3-acetaldehyde reductase (NADPH).	1.1.1.226 4-hydroxycyclohexanecarboxylate dehydrogenase.
1.1.1.192 Long-chain-alcohol dehydrogenase.	1.1.1.227 (-)-borneol dehydrogenase.
1.1.1.193 5-amino-6-(5-phosphoribosylamino)uracil reductase.	1.1.1.228 (+)-sabinol dehydrogenase.
1.1.1.194 Coniferyl-alcohol dehydrogenase.	1.1.1.229 Diethyl 2-methyl-3-oxosuccinate reductase.
1.1.1.195 Cinnamyl-alcohol dehydrogenase.	1.1.1.230 3-alpha-hydroxyglycyrrhetinate dehydrogenase.
1.1.1.196 15-hydroxyprostaglandin-D dehydrogenase (NADP+).	1.1.1.231 15-hydroxyprostaglandin-I dehydrogenase (NADP+).
1.1.1.197 15-hydroxyprostaglandin dehydrogenase (NADP+).	1.1.1.232 15-hydroxyicosatetraenoate dehydrogenase.
1.1.1.198 (+)-borneol dehydrogenase.	1.1.1.233 N-acylmannosamine 1-dehydrogenase.
1.1.1.199 (S)-usnate reductase.	1.1.1.234 Flavanone 4-reductase.
1.1.1.200 Aldose-6-phosphate reductase (NADPH).	1.1.1.235 8-oxocofomycin reductase.
1.1.1.201 7-beta-hydroxysteroid dehydrogenase (NADP+).	1.1.1.236 Tropinone reductase.
1.1.1.202 1,3-propanediol dehydrogenase.	1.1.1.237 Hydroxyphenylpyruvate reductase.
1.1.1.203 Uronate dehydrogenase.	1.1.1.238 12-beta-hydroxysteroid dehydrogenase.
1.1.1.205 IMP dehydrogenase.	1.1.1.239 3-alpha-(17-beta)-hydroxysteroid dehydrogenase (NAD+).
1.1.1.206 Tropine dehydrogenase.	1.1.1.240 N-acetylhexosamine 1-dehydrogenase.

1.1.1.241 6-endo-hydroxycineole dehydrogenase.	1.1.1.281 GDP-4-dehydro-6-deoxy-D-mannose reductase.
1.1.1.243 Carveol dehydrogenase.	1.1.1.282 Quinate/shikimate dehydrogenase.
1.1.1.244 Methanol dehydrogenase.	1.1.2.2 Mannitol dehydrogenase (cytochrome).
1.1.1.245 Cyclohexanol dehydrogenase.	1.1.2.3 L-lactate dehydrogenase (cytochrome).
1.1.1.246 Pterocarpin synthase.	1.1.2.4 D-lactate dehydrogenase (cytochrome).
1.1.1.247 Codeinone reductase (NADPH).	1.1.2.5 D-lactate dehydrogenase (cytochrome c-553).
1.1.1.248 Salutaridine reductase (NADPH).	1.1.3.3 Malate oxidase.
1.1.1.250 D-arabinitol 2-dehydrogenase.	1.1.3.4 Glucose oxidase.
1.1.1.251 Galactitol-1-phosphate 5-dehydrogenase.	1.1.3.5 Hexose oxidase.
1.1.1.252 Tetrahydroxynaphthalene reductase.	1.1.3.6 Cholesterol oxidase.
1.1.1.254 (S)-carnitine 3-dehydrogenase.	1.1.3.7 Aryl-alcohol oxidase.
1.1.1.255 Mannitol dehydrogenase.	1.1.3.8 L-gulonolactone oxidase.
1.1.1.256 Fluoren-9-ol dehydrogenase.	1.1.3.9 Galactose oxidase.

1.1.1.257 4-(hydroxymethyl)benzenesulfonate dehydrogenase.	1.1.3.10 Pyranose oxidase.
1.1.1.258 6-hydroxyhexanoate dehydrogenase.	1.1.3.11 L-sorbose oxidase.
1.1.1.259 3-hydroxypimeloyl-CoA dehydrogenase.	1.1.3.12 Pyridoxine 4-oxidase.
1.1.1.260 Sulcatone reductase.	1.1.3.13 Alcohol oxidase.
1.1.1.261 Glycerol-1-phosphate dehydrogenase (NAD(P) ⁺).	1.1.3.14 Catechol oxidase (dimerizing).
1.1.1.262 4-hydroxythreonine-4-phosphate dehydrogenase.	1.1.3.15 (S)-2-hydroxy-acid oxidase.
1.1.1.263 1,5-anhydro-D-fructose reductase.	1.1.3.16 Ecdysone oxidase.
1.1.1.264 L-idonate 5-dehydrogenase.	1.1.3.17 Choline oxidase.
1.1.1.265 3-methylbutanal reductase.	1.1.3.18 Secondary-alcohol oxidase.
1.1.1.266 dTDP-4-dehydro-6-deoxyglucose reductase.	1.1.3.19 4-hydroxymandelate oxidase.
1.1.1.267 1-deoxy-D-xylulose-5-phosphate reductoisomerase.	1.1.3.20 Long-chain-alcohol oxidase.
1.1.1.268 2-(R)-hydroxypropyl-CoM dehydrogenase.	1.1.3.21 Glycerol-3-phosphate oxidase.
1.1.1.269 2-(S)-hydroxypropyl-CoM dehydrogenase.	1.1.3.23 Thiamine oxidase.
1.1.1.270 3-keto-steroid reductase.	1.1.3.24 L-galactonolactone oxidase.
1.1.1.271 GDP-L-fucose synthase.	1.1.3.25 Cellobiose oxidase.
1.1.1.272 (R)-2-hydroxyacid dehydrogenase.	1.1.3.27 Hydroxyphytanate oxidase.
1.1.1.273 Vellosimine dehydrogenase.	1.1.3.28 Nucleoside oxidase.
1.1.1.274 2,5-didehydrogluconate reductase.	1.1.3.29 N-acylhexosamine oxidase.
1.1.1.275 (+)-trans-carveol dehydrogenase.	1.1.3.30 Polyvinyl-alcohol oxidase.
1.1.1.276 Serine 3-dehydrogenase.	1.1.3.37 D-arabinono-1,4-lactone oxidase.
1.1.1.277 3-beta-hydroxy-5-beta-steroid dehydrogenase.	1.1.3.38 Vanillyl-alcohol oxidase.
1.1.1.278 3-beta-hydroxy-5-alpha-steroid dehydrogenase.	1.1.3.39 Nucleoside oxidase (H ₂ O ₂ -forming).
1.1.1.279 (R)-3-hydroxyacid-ester dehydrogenase.	1.1.3.40 D-mannitol oxidase.
1.1.1.280 (S)-3-hydroxyacid-ester dehydrogenase.	1.1.3.41 Xylitol oxidase.

1.1.4.1 Vitamin-K-epoxide reductase (warfarin-sensitive).	1.2.1.8 Betaine-aldehyde dehydrogenase.
1.1.4.2 Vitamin-K-epoxide reductase (warfarin-insensitive).	1.2.1.9 Glyceraldehyde-3-phosphate dehydrogenase (NADP ⁺).
1.1.5.2 Quinoprotein glucose dehydrogenase.	1.2.1.10 Acetaldehyde dehydrogenase (acetylating).
1.1.99.1 Choline dehydrogenase.	1.2.1.11 Aspartate-semialdehyde dehydrogenase.
1.1.99.2 2-hydroxyglutarate dehydrogenase.	1.2.1.12 Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating).
1.1.99.3 Gluconate 2-dehydrogenase (acceptor).	1.2.1.13 Glyceraldehyde-3-phosphate dehydrogenase (NADP ⁺) (phosphorylating).
1.1.99.4 Dehydrogluconate dehydrogenase.	1.2.1.15 Malonate-semialdehyde dehydrogenase.
1.1.99.5 Glycerol-3-phosphate dehydrogenase.	1.2.1.16 Succinate-semialdehyde dehydrogenase (NAD(P) ⁺).
1.1.99.6 D-2-hydroxy-acid dehydrogenase.	1.2.1.17 Glyoxylate dehydrogenase (acylating).
1.1.99.7 Lactate--malate transhydrogenase.	1.2.1.18 Malonate-semialdehyde dehydrogenase (acetylating).
1.1.99.8 Alcohol dehydrogenase (acceptor).	1.2.1.19 Aminobutyraldehyde dehydrogenase.
1.1.99.9 Pyridoxine 5-dehydrogenase.	1.2.1.20 Glutarate-semialdehyde dehydrogenase.
1.1.99.10 Glucose dehydrogenase (acceptor).	1.2.1.21 Glycolaldehyde dehydrogenase.

1.1.99.11 Fructose 5-dehydrogenase.	1.2.1.22 Lactaldehyde dehydrogenase.
1.1.99.12 Sorbose dehydrogenase.	1.2.1.23 2-oxoaldehyde dehydrogenase (NAD+).
1.1.99.13 Glucoside 3-dehydrogenase.	1.2.1.24 Succinate-semialdehyde dehydrogenase.
1.1.99.14 Glycolate dehydrogenase.	1.2.1.25 2-oxoisovalerate dehydrogenase (acylating).
1.1.99.16 Malate dehydrogenase (acceptor).	1.2.1.26 2,5-dioxovalerate dehydrogenase.
1.1.99.18 Cellobiose dehydrogenase (acceptor).	1.2.1.27 Methylmalonate-semialdehyde dehydrogenase (acylating).
1.1.99.19 Uracil dehydrogenase.	1.2.1.28 Benzaldehyde dehydrogenase (NAD+).
1.1.99.20 Alkan-1-ol dehydrogenase (acceptor).	1.2.1.29 Aryl-aldehyde dehydrogenase.
1.1.99.21 D-sorbitol dehydrogenase (acceptor).	1.2.1.30 Aryl-aldehyde dehydrogenase (NADP+).
1.1.99.22 Glycerol dehydrogenase (acceptor).	1.2.1.31 L-aminoadipate-semialdehyde dehydrogenase.
1.1.99.23 Polyvinyl-alcohol dehydrogenase (acceptor).	1.2.1.32 Aminomuconate-semialdehyde dehydrogenase.
1.1.99.24 Hydroxyacid-oxoacid transhydrogenase.	1.2.1.33 (R)-dehydropantoate dehydrogenase.
1.1.99.25 Quinate dehydrogenase (pyrroloquinoline-quinone).	1.2.1.36 Retinal dehydrogenase.
1.1.99.26 3-hydroxycyclohexanone dehydrogenase.	1.2.1.38 N-acetyl-gamma-glutamyl-phosphate reductase.
1.1.99.27 (R)-pantolactone dehydrogenase (flavin).	1.2.1.39 Phenylacetaldehyde dehydrogenase.
1.1.99.28 Glucose--fructose oxidoreductase.	1.2.1.40 3-alpha,7-alpha,12-alpha-trihydroxycholestan-26-al 26-oxidoreductase.
1.1.99.29 Pyranose dehydrogenase (acceptor).	1.2.1.41 Glutamate-5-semialdehyde dehydrogenase.
1.1.99.30 2-oxo-acid reductase.	1.2.1.42 Hexadecanal dehydrogenase (acylating).
1.2.1.1 Formaldehyde dehydrogenase (glutathione).	1.2.1.43 Formate dehydrogenase (NADP+).
1.2.1.2 Formate dehydrogenase.	1.2.1.44 Cinnamoyl-CoA reductase.
1.2.1.3 Aldehyde dehydrogenase (NAD+).	1.2.1.45 4-carboxy-2-hydroxymuconate-6-semialdehyde dehydrogenase.
1.2.1.4 Aldehyde dehydrogenase (NADP+).	1.2.1.46 Formaldehyde dehydrogenase.
1.2.1.5 Aldehyde dehydrogenase (NAD(P)+).	1.2.1.47 4-trimethylammoniumbutyraldehyde dehydrogenase.
1.2.1.7 Benzaldehyde dehydrogenase (NADP+).	1.2.1.48 Long-chain-aldehyde dehydrogenase.
1.2.1.49 2-oxoaldehyde dehydrogenase (NADP+).	1.2.4.4 3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring).
1.2.1.50 Long-chain-fatty-acyl-CoA reductase.	1.2.7.1 Pyruvate synthase.
1.2.1.51 Pyruvate dehydrogenase (NADP+).	1.2.7.2 2-oxobutyrate synthase.
1.2.1.52 Oxoglutarate dehydrogenase (NADP+).	1.2.7.3 2-oxoglutarate synthase.
1.2.1.53 4-hydroxyphenylacetaldehyde dehydrogenase.	1.2.7.4 Carbon-monoxide dehydrogenase (ferredoxin).
1.2.1.54 Gamma-guanidinobutyraldehyde dehydrogenase.	1.2.7.5 Aldehyde ferredoxin oxidoreductase.
1.2.1.57 Butanal dehydrogenase.	1.2.7.6 Glyceraldehyde-3-phosphate dehydrogenase (ferredoxin).
1.2.1.58 Phenylglyoxylate dehydrogenase (acylating).	1.2.7.7 3-methyl-2-oxobutanoate dehydrogenase (ferredoxin).
1.2.1.59 Glyceraldehyde-3-phosphate dehydrogenase (NAD(P)(+)) (phosphorylating).	1.2.7.8 Indolepyruvate ferredoxin oxidoreductase.
1.2.1.60 5-carboxymethyl-2-hydroxymuconic-semialdehyde dehydrogenase.	1.2.7.9 2-oxoglutarate ferredoxin oxidoreductase.
1.2.1.61 4-hydroxymuconic-semialdehyde dehydrogenase.	1.2.99.2 Carbon-monoxide dehydrogenase (acceptor).

1.2.1.62 4-formylbenzenesulfonate dehydrogenase.	1.2.99.3 Aldehyde dehydrogenase (pyrroloquinoline-quinone).
1.2.1.63 6-oxohexanoate dehydrogenase.	1.2.99.4 Formaldehyde dismutase.
1.2.1.64 4-hydroxybenzaldehyde dehydrogenase.	1.2.99.5 Formylmethanofuran dehydrogenase.
1.2.1.65 Salicylaldehyde dehydrogenase.	1.2.99.6 Carboxylate reductase.
1.2.1.66 Mycothiol-dependent formaldehyde dehydrogenase.	1.2.99.7 Aldehyde dehydrogenase (FAD-independent).
1.2.1.67 Vanillin dehydrogenase.	1.3.1.1 Dihydrouracil dehydrogenase (NAD ⁺).
1.2.1.68 Coniferyl-aldehyde dehydrogenase.	1.3.1.2 Dihydropyrimidine dehydrogenase (NADP ⁺).
1.2.1.69 Fluoroacetaldehyde dehydrogenase.	1.3.1.3 Cortisone beta-reductase.
1.2.2.1 Formate dehydrogenase (cytochrome).	1.3.1.4 Cortisone alpha-reductase.
1.2.2.2 Pyruvate dehydrogenase (cytochrome).	1.3.1.5 Cucurbitacin delta(23)-reductase.
1.2.2.3 Formate dehydrogenase (cytochrome c-553).	1.3.1.6 Fumarate reductase (NADH).
1.2.2.4 Carbon-monoxide dehydrogenase (cytochrome b-561).	1.3.1.7 Meso-tartrate dehydrogenase.
1.2.3.1 Aldehyde oxidase.	1.3.1.8 Acyl-CoA dehydrogenase (NADP ⁺).
1.2.3.3 Pyruvate oxidase.	1.3.1.9 Enoyl-[acyl-carrier-protein] reductase (NADH).
1.2.3.4 Oxalate oxidase.	1.3.1.10 Enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific).
1.2.3.5 Glyoxylate oxidase.	1.3.1.11 2-coumarate reductase.
1.2.3.6 Pyruvate oxidase (CoA-acetylating).	1.3.1.12 Prephenate dehydrogenase.
1.2.3.7 Indole-3-acetaldehyde oxidase.	1.3.1.13 Prephenate dehydrogenase (NADP ⁺).
1.2.3.8 Pyridoxal oxidase.	1.3.1.14 Orotate reductase (NADH).
1.2.3.9 Aryl-aldehyde oxidase.	1.3.1.15 Orotate reductase (NADPH).
1.2.3.11 Retinal oxidase.	1.3.1.16 Beta-nitroacrylate reductase.
1.2.3.13 4-hydroxyphenylpyruvate oxidase.	1.3.1.17 3-methyleneoxindole reductase.
1.2.4.1 Pyruvate dehydrogenase (acetyl-transferring).	1.3.1.18 Kynurenate-7,8-dihydrodiol dehydrogenase.
1.2.4.2 Oxoglutarate dehydrogenase (succinyl-transferring).	1.3.1.19 Cis-1,2-dihydrobenzene-1,2-diol dehydrogenase.

1.3.1.20 Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase.	1.3.1.59 1,6-dihydroxy-5-methylcyclohexa-2,4-dienecarboxylate dehydrogenase.
1.3.1.21 7-dehydrocholesterol reductase.	1.3.1.60 Dibenzothiophene dihydrodiol dehydrogenase.
1.3.1.22 Cholestenone 5-alpha-reductase.	1.3.1.61 Terephthalate 1,2-cis-dihydrodiol dehydrogenase.
1.3.1.23 Cholestenone 5-beta-reductase.	1.3.1.62 Pimeloyl-CoA dehydrogenase.
1.3.1.24 Biliverdin reductase.	1.3.1.63 2,4-dichlorobenzoyl-CoA reductase.
1.3.1.25 1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase.	1.3.1.64 Phthalate 4,5-cis-dihydrodiol dehydrogenase.
1.3.1.26 Dihydrodipicolinate reductase.	1.3.1.65 5,6-dihydroxy-3-methyl-2-oxo-1,2,5,6-tetrahydroquinoline dehydrogenase.
1.3.1.27 2-hexadecenal reductase.	1.3.1.66 Cis-dihydroethylcatechol dehydrogenase.
1.3.1.28 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase.	1.3.1.67 Cis-1,2-dihydroxy-4-methylcyclohexa-3,5-diene-1-carboxylate dehydrogenase.
1.3.1.29 Cis-1,2-dihydro-1,2-dihydroxynaphthalene dehydrogenase.	1.3.1.68 1,2-dihydroxy-6-methylcyclohexa-3,5-dienecarboxylate dehydrogenase.
1.3.1.30 Progesterone 5-alpha-reductase.	1.3.1.69 Zeatin reductase.

1.3.1.31	2-enoate reductase.	1.3.1.70	Delta(14)-sterol reductase.
1.3.1.32	Maleylacetate reductase.	1.3.1.71	Delta(24(24(1)))sterol reductase.
1.3.1.33	Protochlorophyllide reductase.	1.3.1.72	Delta(24)-sterol reductase.
1.3.1.34	2,4-dienoyl-CoA reductase (NADPH).	1.3.1.73	1,2-dihydrovomilenine reductase.
1.3.1.35	Phosphatidylcholine desaturase.	1.3.1.74	2-alkenal reductase.
1.3.1.36	Geissoschizine dehydrogenase.	1.3.1.75	Divinyl chlorophyllide a 8-vinyl-reductase.
1.3.1.37	Cis-2-enoyl-CoA reductase (NADPH).	1.3.1.76	Precorrin-2 dehydrogenase.
1.3.1.38	Trans-2-enoyl-CoA reductase (NADPH).	1.3.2.3	Galactonolactone dehydrogenase.
1.3.1.39	Enoyl-[acyl-carrier-protein] reductase (NADPH, A-specific).	1.3.3.1	Dihydroorotate oxidase.
1.3.1.40	2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate reductase.	1.3.3.2	Lathosterol oxidase.
1.3.1.41	Xanthommatin reductase.	1.3.3.3	Coproporphyrinogen oxidase.
1.3.1.42	12-oxophytodienoate reductase.	1.3.3.4	Protoporphyrinogen oxidase.
1.3.1.43	Cyclohexadienyl dehydrogenase.	1.3.3.5	Bilirubin oxidase.
1.3.1.44	Trans-2-enoyl-CoA reductase (NAD+).	1.3.3.6	Acyl-CoA oxidase.
1.3.1.45	2'-hydroxyisoflavone reductase.	1.3.3.7	Dihydrouracil oxidase.
1.3.1.46	Biochanin-A reductase.	1.3.3.8	Tetrahydroberberine oxidase.
1.3.1.47	Alpha-santonin 1,2-reductase.	1.3.3.9	Secologanin synthase.
1.3.1.48	15-oxoprostaglandin 13-oxidase.	1.3.3.10	Tryptophan alpha,beta-oxidase.
1.3.1.49	Cis-3,4-dihydrophenanthrene-3,4-diol dehydrogenase.	1.3.5.1	Succinate dehydrogenase (ubiquinone).
1.3.1.51	2'-hydroxydaidzein reductase.	1.3.7.1	6-hydroxynicotinate reductase.
1.3.1.52	2-methyl-branched-chain-enoyl-CoA reductase.	1.3.7.2	15,16-dihydrobiliverdin:ferredoxin oxidoreductase.
1.3.1.53	(3S,4R)-3,4-dihydroxycyclohexa-1,5-diene-1,4-dicarboxylate dehydrogenase.	1.3.7.3	Phytoerythrobilin:ferredoxin oxidoreductase.
1.3.1.54	Precorrin-6A reductase.	1.3.7.4	Phytochromobilin:ferredoxin oxidoreductase.
1.3.1.56	Cis-2,3-dihydrobiphenyl-2,3-diol dehydrogenase.	1.3.7.5	Phycocyanobilin:ferredoxin oxidoreductase.
1.3.1.57	Phloroglucinol reductase.	1.3.99.1	Succinate dehydrogenase.
1.3.1.58	2,3-dihydroxy-2,3-dihydro-p-cumate dehydrogenase.	1.3.99.2	Butyryl-CoA dehydrogenase.

1.3.99.3	Acyl-CoA dehydrogenase.	1.4.3.5	Pyridoxamine-phosphate oxidase.
1.3.99.4	3-oxosteroid 1-dehydrogenase.	1.4.3.6	Amine oxidase (copper-containing).
1.3.99.5	3-oxo-5-alpha-steroid 4-dehydrogenase.	1.4.3.7	D-glutamate oxidase.
1.3.99.6	3-oxo-5-beta-steroid 4-dehydrogenase.	1.4.3.8	Ethanolamine oxidase.
1.3.99.7	Glutaryl-CoA dehydrogenase.	1.4.3.10	Putrescine oxidase.
1.3.99.8	2-furoyl-CoA dehydrogenase.	1.4.3.11	L-glutamate oxidase.
1.3.99.10	Isovaleryl-CoA dehydrogenase.	1.4.3.12	Cyclohexylamine oxidase.
1.3.99.11	Dihydroorotate dehydrogenase.	1.4.3.13	Protein-lysine 6-oxidase.
1.3.99.12	2-methylacyl-CoA dehydrogenase.	1.4.3.14	L-lysine oxidase.
1.3.99.13	Long-chain-acyl-CoA dehydrogenase.	1.4.3.15	D-glutamate(D-aspartate) oxidase.
1.3.99.14	Cyclohexanone dehydrogenase.	1.4.3.16	L-aspartate oxidase.
1.3.99.15	Benzoyl-CoA reductase.	1.4.3.19	Glycine oxidase.
1.3.99.16	Isoquinoline 1-oxidoreductase.	1.4.4.2	Glycine dehydrogenase (decarboxylating).
1.3.99.17	Quinoline 2-oxidoreductase.	1.4.7.1	Glutamate synthase (ferredoxin).
1.3.99.18	Quinaldate 4-oxidoreductase.	1.4.99.1	D-amino-acid dehydrogenase.
1.3.99.19	Quinoline-4-carboxylate 2-oxidoreductase.	1.4.99.2	Taurine dehydrogenase.
1.3.99.20	4-hydroxybenzoyl-CoA reductase.	1.4.99.3	Amine dehydrogenase.

1.3.99.21 (R)-benzylsuccinyl-CoA dehydrogenase.	1.4.99.4 Aalkylamine dehydrogenase.
1.4.1.1 Alanine dehydrogenase.	1.4.99.5 Glycine dehydrogenase (cyanide-forming).
1.4.1.2 Glutamate dehydrogenase.	1.5.1.1 Pyrroline-2-carboxylate reductase.
1.4.1.3 Glutamate dehydrogenase (NAD(P)+).	1.5.1.2 Pyrroline-5-carboxylate reductase.
1.4.1.4 Glutamate dehydrogenase (NADP+).	1.5.1.3 Dihydrofolate reductase.
1.4.1.5 L-amino-acid dehydrogenase.	1.5.1.5 Methylene-tetrahydrofolate dehydrogenase (NADP+).
1.4.1.7 Serine 2-dehydrogenase.	1.5.1.6 Formyltetrahydrofolate dehydrogenase.
1.4.1.8 Valine dehydrogenase (NADP+).	1.5.1.7 Saccharopine dehydrogenase (NAD+, L-lysine-forming).
1.4.1.9 Leucine dehydrogenase.	1.5.1.8 Saccharopine dehydrogenase (NADP+, L-lysine-forming).
1.4.1.10 Glycine dehydrogenase.	1.5.1.9 Saccharopine dehydrogenase (NAD+, L-glutamate-forming).
1.4.1.11 L-erythro-3,5-diaminohexanoate dehydrogenase.	1.5.1.10 Saccharopine dehydrogenase (NADP+, L-glutamate-forming).
1.4.1.12 2,4-diaminopentanoate dehydrogenase.	1.5.1.11 D-octopine dehydrogenase.
1.4.1.13 Glutamate synthase (NADPH).	1.5.1.12 1-pyrroline-5-carboxylate dehydrogenase.
1.4.1.14 Glutamate synthase (NADH).	1.5.1.15 Methylene-tetrahydrofolate dehydrogenase (NAD+).
1.4.1.15 Lysine dehydrogenase.	1.5.1.16 D-lysopine dehydrogenase.
1.4.1.16 Diaminopimelate dehydrogenase.	1.5.1.17 Alanopine dehydrogenase.
1.4.1.17 N-methylalanine dehydrogenase.	1.5.1.18 Ephedrine dehydrogenase.
1.4.1.18 Lysine 6-dehydrogenase.	1.5.1.19 D-nopaline dehydrogenase.
1.4.1.19 Tryptophan dehydrogenase.	1.5.1.20 Methylene-tetrahydrofolate reductase (NADPH).
1.4.1.20 Phenylalanine dehydrogenase.	1.5.1.21 Delta(1)-piperidine-2-carboxylate reductase.
1.4.2.1 Glycine dehydrogenase (cytochrome).	1.5.1.22 Strombine dehydrogenase.
1.4.3.1 D-aspartate oxidase.	1.5.1.23 Tauropine dehydrogenase.
1.4.3.2 L-amino-acid oxidase.	1.5.1.24 N(5)-(carboxyethyl)ornithine synthase.
1.4.3.3 D-amino-acid oxidase.	1.5.1.25 Thiomorpholine-carboxylate dehydrogenase.
1.4.3.4 Amine oxidase (flavin-containing).	1.5.1.26 Beta-alanopine dehydrogenase.

1.5.1.27 1,2-dehydroreticulium reductase (NADPH).	1.6.5.7 2-hydroxy-1,4-benzoquinone reductase.
1.5.1.28 Opine dehydrogenase.	1.6.6.9 Trimethylamine-N-oxide reductase.
1.5.1.29 FMN reductase.	1.6.99.1 NADPH dehydrogenase.
1.5.1.30 Flavin reductase.	1.6.99.2 NAD(P)H dehydrogenase (quinone).
1.5.1.31 Berberine reductase.	1.6.99.3 NADH dehydrogenase.
1.5.1.32 Vomilenine reductase.	1.6.99.5 NADH dehydrogenase (quinone).
1.5.1.33 Pteridine reductase.	1.6.99.6 NADPH dehydrogenase (quinone).
1.5.1.34 6,7-dihydropteridine reductase.	1.7.1.1 Nitrate reductase (NADH).
1.5.3.1 Sarcosine oxidase.	1.7.1.2 Nitrate reductase (NAD(P)H).
1.5.3.2 N-methyl-L-amino-acid oxidase.	1.7.1.3 Nitrate reductase (NADPH).
1.5.3.4 N(6)-methyl-lysine oxidase.	1.7.1.4 Nitrite reductase (NAD(P)H).
1.5.3.5 (S)-6-hydroxynicotine oxidase.	1.7.1.5 Hyponitrite reductase.
1.5.3.6 (R)-6-hydroxynicotine oxidase.	1.7.1.6 Azobenzene reductase.
1.5.3.7 L-pipecolate oxidase.	1.7.1.7 GMP reductase.
1.5.3.10 Dimethylglycine oxidase.	1.7.1.9 Nitroquinoline-N-oxide reductase.
1.5.3.11 Polyamine oxidase.	1.7.1.10 Hydroxylamine reductase (NADH).

1.5.3.12 Dihydrobenzophenanthridine oxidase.	1.7.1.11 4-(dimethylamino)phenylazoxybenzene reductase.
1.5.4.1 Pyrimidodiazepine synthase.	1.7.1.12 N-hydroxy-2-acetamidofluorene reductase.
1.5.5.1 Electron-transferring-flavoprotein dehydrogenase.	1.7.2.1 Nitrite reductase (NO-forming).
1.5.8.1 Dimethylamine dehydrogenase.	1.7.2.2 Nitrite reductase (cytochrome; ammonia-forming).
1.5.8.2 Trimethylamine dehydrogenase.	1.7.2.3 Trimethylamine-N-oxide reductase (cytochrome c).
1.5.99.1 Sarcosine dehydrogenase.	1.7.3.1 Nitroethane oxidase.
1.5.99.2 Dimethylglycine dehydrogenase.	1.7.3.2 Acetylindoxyl oxidase.
1.5.99.3 L-pipecolate dehydrogenase.	1.7.3.3 Urate oxidase.
1.5.99.4 Nicotine dehydrogenase.	1.7.3.4 Hydroxylamine oxidase.
1.5.99.5 Methylglutamate dehydrogenase.	1.7.3.5 3-aci-nitropropanoate oxidase.
1.5.99.6 Spermidine dehydrogenase.	1.7.7.1 Ferredoxin-nitrite reductase.
1.5.99.8 Proline dehydrogenase.	1.7.7.2 Ferredoxin-nitrate reductase.
1.5.99.9 Methylenetetrahydromethanopterin dehydrogenase.	1.7.99.1 Hydroxylamine reductase.
1.5.99.11 5,10-methylenetetrahydromethanopterin reductase.	1.7.99.4 Nitrate reductase.
1.5.99.12 Cytokinin dehydrogenase.	1.7.99.5 5,10-methylenetetrahydrofolate reductase (FADH(2)).
1.6.1.1 NAD(P)(+) transhydrogenase (B-specific).	1.7.99.6 Nitrous-oxide reductase.
1.6.1.2 NAD(P)(+) transhydrogenase (AB-specific).	1.7.99.7 Nitric-oxide reductase.
1.6.2.2 Cytochrome-b5 reductase.	1.7.99.8 Hydroxylamine oxidoreductase.
1.6.2.4 NADPH--hemoprotein reductase.	1.8.1.2 Sulfite reductase (NADPH).
1.6.2.5 NADPH--cytochrome-c2 reductase.	1.8.1.3 Hypotaurine dehydrogenase.
1.6.2.6 Leghemoglobin reductase.	1.8.1.4 Dihydrolipoyl dehydrogenase.
1.6.3.1 NAD(P)H oxidase.	1.8.1.5 2-oxopropyl-CoM reductase (carboxylating).
1.6.5.3 NADH dehydrogenase (ubiquinone).	1.8.1.6 Cystine reductase.
1.6.5.4 Monodehydroascorbate reductase (NADH).	1.8.1.7 Glutathione-disulfide reductase.
1.6.5.5 NADPH:quinone reductase.	1.8.1.8 Protein-disulfide reductase.
1.6.5.6 p-benzoquinone reductase (NADPH).	1.8.1.9 Thioredoxin-disulfide reductase.

1.8.1.10 CoA-glutathione reductase.	1.11.1.3 Fatty-acid peroxidase.
1.8.1.11 Asparaguate reductase.	1.11.1.5 Cytochrome-c peroxidase.
1.8.1.12 Trypanothione-disulfide reductase.	1.11.1.6 Catalase.
1.8.1.13 Bis-gamma-glutamylcystine reductase.	1.11.1.7 Peroxidase.
1.8.1.14 CoA-disulfide reductase.	1.11.1.8 Iodide peroxidase.
1.8.1.15 Mycothione reductase.	1.11.1.9 Glutathione peroxidase.
1.8.2.1 Sulfite dehydrogenase.	1.11.1.10 Chloride peroxidase.
1.8.2.2 Thiosulfate dehydrogenase.	1.11.1.11 L-ascorbate peroxidase.
1.8.3.1 Sulfite oxidase.	1.11.1.12 Phospholipid-hydroperoxide glutathione peroxidase.
1.8.3.2 Thiol oxidase.	1.11.1.13 Manganese peroxidase.
1.8.3.3 Glutathione oxidase.	1.11.1.14 Diarylpropane peroxidase.
1.8.3.4 Methanethiol oxidase.	1.12.1.2 Hydrogen dehydrogenase.
1.8.3.5 Prenylcysteine oxidase.	1.12.1.3 Hydrogen dehydrogenase (NADP+).
1.8.4.1 Glutathione-homocystine transhydrogenase.	1.12.2.1 Cytochrome-c3 hydrogenase.
1.8.4.2 Protein-disulfide reductase	1.12.5.1 Hydrogen:quinone oxidoreductase.

(glutathione).	
1.8.4.3 Glutathione-CoA-glutathione transhydrogenase.	1.12.7.2 Ferredoxin hydrogenase.
1.8.4.4 Glutathione-cystine transhydrogenase.	1.12.98.1 Coenzyme F420 hydrogenase.
1.8.4.5 Methionine-S-oxide reductase.	1.12.98.2 5,10-methenyltetrahydromethanopterin hydrogenase.
1.8.4.6 Protein-methionine-S-oxide reductase.	1.12.98.3 Methanosarcina-phenazine hydrogenase.
1.8.4.7 Enzyme-thiol transhydrogenase (glutathione-disulfide).	1.12.99.6 Hydrogenase (acceptor).
1.8.4.8 Phosphoadenylyl-sulfate reductase (thioredoxin).	1.13.11.1 Catechol 1,2-dioxygenase.
1.8.4.9 Adenylyl-sulfate reductase (glutathione).	1.13.11.2 Catechol 2,3-dioxygenase.
1.8.4.10 Adenylyl-sulfate reductase (thioredoxin).	1.13.11.3 Protocatechuate 3,4-dioxygenase.
1.8.5.1 Glutathione dehydrogenase (ascorbate).	1.13.11.4 Gentisate 1,2-dioxygenase.
1.8.7.1 Sulfite reductase (ferredoxin).	1.13.11.5 Homogentisate 1,2-dioxygenase.
1.8.98.1 CoB-CoM heterodisulfide reductase.	1.13.11.6 3-hydroxyanthranilate 3,4-dioxygenase.
1.8.99.1 Sulfite reductase.	1.13.11.8 Protocatechuate 4,5-dioxygenase.
1.8.99.2 Adenylyl-sulfate reductase.	1.13.11.9 2,5-dihydropyridine 5,6-dioxygenase.
1.8.99.3 Hydrogensulfite reductase.	1.13.11.10 7,8-dihydroxykynurenate 8,8a-dioxygenase.
1.9.3.1 Cytochrome-c oxidase.	1.13.11.11 Tryptophan 2,3-dioxygenase.
1.9.6.1 Nitrate reductase (cytochrome).	1.13.11.12 Lipoygenase.
1.9.99.1 Iron-cytochrome-c reductase.	1.13.11.13 Ascorbate 2,3-dioxygenase.
1.10.1.1 Trans-acenaphthene-1,2-diol dehydrogenase.	1.13.11.14 2,3-dihydroxybenzoate 3,4-dioxygenase.
1.10.2.1 L-ascorbate-cytochrome-b5 reductase.	1.13.11.15 3,4-dihydroxyphenylacetate 2,3-dioxygenase.
1.10.2.2 Ubiquinol-cytochrome-c reductase.	1.13.11.16 3-carboxyethylcatechol 2,3-dioxygenase.
1.10.3.1 Catechol oxidase.	1.13.11.17 Indole 2,3-dioxygenase.
1.10.3.2 Laccase.	1.13.11.18 Sulfur dioxygenase.
1.10.3.3 L-ascorbate oxidase.	1.13.11.19 Cysteamine dioxygenase.
1.10.3.4 O-aminophenol oxidase.	1.13.11.20 Cysteine dioxygenase.
1.10.3.5 3-hydroxyanthranilate oxidase.	1.13.11.22 Caffeate 3,4-dioxygenase.
1.10.3.6 Rifamycin-B oxidase.	1.13.11.23 2,3-dihydroxyindole 2,3-dioxygenase.
1.10.99.1 Plastoquinol-plastocyanin reductase.	1.13.11.24 Quercetin 2,3-dioxygenase.
1.11.1.1 NADH peroxidase.	1.13.11.25 3,4-dihydroxy-9,10-secoandrosta-1,3,5(10)-triene-9,17-dione 4,5-dioxygenase.
1.11.1.2 NADPH peroxidase.	1.13.11.26 Peptide-tryptophan 2,3-dioxygenase.

1.13.11.27 4-hydroxyphenylpyruvate dioxygenase.	1.14.11.4 Procollagen-lysine 5-dioxygenase.
1.13.11.28 2,3-dihydroxybenzoate 2,3-dioxygenase.	1.14.11.6 Thymine dioxygenase.
1.13.11.29 Stizolobate synthase.	1.14.11.7 Procollagen-proline 3-dioxygenase.
1.13.11.30 Stizolobinate synthase.	1.14.11.8 Trimethyllysine dioxygenase.
1.13.11.31 Arachidonate 12-lipoxygenase.	1.14.11.9 Naringenin 3-dioxygenase.
1.13.11.32 2-nitropropane dioxygenase.	1.14.11.10 Pyrimidine-deoxynucleoside 1'-dioxygenase.
1.13.11.33 Arachidonate 15-lipoxygenase.	1.14.11.11 Hyoscyamine (6S)-dioxygenase.
1.13.11.34 Arachidonate 5-lipoxygenase.	1.14.11.12 Gibberellin-44 dioxygenase.
1.13.11.35 Pyrogallol 1,2-oxygenase.	1.14.11.13 Gibberellin 2-beta-dioxygenase.
1.13.11.36 Chloridazon-catechol dioxygenase.	1.14.11.14 6-beta-hydroxyhyoscyamine epoxidase.
1.13.11.37 Hydroxyquinol 1,2-dioxygenase.	1.14.11.15 Gibberellin 3-beta-dioxygenase.

1.13.11.38 1-hydroxy-2-naphthoate 1,2-dioxygenase.	1.14.11.16 Peptide-aspartate beta-dioxygenase.
1.13.11.39 Biphenyl-2,3-diol 1,2-dioxygenase.	1.14.11.17 Taurine dioxygenase.
1.13.11.40 Arachidonate 8-lipoxygenase.	1.14.11.18 Phytanoyl-CoA dioxygenase.
1.13.11.41 2,4'-dihydroxyacetophenone dioxygenase.	1.14.11.19 Leucocyanidin oxygenase.
1.13.11.42 Indoleamine-pyrrole 2,3-dioxygenase.	1.14.11.20 Desacetoxyvindoline 4-hydroxylase.
1.13.11.43 Lignostilbene alpha-beta-dioxygenase.	1.14.11.21 Clavamate synthase.
1.13.11.44 Linoleate diol synthase.	1.14.12.1 Anthranilate 1,2-dioxygenase (deaminating, decarboxylating).
1.13.11.45 Linoleate 11-lipoxygenase.	1.14.12.3 Benzene 1,2-dioxygenase.
1.13.11.46 4-hydroxymandelate synthase.	1.14.12.4 3-hydroxy-2-methylpyridinecarboxylate dioxygenase.
1.13.11.47 3-hydroxy-4-oxoquinoline 2,4-dioxygenase.	1.14.12.5 5-pyridoxate dioxygenase.
1.13.11.48 3-hydroxy-2-methylquinolin-4-one 2,4-dioxygenase.	1.14.12.7 Phthalate 4,5-dioxygenase.
1.13.11.49 Chlorite O(2)-lyase.	1.14.12.8 4-sulfobenzoate 3,4-dioxygenase.
1.13.11.50 Acetylacetone-cleaving enzyme.	1.14.12.9 4-chlorophenylacetate 3,4-dioxygenase.
1.13.12.1 Arginine 2-monooxygenase.	1.14.12.10 Benzoate 1,2-dioxygenase.
1.13.12.2 Lysine 2-monooxygenase.	1.14.12.11 Toluene dioxygenase.
1.13.12.3 Tryptophan 2-monooxygenase.	1.14.12.12 Naphthalene 1,2-dioxygenase.
1.13.12.4 Lactate 2-monooxygenase.	1.14.12.13 2-chlorobenzoate 1,2-dioxygenase.
1.13.12.5 Renilla-luciferin 2-monooxygenase.	1.14.12.14 2-aminobenzenesulfonate 2,3-dioxygenase.
1.13.12.6 Cypridina-luciferin 2-monooxygenase.	1.14.12.15 Terephthalate 1,2-dioxygenase.
1.13.12.7 Photinus-luciferin 4-monooxygenase (ATP-hydrolyzing).	1.14.12.16 2-hydroxyquinoline 5,6-dioxygenase.
1.13.12.8 Watasenia-luciferin 2-monooxygenase.	1.14.12.17 Nitric oxide dioxygenase.
1.13.12.9 Phenylalanine 2-monooxygenase.	1.14.12.18 Biphenyl 2,3-dioxygenase.
1.13.12.11 Methylphenyltetrahydropyridine N-monooxygenase.	1.14.13.1 Salicylate 1-monooxygenase.
1.13.12.12 Apo-beta-carotenoid-14',13'-dioxygenase.	1.14.13.2 4-hydroxybenzoate 3-monooxygenase.
1.13.12.13 Oplophorus-luciferin 2-monooxygenase.	1.14.13.3 4-hydroxyphenylacetate 3-monooxygenase.
1.13.99.1 Inositol oxygenase.	1.14.13.4 Melilotate 3-monooxygenase.
1.13.99.3 Tryptophan 2'-dioxygenase.	1.14.13.5 Imidazoleacetate 4-monooxygenase.
1.14.11.1 Gamma-butyrobetaine dioxygenase.	1.14.13.6 Orcinol 2-monooxygenase.
1.14.11.2 Procollagen-proline dioxygenase.	1.14.13.7 Phenol 2-monooxygenase.
1.14.11.3 Pyrimidine-deoxynucleoside 2'-dioxygenase.	1.14.13.8 Dimethylaniline monooxygenase (N-oxide-forming).

1.14.16.4 Tryptophan 5-monooxygenase.	1.14.99.33 Delta(12)-fatty acid dehydrogenase.
1.14.16.5 Glyceryl-ether monooxygenase.	1.14.99.34 Monoprenyl isoflavone epoxidase.
1.14.16.6 Mandelate 4-monooxygenase.	1.14.99.35 Thiophene-2-carbonyl-CoA monooxygenase.
1.14.17.1 Dopamine beta-monooxygenase.	1.14.99.36 Beta-carotene 15,15'-monooxygenase.
1.14.17.3 Peptidylglycine monooxygenase.	1.14.99.37 Taxadiene 5-alpha-hydroxylase.
1.14.17.4 Aminocyclopropanecarboxylate oxidase.	1.15.1.1 Superoxide dismutase.
1.14.18.1 Monophenol monooxygenase.	1.15.1.2 Superoxide reductase.

1.14.18.2	CMP-N-acetylneuraminate monooxygenase.	1.16.1.1	Mercury(II) reductase.
1.14.19.1	Stearoyl-CoA 9-desaturase.	1.16.1.2	Diferriic-transferrin reductase.
1.14.19.2	Acyl-[acyl-carrier-protein] desaturase.	1.16.1.3	Aquacobalamin reductase.
1.14.19.3	Linoleoyl-CoA desaturase.	1.16.1.4	Cob(II)alamin reductase.
1.14.20.1	Deacetoxycephalosporin-C synthase.	1.16.1.5	Aquacobalamin reductase (NADPH).
1.14.21.1	(S)-stylopine synthase.	1.16.1.6	Cyanocobalamin reductase (cyanide-eliminating).
1.14.21.2	(S)-cheilanthifoline synthase.	1.16.1.7	Ferric-chelate reductase.
1.14.21.3	Berbamunine synthase.	1.16.1.8	[Methionine synthase] reductase.
1.14.21.4	Salutaridine synthase.	1.16.3.1	Ferroxidase.
1.14.21.5	(S)-canadine synthase.	1.16.8.1	Cob(II)yrinic acid a,c-diamide reductase.
1.14.99.1	Prostaglandin-endoperoxide synthase.	1.17.1.1	CDP-4-dehydro-6-deoxyglucose reductase.
1.14.99.2	Kynurenine 7,8-hydroxylase.	1.17.1.2	4-hydroxy-3-methylbut-2-enyl diphosphate reductase.
1.14.99.3	Heme oxygenase (decyclizing).	1.17.1.3	Leucoanthocyanidin reductase.
1.14.99.4	Progesterone monooxygenase.	1.17.1.4	Xanthine dehydrogenase.
1.14.99.7	Squalene monooxygenase.	1.17.1.5	Nicotinate dehydrogenase.
1.14.99.9	Steroid 17-alpha-monooxygenase.	1.17.3.1	Pteridine oxidase.
1.14.99.10	Steroid 21-monooxygenase.	1.17.3.2	Xanthine oxidase.
1.14.99.11	Estradiol 6-beta-monooxygenase.	1.17.3.3	6-hydroxynicotinate dehydrogenase.
1.14.99.12	Androst-4-ene-3,17-dione monooxygenase.	1.17.4.1	Ribonucleoside-diphosphate reductase.
1.14.99.14	Progesterone 11-alpha-monooxygenase.	1.17.4.2	Ribonucleoside-triphosphate reductase.
1.14.99.15	4-methoxybenzoate monooxygenase (O-demethylating).	1.17.4.3	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase.
1.14.99.19	Plasmanyethanolamine desaturase.	1.17.5.1	Phenylacetyl-CoA dehydrogenase.
1.14.99.20	Phylloquinone monooxygenase (2,3-epoxidizing).	1.17.99.1	4-cresol dehydrogenase (hydroxylating).
1.14.99.21	Latia-luciferin monooxygenase (demethylating).	1.17.99.2	Ethylbenzene hydroxylase.
1.14.99.22	Ecdysone 20-monooxygenase.	1.18.1.1	Rubredoxin--NAD(+) reductase.
1.14.99.23	3-hydroxybenzoate 2-monooxygenase.	1.18.1.2	Ferredoxin--NADP(+) reductase.
1.14.99.24	Steroid 9-alpha-monooxygenase.	1.18.1.3	Ferredoxin--NAD(+) reductase.
1.14.99.26	2-hydroxypyridine 5-monooxygenase.	1.18.1.4	Rubredoxin--NAD(P)(+) reductase.
1.14.99.27	Juglone 3-monooxygenase.	1.18.6.1	Nitrogenase.
1.14.99.28	Linalool 8-monooxygenase.	1.19.6.1	Nitrogenase (flavodoxin).
1.14.99.29	Deoxyhypusine monooxygenase.	1.20.1.1	Phosphonate dehydrogenase.
1.14.99.30	Carotene 7,8-desaturase.	1.20.4.1	Arsenate reductase (glutaredoxin).
1.14.99.31	Myristoyl-CoA 11-(E) desaturase.	1.20.4.2	Methylarsonate reductase.
1.14.99.32	Myristoyl-CoA 11-(Z) desaturase.	1.20.98.1	Arsenate reductase (azurin).

1.20.99.1	Arsenate reductase (donor).	2.1.1.15	Fatty-acid O-methyltransferase.
1.21.3.1	Isopenicillin-N synthase.	2.1.1.16	Methylene-fatty-acyl-phospholipid synthase.
1.21.3.2	Columbamine oxidase.	2.1.1.17	Phosphatidylethanolamine N-methyltransferase.
1.21.3.3	Reticuline oxidase.	2.1.1.18	Polysaccharide O-methyltransferase.

1.21.3.4	Sulochrin oxidase ((+)-bisdechlorogeodin-forming).	2.1.1.19	Trimethylsulfonium-tetrahydrofolate N-methyltransferase.
1.21.3.5	Sulochrin oxidase ((-)-bisdechlorogeodin-forming).	2.1.1.20	Glycine N-methyltransferase.
1.21.3.6	Aureusidin synthase.	2.1.1.21	Methylamine-glutamate N-methyltransferase.
1.21.4.1	D-proline reductase (dithiol).	2.1.1.22	Carnosine N-methyltransferase.
1.21.4.2	Glycine reductase.	2.1.1.25	Phenol O-methyltransferase.
1.21.4.3	Sarcosine reductase.	2.1.1.26	Iodophenol O-methyltransferase.
1.21.4.4	Betaine reductase.	2.1.1.27	Tyramine N-methyltransferase.
1.21.99.1	Beta-cyclopiazonate dehydrogenase.	2.1.1.28	Phenylethanolamine N-methyltransferase.
1.97.1.1	Chlorate reductase.	2.1.1.29	tRNA (cytosine-5-)-methyltransferase.
1.97.1.2	Pyrogallol hydroxytransferase.	2.1.1.31	tRNA (guanine-N(1)-)-methyltransferase.
1.97.1.3	Sulfur reductase.	2.1.1.32	tRNA (guanine-N(2)-)-methyltransferase.
1.97.1.4	[Formate acetyltransferase] activating enzyme.	2.1.1.33	tRNA (guanine-N(7)-)-methyltransferase.
1.97.1.8	Tetrachloroethene reductive dehalogenase.	2.1.1.34	tRNA (guanosine-2'-O-)-methyltransferase.
1.97.1.9	Selenate reductase.	2.1.1.35	tRNA (uracil-5-)-methyltransferase.
1.97.1.10	Thyroxine 5'-deiodinase.	2.1.1.36	tRNA (adenine-N(1)-)-methyltransferase.
1.97.1.11	Thyroxine 5-deiodinase.	2.1.1.37	DNA (cytosine-5-)-methyltransferase.
		2.1.1.38	O-demethylpuromycin O-methyltransferase.
ENZYME: 2.-.-		2.1.1.39	Inositol 3-methyltransferase.
2.1.1.1	Nicotinamide N-methyltransferase.	2.1.1.40	Inositol 1-methyltransferase.
2.1.1.2	Guanidinoacetate N-methyltransferase.	2.1.1.41	Sterol 24-C-methyltransferase.
2.1.1.3	Thetin-homocysteine S-methyltransferase.	2.1.1.42	Luteolin O-methyltransferase.
2.1.1.4	Acetylserotonin O-methyltransferase.	2.1.1.43	Histone-lysine N-methyltransferase.
2.1.1.5	Betaine-homocysteine S-methyltransferase.	2.1.1.44	Dimethylhistidine N-methyltransferase.
2.1.1.6	Catechol O-methyltransferase.	2.1.1.45	Thymidylate synthase.
2.1.1.7	Nicotinate N-methyltransferase.	2.1.1.46	Isoflavone 4'-O-methyltransferase.
2.1.1.8	Histamine N-methyltransferase.	2.1.1.47	Indolepyruvate C-methyltransferase.
2.1.1.9	Thiol S-methyltransferase.	2.1.1.48	rRNA (adenine-N(6)-)-methyltransferase.
2.1.1.10	Homocysteine S-methyltransferase.	2.1.1.49	Amine N-methyltransferase.
2.1.1.11	Magnesium protoporphyrin IX methyltransferase.	2.1.1.50	Loganate O-methyltransferase.
2.1.1.12	Methionine S-methyltransferase.	2.1.1.51	rRNA (guanine-N(1)-)-methyltransferase.
2.1.1.13	Methionine synthase.	2.1.1.52	rRNA (guanine-N(2)-)-methyltransferase.
2.1.1.14	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase.	2.1.1.53	Putrescine N-methyltransferase.
2.1.1.54	Deoxycytidylate C-methyltransferase.	2.1.1.86	Tetrahydromethanopterin S-methyltransferase.

2.1.1.55 tRNA (adenine-N(6)-)-methyltransferase.	2.1.1.87 Pyridine N-methyltransferase.
2.1.1.56 mRNA (guanine-N(7)-)-methyltransferase.	2.1.1.88 8-hydroxyquercetin 8-O-methyltransferase.
2.1.1.57 mRNA (nucleoside-2'-O)-methyltransferase.	2.1.1.89 Tetrahydrocolumbamine 2-O-methyltransferase.
2.1.1.59 [Cytochrome c]-lysine N-methyltransferase.	2.1.1.90 Methanol--5-hydroxybenzimidazolylcobamide Co-methyltransferase.
2.1.1.60 Calmodulin-lysine N-methyltransferase.	2.1.1.91 Isobutyraldoxime O-methyltransferase.
2.1.1.61 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase.	2.1.1.92 Bergaptol O-methyltransferase.
2.1.1.62 mRNA (2'-O-methyladenosine-N(6)-)-methyltransferase.	2.1.1.93 Xanthoxol O-methyltransferase.
2.1.1.63 Methylated-DNA--[protein]-cysteine S-methyltransferase.	2.1.1.94 11-O-demethyl-17-O-deacetylindoline O-methyltransferase.
2.1.1.64 3-demethylubiquinone-9 3-O-methyltransferase.	2.1.1.95 Tocopherol O-methyltransferase.
2.1.1.65 Licodione 2'-O-methyltransferase.	2.1.1.96 Thioether S-methyltransferase.
2.1.1.66 rRNA (adenosine-2'-O)-methyltransferase.	2.1.1.97 3-hydroxyanthranilate 4-C-methyltransferase.
2.1.1.67 Thiopurine S-methyltransferase.	2.1.1.98 Diphtine synthase.
2.1.1.68 Caffeate O-methyltransferase.	2.1.1.99 16-methoxy-2,3-dihydro-3-hydroxytabersonine N-methyltransferase.
2.1.1.69 5-hydroxyfuranocoumarin 5-O-methyltransferase.	2.1.1.100 Protein-S-isoprenylcysteine O-methyltransferase.
2.1.1.70 8-hydroxyfuranocoumarin 8-O-methyltransferase.	2.1.1.101 Macrocin O-methyltransferase.
2.1.1.71 Phosphatidyl-N-methylethanolamine N-methyltransferase.	2.1.1.102 Demethylmacrocin O-methyltransferase.
2.1.1.72 Site-specific DNA-methyltransferase (adenine-specific).	2.1.1.103 Phosphoethanolamine N-methyltransferase.
2.1.1.74 Methylenetetrahydrofolate-tRNA-(uracil-5-)-methyltransferase (FADH(2)-oxidizing).	2.1.1.104 Caffeoyl-CoA O-methyltransferase.
2.1.1.75 Apigenin 4'-O-methyltransferase.	2.1.1.105 N-benzoyl-4-hydroxyanthranilate 4-O-methyltransferase.
2.1.1.76 Quercetin 3-O-methyltransferase.	2.1.1.106 Tryptophan 2-C-methyltransferase.
2.1.1.77 Protein-L-isoaspartate(D-aspartate) O-methyltransferase.	2.1.1.107 Uroporphyrin-III C-methyltransferase.
2.1.1.78 Isoorientin 3'-O-methyltransferase.	2.1.1.108 6-hydroxymellein O-methyltransferase.
2.1.1.79 Cyclopropane-fatty-acyl-phospholipid synthase.	2.1.1.109 Demethylsterigmatocystin 6-O-methyltransferase.
2.1.1.80 Protein-glutamate O-methyltransferase.	2.1.1.110 Sterigmatocystin 7-O-methyltransferase.
2.1.1.82 3-methylquercetin 7-O-methyltransferase.	2.1.1.111 Anthranilate N-methyltransferase.
2.1.1.83 3,7-dimethylquercetin 4'-O-methyltransferase.	2.1.1.112 Glucuronoxylan 4-O-methyltransferase.
2.1.1.84 Methylquercetagenin 6-O-methyltransferase.	2.1.1.113 Site-specific DNA-methyltransferase (cytosine-N(4)-specific).
2.1.1.85 Protein-histidine N-methyltransferase.	2.1.1.114 Hexaprenyldihydroxybenzoate methyltransferase.

2.1.1.115 (RS)-1-benzyl-1,2,3,4-tetrahydroisoquinoline N-methyltransferase.

2.1.2.1 Glycine hydroxymethyltransferase.

2.1.1.116 3'-hydroxy-N-methyl-(S)-coclaurine 4'-O-methyltransferase.	2.1.2.2 Phosphoribosylglycinamide formyltransferase.
2.1.1.117 (S)-scoulerine 9-O-methyltransferase.	2.1.2.3 Phosphoribosylaminoimidazolecarboxamide formyltransferase.
2.1.1.118 Columbamine O-methyltransferase.	2.1.2.4 Glycine formimidoyltransferase.
2.1.1.119 10-hydroxydihydrosanguinarine 10-O-methyltransferase.	2.1.2.5 Glutamate formimidoyltransferase.
2.1.1.120 12-hydroxydihydrochelirubine 12-O-methyltransferase.	2.1.2.7 D-alanine 2-hydroxymethyltransferase.
2.1.1.121 6-O-methylnorlaudanosoline 5'-O-methyltransferase.	2.1.2.8 Deoxycytidylate 5-hydroxymethyltransferase.
2.1.1.122 (S)-tetrahydroprotoberberine N-methyltransferase.	2.1.2.9 Methionyl-tRNA formyltransferase.
2.1.1.123 [Cytochrome-c]-methionine S-methyltransferase.	2.1.2.10 Aminomethyltransferase.
2.1.1.124 [Cytochrome-c]-arginine N-methyltransferase.	2.1.2.11 3-methyl-2-oxobutanoate hydroxymethyltransferase.
2.1.1.125 Histone-arginine N-methyltransferase.	2.1.3.1 Methylmalonyl-CoA carboxytransferase.
2.1.1.126 [Myelin basic protein]-arginine N-methyltransferase.	2.1.3.2 Aspartate carbamoyltransferase.
2.1.1.127 [Ribulose-bisphosphate carboxylase]-lysine N-methyltransferase.	2.1.3.3 Ornithine carbamoyltransferase.
2.1.1.128 (RS)-norcoclaurine 6-O-methyltransferase.	2.1.3.5 Oxamate carbamoyltransferase.
2.1.1.129 Inositol 4-methyltransferase.	2.1.3.6 Putrescine carbamoyltransferase.
2.1.1.130 Precorrin-2 C(20)-methyltransferase.	2.1.3.7 3-hydroxymethylcephem carbamoyltransferase.
2.1.1.131 Precorrin-3B C(17)-methyltransferase.	2.1.3.8 Lysine carbamoyltransferase.
2.1.1.132 Precorrin-6Y C(5,15)-methyltransferase (decarboxylating).	2.1.4.1 Glycine amidinotransferase.
2.1.1.133 Precorrin-4 C(11)-methyltransferase.	2.1.4.2 Scyllo-inosamine 4-phosphate amidinotransferase.
2.1.1.136 Chlorophenol O-methyltransferase.	2.2.1.1 Transketolase.
2.1.1.137 Arsenite methyltransferase.	2.2.1.2 Transaldolase.
2.1.1.139 3'-demethylstaurosporine O-methyltransferase.	2.2.1.3 Formaldehyde transketolase.
2.1.1.140 (S)-coclaurine-N-methyltransferase.	2.2.1.4 Acetoin-ribose-5-phosphate transaldolase.
2.1.1.141 Jasmonate O-methyltransferase.	2.2.1.5 2-hydroxy-3-oxoadipate synthase.
2.1.1.142 Cycloartenol 24-C-methyltransferase.	2.2.1.6 Acetolactate synthase.
2.1.1.143 24-methylenesterol C-methyltransferase.	2.2.1.7 1-deoxy-D-xylulose-5-phosphate synthase.
2.1.1.144 Trans-aconitate 2-methyltransferase.	2.2.1.8 Fluorothreonine transaldolase.
2.1.1.145 Trans-aconitate 3-methyltransferase.	2.3.1.1 Amino-acid N-acetyltransferase.
2.1.1.146 (Iso)eugenol O-methyltransferase.	2.3.1.2 Imidazole N-acetyltransferase.
2.1.1.147 Corydaline synthase.	2.3.1.3 Glucosamine N-acetyltransferase.
2.1.1.148 Thymidylate synthase (FAD).	2.3.1.4 Glucosamine 6-phosphate N-acetyltransferase.
2.1.1.149 Myricetin O-methyltransferase.	2.3.1.5 Arylamine N-acetyltransferase.
2.1.1.150 Isoflavone 7-O-methyltransferase.	2.3.1.6 Choline O-acetyltransferase.
2.1.1.151 Cobalt-factor II C(20)-methyltransferase.	2.3.1.7 Carnitine O-acetyltransferase.
2.1.1.152 Precorrin-6A synthase (deacetylating).	2.3.1.8 Phosphate acetyltransferase.
2.3.1.9 Acetyl-CoA C-acetyltransferase.	2.3.1.48 Histone acetyltransferase.

2.3.1.10 Hydrogen-sulfide S-acetyltransferase.	2.3.1.49 Deacetyl-[citrate-(pro-3S)-lyase] S-acetyltransferase.
2.3.1.11 Thioethanolamine S-acetyltransferase.	2.3.1.50 Serine C-palmitoyltransferase.
2.3.1.12 Dihydrolipoyllysine-residue acetyltransferase.	2.3.1.51 1-acylglycerol-3-phosphate O-acyltransferase.
2.3.1.13 Glycine N-acyltransferase.	2.3.1.52 2-acylglycerol-3-phosphate O-acyltransferase.
2.3.1.14 Glutamine N-phenylacetyltransferase.	2.3.1.53 Phenylalanine N-acetyltransferase.
2.3.1.15 Glycerol-3-phosphate O-acyltransferase.	2.3.1.54 Formate C-acetyltransferase.
2.3.1.16 Acetyl-CoA C-acyltransferase.	2.3.1.56 Aromatic-hydroxylamine O-acetyltransferase.
2.3.1.17 Aspartate N-acetyltransferase.	2.3.1.57 Diamine N-acetyltransferase.
2.3.1.18 Galactoside O-acetyltransferase.	2.3.1.58 2,3-diaminopropionate N-oxalyltransferase.
2.3.1.19 Phosphate butyryltransferase.	2.3.1.59 Gentamicin 2'-N-acetyltransferase.
2.3.1.20 Diacylglycerol O-acyltransferase.	2.3.1.60 Gentamicin 3'-N-acetyltransferase.
2.3.1.21 Carnitine O-palmitoyltransferase.	2.3.1.61 Dihydrolipoyllysine-residue succinyltransferase.
2.3.1.22 2-acylglycerol O-acyltransferase.	2.3.1.62 2-acylglycerophosphocholine O-acyltransferase.
2.3.1.23 1-acylglycerophosphocholine O-acyltransferase.	2.3.1.63 1-alkylglycerophosphocholine O-acyltransferase.
2.3.1.24 Sphingosine N-acyltransferase.	2.3.1.64 Agmatine N(4)-coumaroyltransferase.
2.3.1.25 Plasmalogen synthase.	2.3.1.65 Glycine N-choloyltransferase.
2.3.1.26 Sterol O-acyltransferase.	2.3.1.66 Leucine N-acetyltransferase.
2.3.1.27 Cortisol O-acetyltransferase.	2.3.1.67 1-alkylglycerophosphocholine O-acetyltransferase.
2.3.1.28 Chloramphenicol O-acetyltransferase.	2.3.1.68 Glutamine N-acyltransferase.
2.3.1.29 Glycine C-acetyltransferase.	2.3.1.69 Monoterpenol O-acetyltransferase.
2.3.1.30 Serine O-acetyltransferase.	2.3.1.70 CDP-acylglycerol O-arachidonoyltransferase.
2.3.1.31 Homoserine O-acetyltransferase.	2.3.1.71 Glycine N-benzoyltransferase.
2.3.1.32 Lysine N-acetyltransferase.	2.3.1.72 Indoleacetylglucose-inositol O-acyltransferase.
2.3.1.33 Histidine N-acetyltransferase.	2.3.1.73 Diacylglycerol--sterol O-acyltransferase.
2.3.1.34 D-tryptophan N-acetyltransferase.	2.3.1.74 Naringenin-chalcone synthase.
2.3.1.35 Glutamate N-acetyltransferase.	2.3.1.75 Long-chain-alcohol O-fatty-acyltransferase.
2.3.1.36 D-amino-acid N-acetyltransferase.	2.3.1.76 Retinol O-fatty-acyltransferase.
2.3.1.37 5-aminolevulinate synthase.	2.3.1.77 Triacylglycerol--sterol O-acyltransferase.
2.3.1.38 [Acyl-carrier-protein] S-acetyltransferase.	2.3.1.78 Heparan-alpha-glucosaminide N-acetyltransferase.
2.3.1.39 [Acyl-carrier-protein] S-malonyltransferase.	2.3.1.79 Maltose O-acetyltransferase.
2.3.1.40 Acyl-[acyl-carrier-protein]--phospholipid O-acyltransferase.	2.3.1.80 Cysteine-S-conjugate N-acetyltransferase.
2.3.1.41 3-oxoacyl-[acyl-carrier-protein] synthase.	2.3.1.81 Aminoglycoside N(3')-acetyltransferase.
2.3.1.42 Glycerone-phosphate O-acyltransferase.	2.3.1.82 Aminoglycoside N(6')-acetyltransferase.
2.3.1.43 Phosphatidylcholine--sterol O-acyltransferase.	2.3.1.83 Phosphatidylcholine--dolichol O-acyltransferase.
2.3.1.44 N-acetylneuraminate 4-O-acetyltransferase.	2.3.1.84 Alcohol O-acetyltransferase.
2.3.1.45 N-acetylneuraminate 7-O(or 9-O)-	2.3.1.85 Fatty-acid synthase.

acetyltransferase.	
2.3.1.46 Homoserine O-succinyltransferase.	2.3.1.86 Fatty-acyl-CoA synthase.
2.3.1.47 8-amino-7-oxononanoate synthase.	2.3.1.87 Aralkylamine N-acetyltransferase.
2.3.1.88 Peptide alpha-N-acetyltransferase.	2.3.1.122 Trehalose O-mycosyltransferase.
2.3.1.89 Tetrahydrodipicolinate N-acetyltransferase.	2.3.1.123 Dolichol O-acyltransferase.
2.3.1.90 Beta-glucogallin O-galloyltransferase.	2.3.1.125 1-alkyl-2-acetyl glycerol O-acyltransferase.
2.3.1.91 Sinapoylglucose--choline O-sinapoyltransferase.	2.3.1.126 Isocitrate O-dihydroxycinnamoyltransferase.
2.3.1.92 Sinapoylglucose--malate O-sinapoyltransferase.	2.3.1.127 Ornithine N-benzoyltransferase.
2.3.1.93 13-hydroxylupinine O-tigloyltransferase.	2.3.1.128 Ribosomal-protein-alanine N-acetyltransferase.
2.3.1.94 Erythronolide synthase.	2.3.1.129 Acyl-[acyl-carrier-protein]--UDP-N-acetylglucosamine O-acyltransferase.
2.3.1.95 Trihydroxystilbene synthase.	2.3.1.130 Galactarate O-hydroxycinnamoyltransferase.
2.3.1.96 Glycoprotein N-palmitoyltransferase.	2.3.1.131 Glucarate O-hydroxycinnamoyltransferase.
2.3.1.97 Glycylpeptide N-tetradecanoyltransferase.	2.3.1.132 Glucarolactone O-hydroxycinnamoyltransferase.
2.3.1.98 Chlorogenate--glucarate O-hydroxycinnamoyltransferase.	2.3.1.133 Shikimate O-hydroxycinnamoyltransferase.
2.3.1.99 Quinate O-hydroxycinnamoyltransferase.	2.3.1.134 Galactolipid O-acyltransferase.
2.3.1.100 Myelin-proteolipid O-palmitoyltransferase.	2.3.1.135 Phosphatidylcholine--retinol O-acyltransferase.
2.3.1.101 Formylmethanofuran--tetrahydromethanopterin N-formyltransferase.	2.3.1.136 Polysialic-acid O-acetyltransferase.
2.3.1.102 N(6)-hydroxyllysine O-acetyltransferase.	2.3.1.137 Carnitine O-octanoyltransferase.
2.3.1.103 Sinapoylglucose--sinapoylglucose O-sinapoyltransferase.	2.3.1.138 Putrescine N-hydroxycinnamoyltransferase.
2.3.1.104 1-alkenylglycerophosphocholine O-acyltransferase.	2.3.1.139 Ecdysone O-acyltransferase.
2.3.1.105 Alkylglycerophosphate 2-O-acetyltransferase.	2.3.1.140 Rosmarinate synthase.
2.3.1.106 Tartronate O-hydroxycinnamoyltransferase.	2.3.1.141 Galactosylacylglycerol O-acyltransferase.
2.3.1.107 17-O-deacetylindoline O-acetyltransferase.	2.3.1.142 Glycoprotein O-fatty-acyltransferase.
2.3.1.108 Tubulin N-acetyltransferase.	2.3.1.143 Beta-glucogallin--tetrakisgalloylglucose O-galloyltransferase.
2.3.1.109 Arginine N-succinyltransferase.	2.3.1.144 Anthranilate N-benzoyltransferase.
2.3.1.110 Tyramine N-feruloyltransferase.	2.3.1.145 Piperidine N-piperoyltransferase.
2.3.1.111 Mycocerosate synthase.	2.3.1.146 Pinosylvin synthase.
2.3.1.112 D-tryptophan N-malonyltransferase.	2.3.1.147 Glycerophospholipid arachidonoyltransferase (CoA-independent).
2.3.1.113 Anthranilate N-malonyltransferase.	2.3.1.148 Glycerophospholipid acyltransferase (CoA-dependent).
2.3.1.114 3,4-dichloroaniline N-malonyltransferase.	2.3.1.149 Platelet-activating factor acetyltransferase.
2.3.1.115 Isoflavone-7-O-beta-glucoside 6"-O-malonyltransferase.	2.3.1.150 Salutaridinol 7-O-acetyltransferase.
2.3.1.116 Flavonol-3-O-beta-glucoside O-malonyltransferase.	2.3.1.151 Benzophenone synthase.
2.3.1.117 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase.	2.3.1.152 Alcohol O-cinnamoyltransferase.
2.3.1.118 N-hydroxyarylamine O-acetyltransferase.	2.3.1.153 Anthocyanin 5-aromatic

	acyltransferase.
2.3.1.119 Icosanoyl-CoA synthase.	2.3.1.154 Propionyl-CoA C(2)-trimethyltridecanoyltransferase.
2.3.1.121 1-alkenylglycerophosphoethanolamine O-acyltransferase.	2.3.1.155 Acetyl-CoA C-myristoyltransferase.

2.3.1.156 Phloroisovalerophenone synthase.	2.3.3.12 3-propylmalate synthase.
2.3.1.157 Glucosamine-1-phosphate N-acetyltransferase.	2.3.3.13 2-isopropylmalate synthase.
2.3.1.158 Phospholipid:diacylglycerol acyltransferase.	2.3.3.14 Homocitrate synthase.
2.3.1.159 Acridone synthase.	2.3.3.15 Sulfoacetaldehyde acetyltransferase.
2.3.1.160 Vinorine synthase.	2.4.1.1 Phosphorylase.
2.3.1.161 Lovastatin nonaketide synthase.	2.4.1.2 Dextrin dextranase.
2.3.1.162 Taxadien-5- α -ol O-acetyltransferase.	2.4.1.4 Amylosucrase.
2.3.1.163 10-hydroxytaxane O-acetyltransferase.	2.4.1.5 Dextransucrase.
2.3.1.164 Isopenicillin-N N-acyltransferase.	2.4.1.7 Sucrose phosphorylase.
2.3.1.165 6-methylsalicylic acid synthase.	2.4.1.8 Maltose phosphorylase.
2.3.1.166 2- α -hydroxytaxane 2-O-benzoyltransferase.	2.4.1.9 Inulosucrase.
2.3.1.167 10-deacetylbaicatin III 10-O-acetyltransferase.	2.4.1.10 Levansucrase.
2.3.1.168 Dihydrolipoyllysine-residue (2-methylpropanoyl)transferase.	2.4.1.11 Glycogen (starch) synthase.
2.3.1.169 CO-methylating acetyl-CoA synthase.	2.4.1.12 Cellulose synthase (UDP-forming).
2.3.2.1 D-glutamyltransferase.	2.4.1.13 Sucrose synthase.
2.3.2.2 Gamma-glutamyltransferase.	2.4.1.14 Sucrose-phosphate synthase.
2.3.2.3 Lysyltransferase.	2.4.1.15 Alpha, alpha-trehalose-phosphate synthase (UDP-forming).
2.3.2.4 Gamma-glutamylcyclotransferase.	2.4.1.16 Chitin synthase.
2.3.2.5 Glutaminy-peptide cyclotransferase.	2.4.1.17 Glucuronosyltransferase.
2.3.2.6 Leucyltransferase.	2.4.1.18 1,4- α -glucan branching enzyme.
2.3.2.7 Aspartyltransferase.	2.4.1.19 Cyclomaltodextrin glucanotransferase.
2.3.2.8 Arginyltransferase.	2.4.1.20 Cellobiose phosphorylase.
2.3.2.9 Agaritine gamma-glutamyltransferase.	2.4.1.21 Starch synthase.
2.3.2.10 UDP-N-acetylmuramoylpentapeptide-lysine N(6)-alanyltransferase.	2.4.1.22 Lactose synthase.
2.3.2.11 Alanylphosphatidylglycerol synthase.	2.4.1.23 Sphingosine beta-galactosyltransferase.
2.3.2.12 Peptidyltransferase.	2.4.1.24 1,4- α -glucan 6- α -glucosyltransferase.
2.3.2.13 Protein-glutamine gamma-glutamyltransferase.	2.4.1.25 4- α -glucanotransferase.
2.3.2.14 D-alanine gamma-glutamyltransferase.	2.4.1.26 DNA alpha-glucosyltransferase.
2.3.2.15 Glutathione gamma-glutamylcysteinyltransferase.	2.4.1.27 DNA beta-glucosyltransferase.
2.3.3.1 Citrate (Si)-synthase.	2.4.1.28 Glucosyl-DNA beta-glucosyltransferase.
2.3.3.2 Decylcitrate synthase.	2.4.1.29 Cellulose synthase (GDP-forming).
2.3.3.3 Citrate (Re)-synthase.	2.4.1.30 1,3-beta-oligoglucan phosphorylase.
2.3.3.4 Decylhomocitrate synthase.	2.4.1.31 Laminaribiose phosphorylase.

2.3.3.5 2-methylcitrate synthase.	2.4.1.32 Glucomannan 4-beta-mannosyltransferase.
2.3.3.6 2-ethylmalate synthase.	2.4.1.33 Alginate synthase.
2.3.3.7 3-ethylmalate synthase.	2.4.1.34 1,3-beta-glucan synthase.
2.3.3.8 ATP citrate synthase.	2.4.1.35 Phenol beta-glucosyltransferase.
2.3.3.9 Malate synthase.	2.4.1.36 Alpha, alpha-trehalose-phosphate synthase (GDP-forming).
2.3.3.10 Hydroxymethylglutaryl-CoA synthase.	2.4.1.37 Fucosylgalactoside 3-alpha-galactosyltransferase.
2.3.3.11 2-hydroxyglutarate synthase.	2.4.1.38 Beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase.

2.4.1.39 Steroid N-acetylglucosaminyltransferase.	2.4.1.71 Arylamine glucosyltransferase.
2.4.1.40 Glycoprotein-fucosylgalactoside alpha-N-acetylglactosaminyltransferase.	2.4.1.73 Lipopolysaccharide glucosyltransferase II.
2.4.1.41 Polypeptide N-acetylglactosaminyltransferase.	2.4.1.74 Glycosaminoglycan galactosyltransferase.
2.4.1.43 Polygalacturonate 4-alpha-galacturonosyltransferase.	2.4.1.75 UDP-galacturonosyltransferase.
2.4.1.44 Lipopolysaccharide 3-alpha-galactosyltransferase.	2.4.1.78 Phosphopolyprenol glucosyltransferase.
2.4.1.45 2-hydroxyacylsphingosine 1-beta-galactosyltransferase.	2.4.1.79 Galactosylgalactosylglucosylceramide beta-D- acetylglactosaminyltransferase.
2.4.1.46 1,2-diacylglycerol 3-beta-galactosyltransferase.	2.4.1.80 Ceramide glucosyltransferase.
2.4.1.47 N-acylsphingosine galactosyltransferase.	2.4.1.81 Flavone 7-O-beta-glucosyltransferase.
2.4.1.48 Heteroglycan alpha-mannosyltransferase.	2.4.1.82 Galactinol-sucrose galactosyltransferase.
2.4.1.49 Cellodextrin phosphorylase.	2.4.1.83 Dolichyl-phosphate beta-D-mannosyltransferase.
2.4.1.50 Procollagen galactosyltransferase.	2.4.1.85 Cyanohydrin beta-glucosyltransferase.
2.4.1.52 Poly(glycerol-phosphate) alpha-glucosyltransferase.	2.4.1.86 Glucosaminylgalactosylglucosylceramide beta-galactosyltransferase.
2.4.1.53 Poly(ribitol-phosphate) beta-glucosyltransferase.	2.4.1.87 N-acetylactosaminide 3-alpha-galactosyltransferase.
2.4.1.54 Undecaprenyl-phosphate mannosyltransferase.	2.4.1.88 Globoside alpha-N-acetylglactosaminyltransferase.
2.4.1.56 Lipopolysaccharide N-acetylglucosaminyltransferase.	2.4.1.90 N-acetylactosamine synthase.
2.4.1.57 Phosphatidylinositol alpha-mannosyltransferase.	2.4.1.91 Flavonol 3-O-glucosyltransferase.
2.4.1.58 Lipopolysaccharide glucosyltransferase I.	2.4.1.92 (N-acetylneuraminy)-galactosylglucosylceramide N-acetylglactosaminyltransferase.
2.4.1.60 Abequosyltransferase.	2.4.1.94 Protein N-acetylglucosaminyltransferase.
2.4.1.62 Ganglioside galactosyltransferase.	2.4.1.95 Bilirubin-glucuronoside glucuronosyltransferase.
2.4.1.63 Linamarin synthase.	2.4.1.96 Sn-glycerol-3-phosphate 1-galactosyltransferase.
2.4.1.64 Alpha, alpha-trehalose phosphorylase.	2.4.1.97 1,3-beta-D-glucan phosphorylase.
2.4.1.65 3-galactosyl-N-acetylglucosaminide 4-alpha-L-fucosyltransferase.	2.4.1.99 Sucrose:sucrose fructosyltransferase.

2.4.1.66 Procollagen glucosyltransferase.	2.4.1.100 2,1-fructan:2,1-fructan 1-fructosyltransferase.
2.4.1.67 Galactinol--raffinose galactosyltransferase.	2.4.1.101 Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase.
2.4.1.68 Glycoprotein 6-alpha-L-fucosyltransferase.	2.4.1.102 Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase.
2.4.1.69 Galactoside 2-alpha-L-fucosyltransferase.	2.4.1.103 Alizarin 2-beta-glucosyltransferase.
2.4.1.70 Poly(ribitol-phosphate) N-acetylglucosaminyltransferase.	2.4.1.104 O-dihydroxycoumarin 7-O-glucosyltransferase.

2.4.1.105 Vitexin beta-glucosyltransferase.	2.4.1.135 Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase.
2.4.1.106 Isovitexin beta-glucosyltransferase.	2.4.1.136 Gallate 1-beta-glucosyltransferase.
2.4.1.109 Dolichyl-phosphate-mannose--protein mannosyltransferase.	2.4.1.137 Sn-glycerol-3-phosphate 2-alpha-galactosyltransferase.
2.4.1.110 tRNA-queuosine beta-mannosyltransferase.	2.4.1.138 Mannotetraose 2-alpha-N-acetylglucosaminyltransferase.
2.4.1.111 Coniferyl-alcohol glucosyltransferase.	2.4.1.139 Maltose synthase.
2.4.1.112 Alpha-1,4-glucan-protein synthase (UDP-forming).	2.4.1.140 Alternansucrase.
2.4.1.113 Alpha-1,4-glucan-protein synthase (ADP-forming).	2.4.1.141 N-acetylglucosaminyldiphosphodolichol N-acetylglucosaminyltransferase.
2.4.1.114 2-coumarate O-beta-glucosyltransferase.	2.4.1.142 Chitobiosyldiphosphodolichol beta-mannosyltransferase.
2.4.1.115 Anthocyanidin 3-O-glucosyltransferase.	2.4.1.143 Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase.
2.4.1.116 Cyanidin-3-rhamnosylglucoside 5-O-glucosyltransferase.	2.4.1.144 Beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase.
2.4.1.117 Dolichyl-phosphate beta-glucosyltransferase.	2.4.1.145 Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase.
2.4.1.118 Cytokinin 7-beta-glucosyltransferase.	2.4.1.146 Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,3-N-acetylglucosaminyltransferase.
2.4.1.119 Dolichyl-diphosphooligosaccharide-protein glycotransferase.	2.4.1.147 Acetylgalactosaminyl-O-glycosyl-glycoprotein beta-1,3-N-acetylglucosaminyltransferase.
2.4.1.120 Sinapate 1-glucosyltransferase.	2.4.1.148 Acetylgalactosaminyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase.
2.4.1.121 Indole-3-acetate beta-glucosyltransferase.	2.4.1.149 N-acetyllactosaminide beta-1,3-N-acetylglucosaminyltransferase.
2.4.1.122 Glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase.	2.4.1.150 N-acetyllactosaminide beta-1,6-N-acetylglucosaminyl-transferase.
2.4.1.123 Inositol 3-alpha-galactosyltransferase.	2.4.1.152 4-galactosyl-N-acetylglucosaminide 3-alpha-L-fucosyltransferase.
2.4.1.125 Sucrose-1,6-alpha-glucan 3(6)-alpha-glucosyltransferase.	2.4.1.153 Dolichyl-phosphate alpha-N-acetylglucosaminyltransferase.
2.4.1.126 Hydroxycinnamate 4-beta-glucosyltransferase.	2.4.1.154 Globotriosylceramide beta-1,6-N-acetylgalactosaminyl-transferase.
2.4.1.127 Monoterpenol beta-glucosyltransferase.	2.4.1.155 Alpha-1,6-mannosyl-glycoprotein 6-beta-N-acetylglucosaminyltransferase.
2.4.1.128 Scopoletin glucosyltransferase.	2.4.1.156 Indolylacetyl-myo-inositol galactosyltransferase.

2.4.1.129 Peptidoglycan glycosyltransferase.	2.4.1.157 1,2-diacylglycerol 3-glucosyltransferase.
2.4.1.130 Dolichyl-phosphate-mannose--glycolipid alpha-mannosyltransferase.	2.4.1.158 13-hydroxydocosanoate 13-beta-glucosyltransferase.
2.4.1.131 Glycolipid 2-alpha-mannosyltransferase.	2.4.1.159 Flavonol-3-O-glucoside L-rhamnosyltransferase.
2.4.1.132 Glycolipid 3-alpha-mannosyltransferase.	2.4.1.160 Pyridoxine 5'-O-beta-D-glucosyltransferase.
2.4.1.133 Xylosylprotein 4-beta-galactosyltransferase.	2.4.1.161 Oligosaccharide 4-alpha-D-glucosyltransferase.
2.4.1.134 Galactosylxylosylprotein 3-beta-galactosyltransferase.	2.4.1.162 Aldose beta-D-fructosyltransferase.

2.4.1.163 Beta-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide beta-1,3-acetylglucosaminyltransferase.	2.4.1.191 Luteolin-7-O-diglucuronide 4'-O-glucuronosyltransferase.
2.4.1.164 Galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide beta-1,6-N-acetylglucosaminyltransferase.	2.4.1.192 Nuatigenin 3-beta-glucosyltransferase.
2.4.1.165 N-acetylneuraminylgalactosylglucosylceramide beta-1,4-N-acetylgalactosaminyltransferase.	2.4.1.193 Sarsapogenin 3-beta-glucosyltransferase.
2.4.1.166 Raffinose--raffinose alpha-galactosyltransferase.	2.4.1.194 4-hydroxybenzoate 4-O-beta-D-glucosyltransferase.
2.4.1.167 Sucrose 6(F)-alpha-galactosyltransferase.	2.4.1.195 Thiohydroximate beta-D-glucosyltransferase.
2.4.1.168 Xyloglucan 4-glucosyltransferase.	2.4.1.196 Nicotinate glucosyltransferase.
2.4.1.170 Isoflavone 7-O-glucosyltransferase.	2.4.1.197 High-mannose-oligosaccharide beta-1,4-N-acetylglucosaminyltransferase.
2.4.1.171 Methyl-ONN-azoxymethanol beta-D-glucosyltransferase.	2.4.1.198 Phosphatidylinositol N-acetylglucosaminyltransferase.
2.4.1.172 Salicyl-alcohol beta-D-glucosyltransferase.	2.4.1.199 Beta-mannosylphosphodecaprenol--mannooligosaccharide 6-mannosyltransferase.
2.4.1.173 Sterol 3-beta-glucosyltransferase.	2.4.1.201 Alpha-1,6-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase.
2.4.1.174 Glucuronylgalactosylproteoglycan 4-beta-N-acetylgalactosaminyltransferase.	2.4.1.202 2,4-dihydroxy-7-methoxy-2H-1,4-benzoxazin-3(4H)-one 2-D-glucosyltransferase.
2.4.1.175 Glucuronosyl-N-acetylgalactosaminyl-proteoglycan 4-beta-N-acetylgalactosaminyltransferase.	2.4.1.203 Trans-zeatin O-beta-D-glucosyltransferase.
2.4.1.176 Gibberellin beta-D-glucosyltransferase.	2.4.1.205 Galactogen 6-beta-galactosyltransferase.
2.4.1.177 Cinnamate beta-D-glucosyltransferase.	2.4.1.206 Lactosylceramide 1,3-N-acetyl-beta-D-glucosaminyltransferase.
2.4.1.178 Hydroxymandelonitrile glucosyltransferase.	2.4.1.207 Xyloglucan:xyloglucosyl transferase.
2.4.1.179 Lactosylceramide beta-1,3-galactosyltransferase.	2.4.1.208 Diglucosyl diacylglycerol synthase.
2.4.1.180 Lipopolysaccharide N-acetylmannosaminouronosyltransferase.	2.4.1.209 Cis-p-coumarate glucosyltransferase.
2.4.1.181 Hydroxyanthraquinone glucosyltransferase.	2.4.1.210 Limonoid glucosyltransferase.
2.4.1.182 Lipid-A-disaccharide synthase.	2.4.1.211 1,3-beta-galactosyl-N-acetylhexosamine phosphorylase.
2.4.1.183 Alpha-1,3-glucan synthase.	2.4.1.212 Hyaluronan synthase.

2.4.1.184 Galactolipid galactosyltransferase.	2.4.1.213 Glucosylglycerol-phosphate synthase.
2.4.1.185 Flavanone 7-O-beta-glucosyltransferase.	2.4.1.214 Glycoprotein 3-alpha-L-fucosyltransferase.
2.4.1.186 Glycogenin glucosyltransferase.	2.4.1.215 Cis-zeatin O-beta-D-glucosyltransferase.
2.4.1.187 N-acetylglucosaminyldiphosphoundecaprenol N-acetyl-beta-D-mannosaminytransferase.	2.4.1.216 Trehalose 6-phosphate phosphorylase.
2.4.1.188 N-acetylglucosaminyldiphosphoundecaprenol glucosyltransferase.	2.4.1.217 Mannosyl-3-phosphoglycerate synthase.
2.4.1.189 Luteolin 7-O-glucuronosyltransferase.	2.4.1.218 Hydroquinone glucosyltransferase.
2.4.1.190 Luteolin-7-O-glucuronide 7-O-glucuronosyltransferase.	2.4.1.219 Vomilenine glucosyltransferase.

2.4.1.220 Indoxyl-UDPG glucosyltransferase.	2.4.2.19 Nicotinate-nucleotide diphosphorylase (carboxylating).
2.4.1.221 Peptide-O-fucosyltransferase.	2.4.2.20 Dioxotetrahydropyrimidine phosphoribosyltransferase.
2.4.1.222 O-fucosylpeptide 3-beta-N-acetylglucosaminytransferase.	2.4.2.21 Nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase.
2.4.1.223 Glucuronyl-galactosyl-proteoglycan 4-alpha-N-acetylglucosaminytransferase.	2.4.2.22 Xanthine phosphoribosyltransferase.
2.4.1.224 Glucuronosyl-N-acetylglucosaminy-proteoglycan 4-alpha-N-acetylglucosaminytransferase.	2.4.2.23 Deoxyuridine phosphorylase.
2.4.1.225 N-acetylglucosaminy-proteoglycan 4-beta-glucuronosyltransferase.	2.4.2.24 1,4-beta-D-xylan synthase.
2.4.1.226 N-acetylglactosaminy-proteoglycan 3-beta-glucuronosyltransferase.	2.4.2.25 Flavone apiosyltransferase.
2.4.1.227 Undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminytransferase.	2.4.2.26 Protein xylosyltransferase.
2.4.1.228 Lactosylceramide 4-alpha-galactosyltransferase.	2.4.2.27 dTDP-dihydrostreptose--streptidine-6-phosphate dihydrostreptosyltransferase.
2.4.1.229 [Skp1-protein]-hydroxyproline N-acetylglucosaminytransferase.	2.4.2.28 S-methyl-5-thioadenosine phosphorylase.
2.4.1.230 Kojibiose phosphorylase.	2.4.2.29 Queuine tRNA-ribosyltransferase.
2.4.1.231 Alpha, alpha-trehalose phosphorylase (configuration-retaining).	2.4.2.30 NAD(+) ADP-ribosyltransferase.
2.4.1.232 Initiation-specific alpha-1,6-mannosyltransferase.	2.4.2.31 NAD(P)(+)-arginine ADP-ribosyltransferase.
2.4.2.1 Purine-nucleoside phosphorylase.	2.4.2.32 Dolichyl-phosphate D-xylosyltransferase.
2.4.2.2 Pyrimidine-nucleoside phosphorylase.	2.4.2.33 Dolichyl-xylosyl-phosphate-protein xylosyltransferase.
2.4.2.3 Uridine phosphorylase.	2.4.2.34 Indolylacetylinoitol arabinosyltransferase.
2.4.2.4 Thymidine phosphorylase.	2.4.2.35 Flavonol-3-O-glycoside xylosyltransferase.
2.4.2.5 Nucleoside ribosyltransferase.	2.4.2.36 NAD(+)-diphthamide ADP-ribosyltransferase.
2.4.2.6 Nucleoside deoxyribosyltransferase.	2.4.2.37 NAD(+)-dinitrogen-reductase ADP-D-ribosyltransferase.
2.4.2.7 Adenine phosphoribosyltransferase.	2.4.2.38 Glycoprotein 2-beta-D-xylosyltransferase.
2.4.2.8 Hypoxanthine phosphoribosyltransferase.	2.4.2.39 Xyloglucan 6-xylosyltransferase.
2.4.2.9 Uracil phosphoribosyltransferase.	2.4.2.40 Zeatin O-beta-D-xylosyltransferase.

2.4.2.10 Orotate phosphoribosyltransferase.	2.4.99.1 Beta-galactoside alpha-2,6-sialyltransferase.
2.4.2.11 Nicotinate phosphoribosyltransferase.	2.4.99.2 Monosialoganglioside sialyltransferase.
2.4.2.12 Nicotinamide phosphoribosyltransferase.	2.4.99.3 Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase.
2.4.2.14 Amidophosphoribosyltransferase.	2.4.99.4 Beta-galactoside alpha-2,3-sialyltransferase.
2.4.2.15 Guanosine phosphorylase.	2.4.99.5 Galactosyldiacylglycerol alpha-2,3-sialyltransferase.
2.4.2.16 Urate-ribonucleotide phosphorylase.	2.4.99.6 N-acetyllactosaminide alpha-2,3-sialyltransferase.
2.4.2.17 ATP phosphoribosyltransferase.	2.4.99.7 (Alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl-galactosaminide 6-alpha-sialyltransferase.
2.4.2.18 Anthranilate phosphoribosyltransferase.	2.4.99.8 Alpha-N-acetylneuraminate alpha-2,8-sialyltransferase.

2.4.99.9 Lactosylceramide alpha-2,3-sialyltransferase.	2.5.1.42 Geranylgeranyl-glycerol-phosphate geranylgeranyltransferase.
2.4.99.10 Neolactotetraosylceramide alpha-2,3-sialyltransferase.	2.5.1.43 Nicotianamine synthase.
2.4.99.11 Lactosylceramide alpha-2,6-N-sialyltransferase.	2.5.1.44 Homospermidine synthase.
2.5.1.1 Dimethylallyltranstransferase.	2.5.1.45 Homospermidine synthase (spermidine-specific).
2.5.1.2 Thiamine pyridinylase.	2.5.1.46 Deoxyhypusine synthase.
2.5.1.3 Thiamine-phosphate diphosphorylase.	2.5.1.47 Cysteine synthase.
2.5.1.4 Adenosylmethionine cyclotransferase.	2.5.1.48 Cystathionine gamma-synthase.
2.5.1.5 Galactose-6-sulfurylase.	2.5.1.49 O-acetylhomoserine aminocarboxypropyltransferase.
2.5.1.6 Methionine adenosyltransferase.	2.5.1.50 Zeatin 9-aminocarboxyethyltransferase.
2.5.1.7 UDP-N-acetylglucosamine 1-carboxyvinyltransferase.	2.5.1.51 Beta-pyrazolylalanine synthase.
2.5.1.8 tRNA isopentenyltransferase.	2.5.1.52 L-mimosine synthase.
2.5.1.9 Riboflavin synthase.	2.5.1.53 Uracilylalanine synthase.
2.5.1.10 Geranyltranstransferase.	2.5.1.54 3-deoxy-7-phosphoheptulonate synthase.
2.5.1.11 Trans-octaprenyltranstransferase.	2.5.1.55 3-deoxy-8-phosphooctulonate synthase.
2.5.1.15 Dihydropteroate synthase.	2.5.1.56 N-acetylneuraminase synthase.
2.5.1.16 Spermidine synthase.	2.5.1.57 N-acetylneuraminate-9-phosphate synthase.
2.5.1.17 Cob(I)yrinic acid a,c-diamide adenosyltransferase.	2.5.1.58 Protein farnesyltransferase.
2.5.1.18 Glutathione transferase.	2.5.1.59 Protein geranylgeranyltransferase type I.
2.5.1.19 3-phosphoshikimate 1-carboxyvinyltransferase.	2.5.1.60 Protein geranylgeranyltransferase type II.
2.5.1.20 Rubber cis-polyprenylcistransferase.	2.5.1.61 Hydroxymethylbilane synthase.
2.5.1.21 Farnesyl-diphosphate farnesyltransferase.	2.5.1.62 Chlorophyll synthase.
2.5.1.22 Spermine synthase.	2.5.1.63 Adenosyl-fluoride synthase.
2.5.1.23 Sym-norspermidine synthase.	2.5.1.64 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase.
2.5.1.24 Discadenine synthase.	2.6.1.1 Aspartate transaminase.
2.5.1.25 tRNA-uridine aminocarboxypropyltransferase.	2.6.1.2 Alanine transaminase.
2.5.1.26 Alkylglycerone-phosphate synthase.	2.6.1.3 Cysteine transaminase.
2.5.1.27 Adenylate dimethylallyltransferase.	2.6.1.4 Glycine transaminase.

2.5.1.28	Dimethylallylcistransferase.	2.6.1.5	Tyrosine transaminase.
2.5.1.29	Farnesyltranstransferase.	2.6.1.6	Leucine transaminase.
2.5.1.30	Trans-hexaprenyltranstransferase.	2.6.1.7	Kynurenine--oxoglutarate transaminase.
2.5.1.31	Di-trans,poly-cis-decaprenylcistransferase.	2.6.1.8	2,5-diaminovalerate transaminase.
2.5.1.32	Geranylgeranyl-diphosphate geranylgeranyltransferase.	2.6.1.9	Histidinol-phosphate transaminase.
2.5.1.33	Trans-pentaprenyltranstransferase.	2.6.1.11	Acetylornithine transaminase.
2.5.1.34	Tryptophan dimethylallyltransferase.	2.6.1.12	Alanine--oxo-acid transaminase.
2.5.1.35	Aspulinone dimethylallyltransferase.	2.6.1.13	Ornithine--oxo-acid transaminase.
2.5.1.36	Trihydroxypterocarpan dimethylallyltransferase.	2.6.1.14	Asparagine--oxo-acid transaminase.
2.5.1.38	Isonocardicin synthase.	2.6.1.15	Glutamine--pyruvate transaminase.
2.5.1.39	4-hydroxybenzoate nonaprenyltransferase.	2.6.1.16	Glutamine--fructose-6-phosphate transaminase (isomerizing).
2.5.1.41	Phosphoglycerol geranylgeranyltransferase.	2.6.1.17	Succinyldiaminopimelate transaminase.

2.6.1.18	Beta-alanine--pyruvate transaminase.	2.6.1.62	Adenosylmethionine--8-amino-7-oxononanoate transaminase.
2.6.1.19	4-aminobutyrate transaminase.	2.6.1.63	Kynurenine--glyoxylate transaminase.
2.6.1.21	D-alanine transaminase.	2.6.1.64	Glutamine--phenylpyruvate transaminase.
2.6.1.22	(S)-3-amino-2-methylpropionate transaminase.	2.6.1.65	N(6)-acetyl-beta-lysine transaminase.
2.6.1.23	4-hydroxyglutamate transaminase.	2.6.1.66	Valine--pyruvate transaminase.
2.6.1.24	Diiodotyrosine transaminase.	2.6.1.67	2-aminohexanoate transaminase.
2.6.1.26	Thyroid-hormone transaminase.	2.6.1.68	Ornithine(lysine) transaminase.
2.6.1.27	Tryptophan transaminase.	2.6.1.70	Aspartate--phenylpyruvate transaminase.
2.6.1.28	Tryptophan--phenylpyruvate transaminase.	2.6.1.71	Lysine--pyruvate 6-transaminase.
2.6.1.29	Diamine transaminase.	2.6.1.72	D-4-hydroxyphenylglycine transaminase.
2.6.1.30	Pyridoxamine--pyruvate transaminase.	2.6.1.73	Methionine--glyoxylate transaminase.
2.6.1.31	Pyridoxamine--oxaloacetate transaminase.	2.6.1.74	Cephalosporin-C transaminase.
2.6.1.32	Valine--3-methyl-2-oxovalerate transaminase.	2.6.1.75	Cysteine-conjugate transaminase.
2.6.1.33	dTDP-4-amino-4,6-dideoxy-D-glucose transaminase.	2.6.1.76	Diaminobutyrate--2-oxoglutarate transaminase.
2.6.1.34	UDP-2-acetamido-4-amino-2,4,6-trideoxyglucose transaminase.	2.6.1.77	Taurine--pyruvate aminotransferase.
2.6.1.35	Glycine--oxaloacetate transaminase.	2.6.3.1	Oximinotransferase.
2.6.1.36	L-lysine 6-transaminase.	2.6.99.1	dATP(dGTP)--DNA purinetransferase.
2.6.1.37	2-aminoethylphosphonate--pyruvate transaminase.	2.7.1.1	Hexokinase.
2.6.1.38	Histidine transaminase.	2.7.1.2	Glucokinase.
2.6.1.39	2-aminoadipate transaminase.	2.7.1.3	Ketohexokinase.
2.6.1.40	(R)-3-amino-2-methylpropionate--pyruvate transaminase.	2.7.1.4	Fructokinase.
2.6.1.41	D-methionine--pyruvate transaminase.	2.7.1.5	Rhamnulokinase.
2.6.1.42	Branched-chain-amino-acid transaminase.	2.7.1.6	Galactokinase.
2.6.1.43	Aminolevulinate transaminase.	2.7.1.7	Mannokinase.
2.6.1.44	Alanine--glyoxylate transaminase.	2.7.1.8	Glucosamine kinase.
2.6.1.45	Serine--glyoxylate transaminase.	2.7.1.10	Phosphoglucokinase.

2.6.1.46 Diaminobutyrate-pyruvate transaminase.	2.7.1.11 6-phosphofructokinase.
2.6.1.47 Alanine-oxomalonate transaminase.	2.7.1.12 Gluconokinase.
2.6.1.48 5-aminovalerate transaminase.	2.7.1.13 Dehydrogluconokinase.
2.6.1.49 Dihydroxyphenylalanine transaminase.	2.7.1.14 Sedoheptulokinase.
2.6.1.50 Glutamine-scylo-inositol transaminase.	2.7.1.15 Ribokinase.
2.6.1.51 Serine-pyruvate transaminase.	2.7.1.16 Ribulokinase.
2.6.1.52 Phosphoserine transaminase.	2.7.1.17 Xylulokinase.
2.6.1.54 Pyridoxamine-phosphate transaminase.	2.7.1.18 Phosphoribokinase.
2.6.1.55 Taurine-2-oxoglutarate transaminase.	2.7.1.19 Phosphoribulokinase.
2.6.1.56 1D-1-guanidino-3-amino-1,3-dideoxy-scylo-inositol transaminase.	2.7.1.20 Adenosine kinase.
2.6.1.57 Aromatic-amino-acid transaminase.	2.7.1.21 Thymidine kinase.
2.6.1.58 Phenylalanine(histidine) transaminase.	2.7.1.22 Ribosylnicotinamide kinase.
2.6.1.59 dTDP-4-amino-4,6-dideoxygalactose transaminase.	2.7.1.23 NAD(+) kinase.
2.6.1.60 Aromatic-amino-acid-glyoxylate transaminase.	2.7.1.24 Dephospho-CoA kinase.

2.7.1.25 Adenylyl-sulfate kinase.	2.7.1.69 Protein-N(pi)-phosphohistidine-sugar phosphotransferase.
2.7.1.26 Riboflavin kinase.	2.7.1.71 Shikimate kinase.
2.7.1.27 Erythritol kinase.	2.7.1.72 Streptomycin 6-kinase.
2.7.1.28 Triokinase.	2.7.1.73 Inosine kinase.
2.7.1.29 Glycerone kinase.	2.7.1.74 Deoxycytidine kinase.
2.7.1.30 Glycerol kinase.	2.7.1.76 Deoxyadenosine kinase.
2.7.1.31 Glycerate kinase.	2.7.1.77 Nucleoside phosphotransferase.
2.7.1.32 Choline kinase.	2.7.1.78 Polynucleotide 5'-hydroxy-kinase.
2.7.1.33 Pantothenate kinase.	2.7.1.79 Diphosphate-glycerol phosphotransferase.
2.7.1.34 Pantetheine kinase.	2.7.1.80 Diphosphate-serine phosphotransferase.
2.7.1.35 Pyridoxal kinase.	2.7.1.81 Hydroxyllysine kinase.
2.7.1.36 Mevalonate kinase.	2.7.1.82 Ethanolamine kinase.
2.7.1.37 Protein kinase.	2.7.1.83 Pseudouridine kinase.
2.7.1.38 Phosphorylase kinase.	2.7.1.84 Alkylglycerone kinase.
2.7.1.39 Homoserine kinase.	2.7.1.85 Beta-glucoside kinase.
2.7.1.40 Pyruvate kinase.	2.7.1.86 NADH kinase.
2.7.1.41 Glucose-1-phosphate phosphodismutase.	2.7.1.87 Streptomycin 3"-kinase.
2.7.1.42 Riboflavin phosphotransferase.	2.7.1.88 Dihydrostreptomycin-6-phosphate 3'-alpha-kinase.
2.7.1.43 Glucuronokinase.	2.7.1.89 Thiamine kinase.
2.7.1.44 Galacturonokinase.	2.7.1.90 Diphosphate-fructose-6-phosphate 1-phosphotransferase.
2.7.1.45 2-dehydro-3-deoxygluconokinase.	2.7.1.91 Sphinganine kinase.
2.7.1.46 L-arabinokinase.	2.7.1.92 5-dehydro-2-deoxygluconokinase.
2.7.1.47 D-ribulokinase.	2.7.1.93 Alkylglycerol kinase.
2.7.1.48 Uridine kinase.	2.7.1.94 Acylglycerol kinase.
2.7.1.49 Hydroxymethylpyrimidine kinase.	2.7.1.95 Kanamycin kinase.
2.7.1.50 Hydroxyethylthiazole kinase.	2.7.1.99 [Pyruvate dehydrogenase (lipoamide)] kinase.
2.7.1.51 L-fuculokinase.	2.7.1.100 S-methyl-5-thioribose kinase.
2.7.1.52 Fucokinase.	2.7.1.101 Tagatose kinase.
2.7.1.53 L-xylulokinase.	2.7.1.102 Hamamelose kinase.
2.7.1.54 D-arabinokinase.	2.7.1.103 Viomycin kinase.

2.7.1.55	Allose kinase.	2.7.1.104	Diphosphate-protein phosphotransferase.
2.7.1.56	1-phosphofructokinase.	2.7.1.105	6-phosphofructo-2-kinase.
2.7.1.58	2-dehydro-3-deoxygalactonokinase.	2.7.1.106	Glucose-1,6-bisphosphate synthase.
2.7.1.59	N-acetylglucosamine kinase.	2.7.1.107	Diacylglycerol kinase.
2.7.1.60	N-acylmannosamine kinase.	2.7.1.108	Dolichol kinase.
2.7.1.61	Acyl-phosphate-hexose phosphotransferase.	2.7.1.109	[Hydroxymethylglutaryl-CoA reductase (NADPH)] kinase.
2.7.1.62	Phosphoramidate-hexose phosphotransferase.	2.7.1.110	Dephospho-[reductase kinase] kinase.
2.7.1.63	Polyphosphate-glucose phosphotransferase.	2.7.1.112	Protein-tyrosine kinase.
2.7.1.64	Inositol 3-kinase.	2.7.1.113	Deoxyguanosine kinase.
2.7.1.65	Scyllo-inosamine 4-kinase.	2.7.1.114	AMP-thymidine kinase.
2.7.1.66	Undecaprenol kinase.	2.7.1.115	[3-methyl-2-oxobutanoate dehydrogenase (lipoamide)] kinase.
2.7.1.67	1-phosphatidylinositol 4-kinase.	2.7.1.116	[Isocitrate dehydrogenase (NADP+)] kinase.
2.7.1.68	1-phosphatidylinositol-4-phosphate 5-kinase.	2.7.1.117	[Myosin light-chain] kinase.

2.7.1.118	ADP-thymidine kinase.	2.7.2.6	Formate kinase.
2.7.1.119	Hygromycin-B kinase.	2.7.2.7	Butyrate kinase.
2.7.1.120	Caldesmon kinase.	2.7.2.8	Acetylglutamate kinase.
2.7.1.121	Phosphoenolpyruvate-glycerone phosphotransferase.	2.7.2.10	Phosphoglycerate kinase (GTP).
2.7.1.122	Xylitol kinase.	2.7.2.11	Glutamate 5-kinase.
2.7.1.123	Calcium/calmodulin-dependent protein kinase.	2.7.2.12	Acetate kinase (diphosphate).
2.7.1.124	[Tyrosine 3-monooxygenase] kinase.	2.7.2.13	Glutamate 1-kinase.
2.7.1.125	Rhodopsin kinase.	2.7.2.14	Branched-chain-fatty-acid kinase.
2.7.1.126	[Beta-adrenergic-receptor] kinase.	2.7.3.1	Guanidinoacetate kinase.
2.7.1.127	Inositol-trisphosphate 3-kinase.	2.7.3.2	Creatine kinase.
2.7.1.128	[Acetyl-CoA carboxylase] kinase.	2.7.3.3	Arginine kinase.
2.7.1.129	[Myosin heavy-chain] kinase.	2.7.3.4	Taurocyamine kinase.
2.7.1.130	Tetraacyldisaccharide 4'-kinase.	2.7.3.5	Lombricine kinase.
2.7.1.131	[Low-density lipoprotein receptor] kinase.	2.7.3.6	Hypotaurocyamine kinase.
2.7.1.132	Tropomyosin kinase.	2.7.3.7	Opheline kinase.
2.7.1.134	Inositol-tetrakisphosphate 1-kinase.	2.7.3.8	Ammonia kinase.
2.7.1.135	[Tau protein] kinase.	2.7.3.9	Phosphoenolpyruvate-protein phosphotransferase.
2.7.1.136	Macrolide 2'-kinase.	2.7.3.10	Agmatine kinase.
2.7.1.137	Phosphatidylinositol 3-kinase.	2.7.3.11	Protein-histidine pros-kinase.
2.7.1.138	Ceramide kinase.	2.7.3.12	Protein-histidine tele-kinase.
2.7.1.140	Inositol-tetrakisphosphate 5-kinase.	2.7.4.1	Polyphosphate kinase.
2.7.1.141	[RNA-polymerase]-subunit kinase.	2.7.4.2	Phosphomevalonate kinase.
2.7.1.142	Glycerol-3-phosphate-glucose phosphotransferase.	2.7.4.3	Adenylate kinase.
2.7.1.143	Diphosphate-purine nucleoside kinase.	2.7.4.4	Nucleoside-phosphate kinase.
2.7.1.144	Tagatose-6-phosphate kinase.	2.7.4.6	Nucleoside-diphosphate kinase.
2.7.1.145	Deoxynucleoside kinase.	2.7.4.7	Phosphomethylpyrimidine kinase.
2.7.1.146	ADP-specific phosphofructokinase.	2.7.4.8	Guanylate kinase.
2.7.1.147	ADP-specific glucokinase.	2.7.4.9	dTMP kinase.

2.7.1.148 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase.	2.7.4.10 Nucleoside-triphosphate--adenylate kinase.
2.7.1.149 1-phosphatidylinositol-5-phosphate 4-kinase.	2.7.4.11 (Deoxy)adenylate kinase.
2.7.1.150 1-phosphatidylinositol-3-phosphate 5-kinase.	2.7.4.12 T(2)-induced deoxynucleotide kinase.
2.7.1.151 Inositol-polyphosphate multikinase.	2.7.4.13 (Deoxy)nucleoside-phosphate kinase.
2.7.1.153 Phosphatidylinositol-4,5-bisphosphate 3-kinase.	2.7.4.14 Cytidylate kinase.
2.7.1.154 Phosphatidylinositol-4-phosphate 3-kinase.	2.7.4.15 Thiamine-diphosphate kinase.
2.7.1.155 Diphosphoinositol-pentakisphosphate kinase.	2.7.4.16 Thiamine-phosphate kinase.
2.7.1.156 Adenosylcobinamide kinase.	2.7.4.17 3-phosphoglyceroyl-phosphate--polyphosphate phosphotransferase.
2.7.2.1 Acetate kinase.	2.7.4.18 Farnesyl-diphosphate kinase.
2.7.2.2 Carbamate kinase.	2.7.4.19 5-methyldeoxycytidine-5'-phosphate kinase.
2.7.2.3 Phosphoglycerate kinase.	2.7.4.20 Dolichyl-diphosphate--polyphosphate phosphotransferase.
2.7.2.4 Aspartate kinase.	2.7.4.21 Inositol-hexakisphosphate kinase.

2.7.6.1 Ribose-phosphate diphosphokinase.	2.7.7.34 Glucose-1-phosphate guanylyltransferase.
2.7.6.2 Thiamine diphosphokinase.	2.7.7.35 Ribose-5-phosphate adenylyltransferase.
2.7.6.3 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase.	2.7.7.36 Aldose-1-phosphate adenylyltransferase.
2.7.6.4 Nucleotide diphosphokinase.	2.7.7.37 Aldose-1-phosphate nucleotidyltransferase.
2.7.6.5 GTP diphosphokinase.	2.7.7.38 3-deoxy-manno-octulosonate cytidyltransferase.
2.7.7.1 Nicotinamide-nucleotide adenylyltransferase.	2.7.7.39 Glycerol-3-phosphate cytidyltransferase.
2.7.7.2 FMN adenylyltransferase.	2.7.7.40 D-ribitol-5-phosphate cytidyltransferase.
2.7.7.3 Pantetheine-phosphate adenylyltransferase.	2.7.7.41 Phosphatidate cytidyltransferase.
2.7.7.4 Sulfate adenylyltransferase.	2.7.7.42 [Glutamate--ammonia-ligase] adenylyltransferase.
2.7.7.5 Sulfate adenylyltransferase (ADP).	2.7.7.43 N-acylneuraminate cytidyltransferase.
2.7.7.6 DNA-directed RNA polymerase.	2.7.7.44 Glucuronate-1-phosphate uridylyltransferase.
2.7.7.7 DNA-directed DNA polymerase.	2.7.7.45 Guanosine-triphosphate guanylyltransferase.
2.7.7.8 Polyribonucleotide nucleotidyltransferase.	2.7.7.46 Gentamicin 2"-nucleotidyltransferase.
2.7.7.9 UTP--glucose-1-phosphate uridylyltransferase.	2.7.7.47 Streptomycin 3"-adenylyltransferase.
2.7.7.10 UTP--hexose-1-phosphate uridylyltransferase.	2.7.7.48 RNA-directed RNA polymerase.
2.7.7.11 UTP--xylose-1-phosphate uridylyltransferase.	2.7.7.49 RNA-directed DNA polymerase.
2.7.7.12 UDP-glucose--hexose-1-phosphate uridylyltransferase.	2.7.7.50 mRNA guanylyltransferase.
2.7.7.13 Mannose-1-phosphate guanylyltransferase.	2.7.7.51 Adenylylsulfate--ammonia adenylyltransferase.

2.7.7.14 Ethanolamine-phosphate cytidylyltransferase.	2.7.7.52 RNA uridylyltransferase.
2.7.7.15 Choline-phosphate cytidylyltransferase.	2.7.7.53 ATP adenylyltransferase.
2.7.7.18 Nicotinate-nucleotide adenylyltransferase.	2.7.7.54 Phenylalanine adenylyltransferase.
2.7.7.19 Polynucleotide adenylyltransferase.	2.7.7.55 Anthranilate adenylyltransferase.
2.7.7.21 tRNA cytidylyltransferase.	2.7.7.56 tRNA nucleotidylyltransferase.
2.7.7.22 Mannose-1-phosphate guanylyltransferase (GDP).	2.7.7.57 N-methylphosphoethanolamine cytidylyltransferase.
2.7.7.23 UDP-N-acetylglucosamine diphosphorylase.	2.7.7.58 (2,3-dihydroxybenzoyl)adenylate synthase.
2.7.7.24 Glucose-1-phosphate thymidylyltransferase.	2.7.7.59 [Protein-P _{II}] uridylyltransferase.
2.7.7.25 tRNA adenylyltransferase.	2.7.7.60 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase.
2.7.7.27 Glucose-1-phosphate adenylyltransferase.	2.7.7.61 Holo-ACP synthase.
2.7.7.28 Nucleoside-triphosphate-aldose 1-phosphate nucleotidylyltransferase.	2.7.7.62 Adenosylcobinamide-phosphate guanylyltransferase.
2.7.7.30 Fucose-1-phosphate guanylyltransferase.	2.7.8.1 Ethanolaminephosphotransferase.
2.7.7.31 DNA nucleotidylexotransferase.	2.7.8.2 Diacylglycerol cholinephosphotransferase.
2.7.7.32 Galactose-1-phosphate thymidylyltransferase.	2.7.8.3 Ceramide cholinephosphotransferase.
2.7.7.33 Glucose-1-phosphate cytidylyltransferase.	2.7.8.4 Serine-phosphoethanolamine synthase.

2.7.8.5 CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidylyltransferase.	2.8.2.1 Aryl sulfotransferase.
2.7.8.6 Undecaprenyl-phosphate galactose phosphotransferase.	2.8.2.2 Alcohol sulfotransferase.
2.7.8.7 Holo-[acyl-carrier-protein] synthase.	2.8.2.3 Amine sulfotransferase.
2.7.8.8 CDP-diacylglycerol-serine O-phosphatidylyltransferase.	2.8.2.4 Estrone sulfotransferase.
2.7.8.9 Phosphomannan mannosephosphotransferase.	2.8.2.5 Chondroitin 4-sulfotransferase.
2.7.8.10 Sphingosine cholinephosphotransferase.	2.8.2.6 Choline sulfotransferase.
2.7.8.11 CDP-diacylglycerol--inositol 3-phosphatidylyltransferase.	2.8.2.7 UDP-N-acetylgalactosamine-4-sulfate sulfotransferase.
2.7.8.12 CDP-glycerol glycerophosphotransferase.	2.8.2.8 [Heparan sulfate]-glucosamine N-sulfotransferase.
2.7.8.13 Phospho-N-acetylmuramoyl-pentapeptide-transferase.	2.8.2.9 Tyrosine-ester sulfotransferase.
2.7.8.14 CDP-ribitol ribitolphosphotransferase.	2.8.2.10 Renilla-luciferin sulfotransferase.
2.7.8.15 UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase.	2.8.2.11 Galactosylceramide sulfotransferase.
2.7.8.17 UDP-N-acetylglucosamine--lysosomal-enzyme N-acetylglucosaminephosphotransferase.	2.8.2.13 Psychosine sulfotransferase.
2.7.8.18 UDP-galactose--UDP-N-acetylglucosamine galactose phosphotransferase.	2.8.2.14 Bile-salt sulfotransferase.
2.7.8.19 UDP-glucose-glycoprotein glucose phosphotransferase.	2.8.2.15 Steroid sulfotransferase.
2.7.8.20 Phosphatidylglycerol--membrane-oligosaccharide glycerophosphotransferase.	2.8.2.16 Thiol sulfotransferase.
2.7.8.21 Membrane-oligosaccharide glycerophosphotransferase.	2.8.2.17 Chondroitin 6-sulfotransferase.

2.7.8.22 1-alkenyl-2-acylglycerol choline phosphotransferase.	2.8.2.18 Cortisol sulfotransferase.
2.7.8.23 Carboxyvinyl-carboxyphosphonate phosphorylmutase.	2.8.2.19 Triglycosylalkylacylglycerol sulfotransferase.
2.7.8.24 Phosphatidylcholine synthase.	2.8.2.20 Protein-tyrosine sulfotransferase.
2.7.8.25 Triphosphoribosyl-dephospho-CoA synthase.	2.8.2.21 Keratan sulfotransferase.
2.7.8.26 Adenosylcobinamide-GDP ribazoletransferase.	2.8.2.22 Arylsulfate sulfotransferase.
2.7.9.1 Pyruvate, phosphate dikinase.	2.8.2.23 [Heparan sulfate]-glucosamine 3-sulfotransferase 1.
2.7.9.2 Pyruvate, water dikinase.	2.8.2.24 Desulfoglucosinolate sulfotransferase.
2.7.9.3 Selenide, water dikinase.	2.8.2.25 Flavonol 3-sulfotransferase.
2.7.9.4 Alpha-glucan, water dikinase.	2.8.2.26 Quercetin-3-sulfate 3'-sulfotransferase.
2.8.1.1 Thiosulfate sulfur-transferase.	2.8.2.27 Quercetin-3-sulfate 4'-sulfotransferase.
2.8.1.2 3-mercaptopyruvate sulfur-transferase.	2.8.2.28 Quercetin-3,3'-bissulfate 7-sulfotransferase.
2.8.1.3 Thiosulfate--thiol sulfur-transferase.	2.8.2.29 [Heparan sulfate]-glucosamine 3-sulfotransferase 2.
2.8.1.4 tRNA sulfur-transferase.	2.8.2.30 [Heparan sulfate]-glucosamine 3-sulfotransferase 3.
2.8.1.5 Thiosulfate--dithiol sulfur-transferase.	2.8.3.1 Propionate CoA-transferase.
2.8.1.6 Biotin synthase.	2.8.3.2 Oxalate CoA-transferase.
2.8.1.7 Cysteine desulfurase.	2.8.3.3 Malonate CoA-transferase.

2.8.3.5 3-oxoacid CoA-transferase.	3.1.1.34 Lipoprotein lipase.
2.8.3.6 3-oxoadipate CoA-transferase.	3.1.1.35 Dihydrocoumarin hydrolase.
2.8.3.7 Succinate--citramalate CoA-transferase.	3.1.1.36 Limonin-D-ring-lactonase.
2.8.3.8 Acetate CoA-transferase.	3.1.1.37 Steroid-lactonase.
2.8.3.9 Butyrate--acetoacetate CoA-transferase.	3.1.1.38 Triacetate-lactonase.
2.8.3.10 Citrate CoA-transferase.	3.1.1.39 Actinomycin lactonase.
2.8.3.11 Citramalate CoA-transferase.	3.1.1.40 Orsellinate-depside hydrolase.
2.8.3.12 Glutaconate CoA-transferase.	3.1.1.41 Cephalosporin-C deacetylase.
2.8.3.13 Succinate--hydroxymethylglutarate CoA-transferase.	3.1.1.42 Chlorogenate hydrolase.
2.8.3.14 5-hydroxypentanoate CoA-transferase.	3.1.1.43 Alpha-amino-acid esterase.
2.8.3.15 Succinyl-CoA:(R)-benzylsuccinate CoA-transferase.	3.1.1.44 4-methyloxaloacetate esterase.
2.8.3.16 Formyl-CoA transferase.	3.1.1.45 Carboxymethylenebutenolidase.
2.8.3.17 Cinnamoyl-CoA:phenyllactate CoA-transferase.	3.1.1.46 Deoxylimonate A-ring-lactonase.
2.8.4.1 Coenzyme-B sulfoethylthiotransferase.	3.1.1.47 1-alkyl-2-acetylgllycerophosphocholine esterase.
2.9.1.1 L-seryl-tRNA(Sec) selenium transferase.	3.1.1.48 Fusarinine-C ornithinesterase.
ENZYME: 3.-.-.-	3.1.1.49 Sinapine esterase.
3.1.1.1 Carboxylesterase.	3.1.1.50 Wax-ester hydrolase.
3.1.1.2 Arylesterase.	3.1.1.51 Phorbol-diester hydrolase.
3.1.1.3 Triacylglycerol lipase.	3.1.1.52 Phosphatidylinositol deacylase.
3.1.1.4 Phospholipase A(2).	3.1.1.53 Sialate O-acylesterase.
3.1.1.5 Lysophospholipase.	3.1.1.54 Acetoxybutynylbithiophene deacetylase.
3.1.1.6 Acylesterase.	3.1.1.55 Acetylsalicylate deacetylase.
3.1.1.7 Acetylcholinesterase.	3.1.1.56 Methylumbelliferyl-acetate deacetylase.
3.1.1.8 Cholinesterase.	3.1.1.57 2-pyrone-4,6-dicarboxylate lactonase.
	3.1.1.58 N-acetylgalactosaminoglycan

	deacetylase.
3.1.1.10 Tropinesterase.	3.1.1.59 Juvenile-hormone esterase.
3.1.1.11 Pectinesterase.	3.1.1.60 Bis(2-ethylhexyl)phthalate esterase.
3.1.1.13 Sterol esterase.	3.1.1.61 Protein-glutamate methylesterase.
3.1.1.14 Chlorophyllase.	3.1.1.63 11-cis-retinyl-palmitate hydrolase.
3.1.1.15 L-arabinonolactonase.	3.1.1.64 All-trans-retinyl-palmitate hydrolase.
3.1.1.17 Gluconolactonase.	3.1.1.65 L-rhamnono-1,4-lactonase.
3.1.1.19 Uronolactonase.	3.1.1.66 5-(3,4-diacetoxybut-1-ynyl)-2,2'-bithiophene deacetylase.
3.1.1.20 Tannase.	3.1.1.67 Fatty-acyl-ethyl-ester synthase.
3.1.1.21 Retinyl-palmitate esterase.	3.1.1.68 Xylono-1,4-lactonase.
3.1.1.22 Hydroxybutyrate-dimer hydrolase.	3.1.1.70 Cetraxate benzylesterase.
3.1.1.23 Acylglycerol lipase.	3.1.1.71 Acetylalkylglycerol acetylhydrolase.
3.1.1.24 3-oxoadipate enol-lactonase.	3.1.1.72 Acetylxytan esterase.
3.1.1.25 1,4-lactonase.	3.1.1.73 Feruloyl esterase.
3.1.1.26 Galactolipase.	3.1.1.74 Cutinase.
3.1.1.27 4-pyridoxolactonase.	3.1.1.75 Poly(3-hydroxybutyrate) depolymerase.
3.1.1.28 Acylcarnitine hydrolase.	3.1.1.76 Poly(3-hydroxyoctanoate) depolymerase.
3.1.1.29 Aminoacyl-tRNA hydrolase.	3.1.1.77 Acyloxyacyl hydrolase.
3.1.1.30 D-arabinonolactonase.	3.1.1.78 Polyneuridine-aldehyde esterase.
3.1.1.31 6-phosphogluconolactonase.	3.1.1.79 Hormone-sensitive lipase.
3.1.1.32 Phospholipase A(1).	3.1.2.1 Acetyl-CoA hydrolase.
3.1.1.33 6-acetylglucose deacetylase.	3.1.2.2 Palmitoyl-CoA hydrolase.

3.1.2.3 Succinyl-CoA hydrolase.	3.1.3.23 Sugar-phosphatase.
3.1.2.4 3-hydroxyisobutyryl-CoA hydrolase.	3.1.3.24 Sucrose-phosphatase.
3.1.2.5 Hydroxymethylglutaryl-CoA hydrolase.	3.1.3.25 Inositol-1(or 4)-monophosphatase.
3.1.2.6 Hydroxyacylglutathione hydrolase.	3.1.3.26 4-phytase.
3.1.2.7 Glutathione thioesterase.	3.1.3.27 Phosphatidylglycerophosphatase.
3.1.2.10 Formyl-CoA hydrolase.	3.1.3.28 ADP-phosphoglycerate phosphatase.
3.1.2.11 Acetoacetyl-CoA hydrolase.	3.1.3.29 N-acylneuraminate-9-phosphatase.
3.1.2.12 S-formylglutathione hydrolase.	3.1.3.31 Nucleotidase.
3.1.2.13 S-succinylglutathione hydrolase.	3.1.3.32 Polynucleotide 3'-phosphatase.
3.1.2.14 Oleoyl-[acyl-carrier-protein] hydrolase.	3.1.3.33 Polynucleotide 5'-phosphatase.
3.1.2.15 Ubiquitin thioesterase.	3.1.3.34 Deoxynucleotide 3'-phosphatase.
3.1.2.16 [Citrate-(pro-3S)-lyase] thioesterase.	3.1.3.35 Thymidylate 5'-phosphatase.
3.1.2.17 (S)-methylmalonyl-CoA hydrolase.	3.1.3.36 Phosphoinositide 5-phosphatase.
3.1.2.18 ADP-dependent short-chain-acyl-CoA hydrolase.	3.1.3.37 Sedoheptulose-bisphosphatase.
3.1.2.19 ADP-dependent medium-chain-acyl-CoA hydrolase.	3.1.3.38 3-phosphoglycerate phosphatase.
3.1.2.20 Acyl-CoA hydrolase.	3.1.3.39 Streptomycin-6-phosphatase.
3.1.2.21 Dodecanoyl-[acyl-carrier protein] hydrolase.	3.1.3.40 Guanidinodeoxy-scylo-inositol-4-phosphatase.
3.1.2.22 Palmitoyl-protein hydrolase.	3.1.3.41 4-nitrophenylphosphatase.
3.1.2.23 4-hydroxybenzoyl-CoA thioesterase.	3.1.3.42 [Glycogen-synthase-D] phosphatase.
3.1.2.24 2-(2-hydroxyphenyl)benzenesulfinate hydrolase.	3.1.3.43 [Pyruvate dehydrogenase (lipoamide)]-phosphatase.
3.1.2.25 Phenylacetyl-CoA hydrolase.	3.1.3.44 [Acetyl-CoA carboxylase]-phosphatase.
3.1.3.1 Alkaline phosphatase.	3.1.3.45 3-deoxy-manno-octulosonate-8-phosphatase.
3.1.3.2 Acid phosphatase.	3.1.3.46 Fructose-2,6-bisphosphate 2-

	phosphatase.
3.1.3.3 Phosphoserine phosphatase.	3.1.3.47 [Hydroxymethylglutaryl-CoA reductase (NADPH)]-phosphatase.
3.1.3.4 Phosphatidate phosphatase.	3.1.3.48 Protein-tyrosine-phosphatase.
3.1.3.5 5'-nucleotidase.	3.1.3.49 [Pyruvate kinase]-phosphatase.
3.1.3.6 3'-nucleotidase.	3.1.3.50 Sorbitol-6-phosphatase.
3.1.3.7 3'(2'),5'-bisphosphate nucleotidase.	3.1.3.51 Dolichyl-phosphatase.
3.1.3.8 3-phytase.	3.1.3.52 [3-methyl-2-oxobutanoate dehydrogenase (lipoamide)]-phosphatase.
3.1.3.9 Glucose-6-phosphatase.	3.1.3.53 [Myosin light-chain]-phosphatase.
3.1.3.10 Glucose-1-phosphatase.	3.1.3.54 Fructose-2,6-bisphosphate 6-phosphatase.
3.1.3.11 Fructose-bisphosphatase.	3.1.3.55 Caldesmon-phosphatase.
3.1.3.12 Trehalose-phosphatase.	3.1.3.56 Inositol-polyphosphate 5-phosphatase.
3.1.3.13 Bisphosphoglycerate phosphatase.	3.1.3.57 Inositol-1,4-bisphosphate 1-phosphatase.
3.1.3.14 Methylphosphothioglycerate phosphatase.	3.1.3.58 Sugar-terminal-phosphatase.
3.1.3.15 Histidinol-phosphatase.	3.1.3.59 Alkylacetylgllycerophosphatase.
3.1.3.16 Phosphoprotein phosphatase.	3.1.3.60 Phosphoenolpyruvate phosphatase.
3.1.3.17 [Phosphorylase] phosphatase.	3.1.3.62 Multiple inositol-polyphosphate phosphatase.
3.1.3.18 Phosphoglycolate phosphatase.	3.1.3.63 2-carboxy-D-arabinitol-1-phosphatase.
3.1.3.19 Glycerol-2-phosphatase.	3.1.3.64 Phosphatidylinositol-3-phosphatase.
3.1.3.20 Phosphoglycerate phosphatase.	3.1.3.66 Phosphatidylinositol-3,4-bisphosphate 4-phosphatase.
3.1.3.21 Glycerol-1-phosphatase.	3.1.3.67 Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase.
3.1.3.22 Mannitol-1-phosphatase.	3.1.3.68 2-deoxyglucose-6-phosphatase.

3.1.3.69 Glucosylglycerol 3-phosphatase.	3.1.13.3 Oligonucleotidase.
3.1.3.70 Mannosyl-3-phosphoglycerate phosphatase.	3.1.13.4 Poly(A)-specific ribonuclease.
3.1.3.71 2-phosphosulfolactate phosphatase.	3.1.14.1 Yeast ribonuclease.
3.1.3.72 5-phytase.	3.1.15.1 Venom exonuclease.
3.1.3.73 Alpha-ribose phosphatase.	3.1.16.1 Spleen exonuclease.
3.1.4.1 Phosphodiesterase I.	3.1.21.1 Deoxyribonuclease I.
3.1.4.2 Glycerophosphocholine phosphodiesterase.	3.1.6.3 Glycosulfatase.
3.1.4.3 Phospholipase C.	3.1.6.4 N-acetylgalactosamine-6-sulfatase.
3.1.4.4 Phospholipase D.	3.1.6.6 Choline-sulfatase.
3.1.4.11 Phosphoinositide phospholipase C.	3.1.6.7 Cellulose-polysulfatase.
3.1.4.12 Sphingomyelin phosphodiesterase.	3.1.6.8 Cerebroside-sulfatase.
3.1.4.13 Serine-ethanolaminephosphate phosphodiesterase.	3.1.6.9 Chondro-4-sulfatase.
3.1.4.14 [Acyl-carrier-protein] phosphodiesterase.	3.1.6.10 Chondro-6-sulfatase.
3.1.4.15 Adenyl-[glutamate--ammonia ligase] hydrolase.	3.1.6.11 Disulfoglucosamine-6-sulfatase.
3.1.4.16 2',3'-cyclic-nucleotide 2'-phosphodiesterase.	3.1.6.12 N-acetylgalactosamine-4-sulfatase.
3.1.4.17 3',5'-cyclic-nucleotide phosphodiesterase.	3.1.6.13 Iduronate-2-sulfatase.
3.1.4.35 3',5'-cyclic-GMP phosphodiesterase.	3.1.6.14 N-acetylglucosamine-6-sulfatase.
3.1.4.37 2',3'-cyclic-nucleotide 3'-phosphodiesterase.	3.1.6.15 N-sulfoglucosamine-3-sulfatase.

3.1.4.38 Glycerophosphocholine cholinephosphodiesterase.	3.1.6.16 Monomethyl-sulfatase.
3.1.4.39 Alkylglycerophosphoethanolamine phosphodiesterase.	3.1.6.17 D-lactate-2-sulfatase.
3.1.4.40 CMP-N-acylneuraminate phosphodiesterase.	3.1.6.18 Glucuronate-2-sulfatase.
3.1.4.41 Sphingomyelin phosphodiesterase D.	3.1.7.1 Prenyl-diphosphatase.
3.1.4.42 Glycerol-1,2-cyclic-phosphate 2-phosphodiesterase.	3.1.7.2 Guanosine-3',5'-bis(diphosphate) 3'-diphosphatase.
3.1.4.43 Glycerophosphoinositol inositolphosphodiesterase.	3.1.7.3 Monoterpenyl-diphosphatase.
3.1.4.44 Glycerophosphoinositol glycerophosphodiesterase.	3.1.8.1 Aryldialkylphosphatase.
3.1.4.45 N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase.	3.1.8.2 Diisopropyl-fluorophosphatase.
3.1.4.46 Glycerophosphodiester phosphodiesterase.	3.1.11.1 Exodeoxyribonuclease I.
3.1.4.48 Dolichylphosphate-glucose phosphodiesterase.	3.1.11.2 Exodeoxyribonuclease III.
3.1.4.49 Dolichylphosphate-mannose phosphodiesterase.	3.1.11.3 Exodeoxyribonuclease (lambda-induced).
3.1.4.50 Glycosylphosphatidylinositol phospholipase D.	3.1.11.4 Exodeoxyribonuclease (phage Sp3-induced).
3.1.4.51 Glucose-1-phospho-D-mannosylglycoprotein phosphodiesterase.	3.1.11.5 Exodeoxyribonuclease V.
3.1.5.1 dGTPase.	3.1.11.6 Exodeoxyribonuclease VII.
3.1.6.1 Arylsulfatase.	3.1.13.1 Exoribonuclease II.
3.1.6.2 Steryl-sulfatase.	3.1.13.2 Exoribonuclease H.

3.1.21.2 Deoxyribonuclease IV (phage-T(4)-induced).	3.2.1.23 Beta-galactosidase.
3.1.21.3 Type I site-specific deoxyribonuclease.	3.2.1.24 Alpha-mannosidase.
3.1.21.4 Type II site-specific deoxyribonuclease.	3.2.1.25 Beta-mannosidase.
3.1.21.5 Type III site-specific deoxyribonuclease.	3.2.1.26 Beta-fructofuranosidase.
3.1.21.6 CC-preferring endodeoxyribonuclease.	3.2.1.28 Alpha, alpha-trehalase.
3.1.21.7 Deoxyribonuclease V.	3.2.1.31 Beta-glucuronidase.
3.1.22.1 Deoxyribonuclease II.	3.2.1.32 Xylan endo-1,3-beta-xylosidase.
3.1.22.2 Aspergillus deoxyribonuclease K(1).	3.2.1.33 Amylo-alpha-1,6-glucosidase.
3.1.22.4 Crossover junction endoribonuclease.	3.2.1.35 Hyaluronoglucosaminidase.
3.1.22.5 Deoxyribonuclease X.	3.2.1.36 Hyaluronoglucuronidase.
3.1.25.1 Deoxyribonuclease (pyrimidine dimer).	3.2.1.37 Xylan 1,4-beta-xylosidase.
3.1.26.1 Physarum polycephalum ribonuclease.	3.2.1.38 Beta-D-fucosidase.
3.1.26.2 Ribonuclease alpha.	3.2.1.39 Glucan endo-1,3-beta-D-glucosidase.
3.1.26.3 Ribonuclease III.	3.2.1.40 Alpha-L-rhamnosidase.
3.1.26.4 Ribonuclease H.	3.2.1.41 Pullulanase.
3.1.26.5 Ribonuclease P.	3.2.1.42 GDP-glucosidase.
3.1.26.6 Ribonuclease IV.	3.2.1.43 Beta-L-rhamnosidase.
3.1.26.7 Ribonuclease P4.	3.2.1.44 Fucoidanase.
3.1.26.8 Ribonuclease M5.	3.2.1.45 Glucosylceramidase.
3.1.26.9 Ribonuclease (poly-(U)-specific).	3.2.1.46 Galactosylceramidase.
3.1.26.10 Ribonuclease IX.	3.2.1.47 Galactosylgalactosylglucosylceramidase.
3.1.26.11 Ribonuclease Z.	3.2.1.48 Sucrose alpha-glucosidase.
3.1.27.1 Ribonuclease T(2).	3.2.1.49 Alpha-N-acetylgalactosaminidase.

3.1.27.2	Bacillus subtilis ribonuclease.	3.2.1.50	Alpha-N-acetylglucosaminidase.
3.1.27.3	Ribonuclease T(1).	3.2.1.51	Alpha-L-fucosidase.
3.1.27.4	Ribonuclease U(2).	3.2.1.52	Beta-N-acetylhexosaminidase.
3.1.27.5	Pancreatic ribonuclease.	3.2.1.53	Beta-N-acetylgalactosaminidase.
3.1.27.6	Enterobacter ribonuclease.	3.2.1.54	Cyclomaltodextrinase.
3.1.27.7	Ribonuclease F.	3.2.1.55	Alpha-N-arabinofuranosidase.
3.1.27.8	Ribonuclease V.	3.2.1.56	Glucuronosyl-disulfoglucosamine glucuronidase.
3.1.27.9	tRNA-intron endonuclease.	3.2.1.57	Isopullulanase.
3.1.27.10	rRNA endonuclease.	3.2.1.58	Glucan 1,3-beta-glucosidase.
3.1.30.1	Aspergillus nuclease S(1).	3.2.1.59	Glucan endo-1,3-alpha-glucosidase.
3.1.30.2	Serratia marcescens nuclease.	3.2.1.60	Glucan 1,4-alpha-maltotetraohydrolase.
3.1.31.1	Micrococcal nuclease.	3.2.1.61	Mycodextranase.
3.2.1.1	Alpha-amylase.	3.2.1.62	Glycosylceramidase.
3.2.1.2	Beta-amylase.	3.2.1.63	1,2-alpha-L-fucosidase.
3.2.1.3	Glucan 1,4-alpha-glucosidase.	3.2.1.64	2,6-beta-fructan 6-levanbiohydrolase.
3.2.1.4	Cellulase.	3.2.1.65	Levanase.
3.2.1.6	Endo-1,3(4)-beta-glucanase.	3.2.1.66	Quercitrinase.
3.2.1.7	Inulinase.	3.2.1.67	Galacturan 1,4-alpha-galacturonidase.
3.2.1.8	Endo-1,4-beta-xylanase.	3.2.1.68	Isoamylase.
3.2.1.10	Oligo-1,6-glucosidase.	3.2.1.70	Glucan 1,6-alpha-glucosidase.
3.2.1.11	Dextranase.	3.2.1.71	Glucan endo-1,2-beta-glucosidase.
3.2.1.14	Chitinase.	3.2.1.72	Xylan 1,3-beta-xylosidase.
3.2.1.15	Polygalacturonase.	3.2.1.73	Licheninase.
3.2.1.17	Lysozyme.	3.2.1.74	Glucan 1,4-beta-glucosidase.
3.2.1.18	Exo-alpha-sialidase.	3.2.1.75	Glucan endo-1,6-beta-glucosidase.
3.2.1.20	Alpha-glucosidase.	3.2.1.76	L-iduronidase.
3.2.1.21	Beta-glucosidase.	3.2.1.77	Mannan 1,2-(1,3)-alpha-mannosidase.
3.2.1.22	Alpha-galactosidase.	3.2.1.78	Mannan endo-1,4-beta-mannosidase.

3.2.1.80	Fructan beta-fructosidase.	3.2.1.121	Polymannuronate hydrolase.
3.2.1.81	Agarase.	3.2.1.122	Maltose-6'-phosphate glucosidase.
3.2.1.82	Exo-poly-alpha-galacturonosidase.	3.2.1.123	Endoglycosylceramidase.
3.2.1.83	Kappa-carrageenase.	3.2.1.124	3-deoxy-2-octulosonidase.
3.2.1.84	Glucan 1,3-alpha-glucosidase.	3.2.1.125	Raucaffricine beta-glucosidase.
3.2.1.85	6-phospho-beta-galactosidase.	3.2.1.126	Coniferin beta-glucosidase.
3.2.1.86	6-phospho-beta-glucosidase.	3.2.1.127	1,6-alpha-L-fucosidase.
3.2.1.87	Capsular-polysaccharide endo-1,3-alpha-galactosidase.	3.2.1.128	Glycyrrhizinate beta-glucuronidase.
3.2.1.88	Beta-L-arabinosidase.	3.2.1.129	Endo-alpha-sialidase.
3.2.1.89	Arabinogalactan endo-1,4-beta-galactosidase.	3.2.1.130	Glycoprotein endo-alpha-1,2-mannosidase.
3.2.1.91	Cellulose 1,4-beta-cellobiosidase.	3.2.1.131	Xylan alpha-1,2-glucuronosidase.
3.2.1.92	Peptidoglycan beta-N-acetylmuramidase.	3.2.1.132	Chitosanase.
3.2.1.93	Alpha, alpha-phosphotrehalase.	3.2.1.133	Glucan 1,4-alpha-maltohydrolase.
3.2.1.94	Glucan 1,6-alpha-isomaltosidase.	3.2.1.134	Difructose-anhydride synthase.
3.2.1.95	Dextran 1,6-alpha-isomaltotriosidase.	3.2.1.135	Neopullulanase.
3.2.1.96	Mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase.	3.2.1.136	Glucuronoarabinoxylan endo-1,4-beta-xylanase.
3.2.1.97	Glycopeptide alpha-N-acetylgalactosaminidase.	3.2.1.137	Mannan exo-1,2-1,6-alpha-mannosidase.
3.2.1.98	Glucan 1,4-alpha-maltohexaosidase.	3.2.1.139	Alpha-glucuronidase.

3.2.1.99 Arabinan endo-1,5- α -L-arabinosidase.	3.2.1.140 Lacto-N-biosidase.
3.2.1.100 Mannan 1,4-mannobiosidase.	3.2.1.141 4- α -D- $\{(1\rightarrow4)\}$ - α -D-glucano}trehalose trehalohydrolase.
3.2.1.101 Mannan endo-1,6- α -mannosidase.	3.2.1.142 Limit dextrinase.
3.2.1.102 Blood-group-substance endo-1,4- β -galactosidase.	3.2.1.143 Poly(ADP-ribose) glycohydrolase.
3.2.1.103 Keratan-sulfate endo-1,4- β -galactosidase.	3.2.1.144 3-deoxyoctulosonase.
3.2.1.104 Steryl- β -glucosidase.	3.2.1.145 Galactan 1,3- β -galactosidase.
3.2.1.105 Strictosidine β -glucosidase.	3.2.1.146 β -galactofuranosidase.
3.2.1.106 Mannosyl-oligosaccharide glucosidase.	3.2.1.147 Thioglucosidase.
3.2.1.107 Protein-glucosylgalactosylhydroxylysine glucosidase.	3.2.1.148 Ribosylhomocysteinase.
3.2.1.108 Lactase.	3.2.1.149 β -primeverosidase.
3.2.1.109 Endogalactosaminidase.	3.2.1.150 Oligoxyloglucan reducing-end-specific cellobiohydrolase.
3.2.1.110 Mucinaminyserine mucinaminidase.	3.2.1.151 Xyloglucan-specific endo- β -1,4-glucanase.
3.2.1.111 1,3- α -L-fucosidase.	3.2.2.1 Purine nucleosidase.
3.2.1.112 2-deoxyglucosidase.	3.2.2.2 Inosine nucleosidase.
3.2.1.113 Mannosyl-oligosaccharide 1,2- α -mannosidase.	3.2.2.3 Uridine nucleosidase.
3.2.1.114 Mannosyl-oligosaccharide 1,3-1,6- α -mannosidase.	3.2.2.4 AMP nucleosidase.
3.2.1.115 Branched-dextran exo-1,2- α -glucosidase.	3.2.2.5 NAD(+) nucleosidase.
3.2.1.116 Glucan 1,4- α -maltotriohydrolase.	3.2.2.6 NAD(P)(+) nucleosidase.
3.2.1.117 Amygdalin β -glucosidase.	3.2.2.7 Adenosine nucleosidase.
3.2.1.118 Prunasin β -glucosidase.	3.2.2.8 Ribosylpyrimidine nucleosidase.
3.2.1.119 Vicianin β -glucosidase.	3.2.2.9 Adenosylhomocysteine nucleosidase.
3.2.1.120 Oligoxyloglucan β -glycosidase.	3.2.2.10 Pyrimidine-5'-nucleotide nucleosidase.

3.2.2.11 β -aspartyl-N-acetylglucosaminidase.	3.4.13.18 Cytosol nonspecific dipeptidase.
3.2.2.12 Inosinate nucleosidase.	3.4.13.19 Membrane dipeptidase.
3.2.2.13 1-methyladenosine nucleosidase.	3.4.13.20 β -Ala-His dipeptidase.
3.2.2.14 NMN nucleosidase.	3.4.13.21 Dipeptidase E.
3.2.2.15 DNA-deoxyinosine glycosylase.	3.4.14.1 Dipeptidyl-peptidase I.
3.2.2.16 Methylthioadenosine nucleosidase.	3.4.14.2 Dipeptidyl-peptidase II.
3.2.2.17 Deoxyribodipyrimidine endonucleosidase.	3.4.14.4 Dipeptidyl-peptidase III.
3.2.2.19 [Protein ADP-ribosylarginine] hydrolase.	3.4.14.5 Dipeptidyl-peptidase IV.
3.2.2.20 DNA-3-methyladenine glycosylase I.	3.4.14.6 Dipeptidyl-dipeptidase.
3.2.2.21 DNA-3-methyladenine glycosylase II.	3.4.14.9 Tripeptidyl-peptidase I.
3.2.2.22 rRNA N-glycosylase.	3.4.14.10 Tripeptidyl-peptidase II.
3.2.2.23 DNA-formamidopyrimidine glycosylase.	3.4.14.11 Xaa-Pro dipeptidyl-peptidase.
3.2.2.24 ADP-ribosyl-[dinitrogen reductase] hydrolase.	3.4.15.1 Peptidyl-dipeptidase A.
3.3.1.1 Adenosylhomocysteinase.	3.4.15.4 Peptidyl-dipeptidase B.
3.3.1.2 Adenosylmethionine hydrolase.	3.4.15.5 Peptidyl-dipeptidase Dcp.
3.3.2.1 Isochorismatase.	3.4.16.2 Lysosomal Pro-X carboxypeptidase.
3.3.2.2 Alkenylglycerophosphocholine hydrolase.	3.4.16.4 Serine-type D-Ala-D-Ala carboxypeptidase.
3.3.2.3 Epoxide hydrolase.	3.4.16.5 Carboxypeptidase C.
3.3.2.4 Trans-epoxysuccinate hydrolase.	3.4.16.6 Carboxypeptidase D.

3.3.2.5 Alkenylglycerophosphoethanolamine hydrolase.	3.4.17.1 Carboxypeptidase A.
3.3.2.6 Leukotriene-A(4) hydrolase.	3.4.17.2 Carboxypeptidase B.
3.3.2.7 Hepoxilin-epoxide hydrolase.	3.4.17.3 Lysine carboxypeptidase.
3.3.2.8 Limonene-1,2-epoxide hydrolase.	3.4.17.4 Gly-X carboxypeptidase.
3.4.11.1 Leucyl aminopeptidase.	3.4.17.6 Alanine carboxypeptidase.
3.4.11.2 Membrane alanyl aminopeptidase.	3.4.17.8 Muramoylpentapeptide carboxypeptidase.
3.4.11.3 Cystinyl aminopeptidase.	3.4.17.10 Carboxypeptidase E.
3.4.11.4 Tripeptide aminopeptidase.	3.4.17.11 Glutamate carboxypeptidase.
3.4.11.5 Prolyl aminopeptidase.	3.4.17.12 Carboxypeptidase M.
3.4.11.6 Aminopeptidase B.	3.4.17.13 Muramoyltetrapeptide carboxypeptidase.
3.4.11.7 Glutamyl aminopeptidase.	3.4.17.14 Zinc D-Ala-D-Ala carboxypeptidase.
3.4.11.9 Xaa-Pro aminopeptidase.	3.4.17.15 Carboxypeptidase A2.
3.4.11.10 Bacterial leucyl aminopeptidase.	3.4.17.16 Membrane Pro-X carboxypeptidase.
3.4.11.13 Clostridial aminopeptidase.	3.4.17.17 Tubuliny-Tyr carboxypeptidase.
3.4.11.14 Cytosol alanyl aminopeptidase.	3.4.17.18 Carboxypeptidase T.
3.4.11.15 Aminopeptidase Y.	3.4.17.19 Carboxypeptidase Taq.
3.4.11.16 Xaa-Trp aminopeptidase.	3.4.17.20 Carboxypeptidase U.
3.4.11.17 Tryptophanyl aminopeptidase.	3.4.17.21 Glutamate carboxypeptidase II.
3.4.11.18 Methionyl aminopeptidase.	3.4.17.22 Metallo-carboxypeptidase D.
3.4.11.19 D-stereospecific aminopeptidase.	3.4.18.1 Cathepsin X.
3.4.11.20 Aminopeptidase Ey.	3.4.19.1 Acylaminoacyl-peptidase.
3.4.11.21 Aspartyl aminopeptidase.	3.4.19.2 Peptidyl-glycinamidase.
3.4.11.22 Aminopeptidase I.	3.4.19.3 Pyroglutamyl-peptidase I.
3.4.11.23 PepB aminopeptidase.	3.4.19.5 Beta-aspartyl-peptidase.
3.4.13.3 Xaa-His dipeptidase.	3.4.19.6 Pyroglutamyl-peptidase II.
3.4.13.4 Xaa-Arg dipeptidase.	3.4.19.7 N-formylmethionyl-peptidase.
3.4.13.5 Xaa-methyl-His dipeptidase.	3.4.19.9 Gamma-glutamyl hydrolase.
3.4.13.7 Glu-Glu dipeptidase.	3.4.19.11 Gamma-D-glutamyl-meso-diaminopimelate peptidase.
3.4.13.9 Xaa-Pro dipeptidase.	3.4.19.12 Ubiquitinyl hydrolase 1.
3.4.13.12 Met-Xaa dipeptidase.	3.4.21.1 Chymotrypsin.
3.4.13.17 Non-stereospecific dipeptidase.	3.4.21.2 Chymotrypsin C.

3.4.21.3 Metridin.	3.4.21.74 Venombin A.
3.4.21.4 Trypsin.	3.4.21.75 Furin.
3.4.21.5 Thrombin.	3.4.21.76 Myeloblastin.
3.4.21.6 Coagulation factor Xa.	3.4.21.77 Semenogelase.
3.4.21.7 Plasmin.	3.4.21.78 Granzyme A.
3.4.21.9 Enteropeptidase.	3.4.21.79 Granzyme B.
3.4.21.10 Acrosin.	3.4.21.80 Streptogrisin A.
3.4.21.12 Alpha-lytic endopeptidase.	3.4.21.81 Streptogrisin B.
3.4.21.19 Glutamyl endopeptidase.	3.4.21.82 Glutamyl endopeptidase II.
3.4.21.20 Cathepsin G.	3.4.21.83 Oligopeptidase B.
3.4.21.21 Coagulation factor VIIa.	3.4.21.84 Limulus clotting factor C.
3.4.21.22 Coagulation factor IXa.	3.4.21.85 Limulus clotting factor B.
3.4.21.25 Cucumisin.	3.4.21.86 Limulus clotting enzyme.
3.4.21.26 Prolyl oligopeptidase.	3.4.21.87 Omptin.
3.4.21.27 Coagulation factor XIa.	3.4.21.88 Repressor lexA.
3.4.21.32 Brachyurin.	3.4.21.89 Signal peptidase I.
3.4.21.34 Plasma kallikrein.	3.4.21.90 Togavirin.

3.4.21.35	Tissue kallikrein.	3.4.21.91	Flavivirin.
3.4.21.36	Pancreatic elastase.	3.4.21.92	Endopeptidase Clp.
3.4.21.37	Leukocyte elastase.	3.4.21.93	Proprotein convertase 1.
3.4.21.38	Coagulation factor XIIa.	3.4.21.94	Proprotein convertase 2.
3.4.21.39	Chymase.	3.4.21.95	Snake venom factor V activator.
3.4.21.41	Complement subcomponent C1r.	3.4.21.96	Lactocepin.
3.4.21.42	Complement subcomponent C1s.	3.4.21.97	Assemblin.
3.4.21.43	Classical-complement-pathway C3/C5 convertase.	3.4.21.98	Hepacivirin.
3.4.21.45	Complement factor I.	3.4.21.99	Spermosin.
3.4.21.46	Complement factor D.	3.4.21.100	Pseudomonalisin.
3.4.21.47	Alternative-complement-pathway C3/C5 convertase.	3.4.21.101	Xanthomonalisin.
3.4.21.48	Cerevisin.	3.4.21.102	C-terminal processing peptidase.
3.4.21.49	Hypodermin C.	3.4.21.103	Physarolisin.
3.4.21.50	Lysyl endopeptidase.	3.4.22.1	Cathepsin B.
3.4.21.53	Endopeptidase La.	3.4.22.2	Papain.
3.4.21.54	Gamma-renin.	3.4.22.3	Ficain.
3.4.21.55	Venombin AB.	3.4.22.6	Chymopapain.
3.4.21.57	Leucyl endopeptidase.	3.4.22.7	Asclepain.
3.4.21.59	Tryptase.	3.4.22.8	Clostripain.
3.4.21.60	Scutellarin.	3.4.22.10	Streptopain.
3.4.21.61	Kexin.	3.4.22.14	Actinidain.
3.4.21.62	Subtilisin.	3.4.22.15	Cathepsin L.
3.4.21.63	Oryzin.	3.4.22.16	Cathepsin H.
3.4.21.64	Endopeptidase K.	3.4.22.24	Cathepsin T.
3.4.21.65	Thermomycolin.	3.4.22.25	Glycyl endopeptidase.
3.4.21.66	Thermitase.	3.4.22.26	Cancer procoagulant.
3.4.21.67	Endopeptidase So.	3.4.22.27	Cathepsin S.
3.4.21.68	T-plasminogen activator.	3.4.22.28	Picornain 3C.
3.4.21.69	Protein C (activated).	3.4.22.29	Picornain 2A.
3.4.21.70	Pancreatic endopeptidase E.	3.4.22.30	Caricain.
3.4.21.71	Pancreatic elastase II.	3.4.22.31	Ananain.
3.4.21.72	IgA-specific serine endopeptidase.	3.4.22.32	Stem bromelain.
3.4.21.73	U-plasminogen activator.	3.4.22.33	Fruit bromelain.

3.4.22.34	Legumain.	3.4.23.44	Nodavirus endopeptidase.
3.4.22.35	Histolysain.	3.4.23.45	Memapsin 1.
3.4.22.36	Caspase-1.	3.4.23.46	Memapsin 2.
3.4.22.37	Gingipain R.	3.4.23.47	HIV-2 retropepsin.
3.4.22.38	Cathepsin K.	3.4.23.48	Plasminogen activator Pla.
3.4.22.39	Adenain.	3.4.24.1	Atrolysin A.
3.4.22.40	Bleomycin hydrolase.	3.4.24.3	Microbial collagenase.
3.4.22.41	Cathepsin F.	3.4.24.6	Leucolysin.
3.4.22.42	Cathepsin O.	3.4.24.7	Interstitial collagenase.
3.4.22.43	Cathepsin V.	3.4.24.11	Neprilysin.
3.4.22.44	Nuclear-inclusion-a endopeptidase.	3.4.24.12	Envelysin.
3.4.22.45	Helper-component proteinase.	3.4.24.13	IgA-specific metalloendopeptidase.
3.4.22.46	L-peptidase.	3.4.24.14	Procollagen N-endopeptidase.
3.4.22.47	Gingipain K.	3.4.24.15	Thimet oligopeptidase.
3.4.22.48	Staphopain.	3.4.24.16	Neurolysin.
3.4.22.49	Separase.	3.4.24.17	Stromelysin 1.
3.4.22.50	V-cath endopeptidase.	3.4.24.18	Meprin A.

3.4.22.51	Cruzipain.	3.4.24.19	Procollagen C-endorpeptidase.
3.4.22.52	Calpain-1.	3.4.24.20	Peptidyl-Lys metalloendorpeptidase.
3.4.22.53	Calpain-2.	3.4.24.21	Astacin.
3.4.23.1	Pepsin A.	3.4.24.22	Stromelysin 2.
3.4.23.2	Pepsin B.	3.4.24.23	Matrilysin.
3.4.23.3	Gastricsin.	3.4.24.24	Gelatinase A.
3.4.23.4	Chymosin.	3.4.24.25	Vibriolysin.
3.4.23.5	Cathepsin D.	3.4.24.26	Pseudolysin.
3.4.23.12	Nepenthesin.	3.4.24.27	Thermolysin.
3.4.23.15	Renin.	3.4.24.28	Bacillolysin.
3.4.23.16	HIV-1 retropepsin.	3.4.24.29	Aureolysin.
3.4.23.17	Pro-opiomelanocortin converting enzyme.	3.4.24.30	Coccolysin.
3.4.23.18	Aspergillopepsin I.	3.4.24.31	Mycolysin.
3.4.23.19	Aspergillopepsin II.	3.4.24.32	Beta-lytic metalloendorpeptidase.
3.4.23.20	Penicillopepsin.	3.4.24.33	Peptidyl-Asp metalloendorpeptidase.
3.4.23.21	Rhizopuspepsin.	3.4.24.34	Neutrophil collagenase.
3.4.23.22	Endothiapepsin.	3.4.24.35	Gelatinase B.
3.4.23.23	Mucorpepsin.	3.4.24.36	Leishmanolysin.
3.4.23.24	Candidapepsin.	3.4.24.37	Saccharolysin.
3.4.23.25	Saccharopepsin.	3.4.24.38	Gametolysin.
3.4.23.26	Rhodotorulapepsin.	3.4.24.39	Deuterolysin.
3.4.23.28	Acrocylindropepsin.	3.4.24.40	Serralysin.
3.4.23.29	Polyporopepsin.	3.4.24.41	Atrolysin B.
3.4.23.30	Pycnoporopepsin.	3.4.24.42	Atrolysin C.
3.4.23.31	Scytalidopepsin A.	3.4.24.43	Atroxase.
3.4.23.32	Scytalidopepsin B.	3.4.24.44	Atrolysin E.
3.4.23.34	Cathepsin E.	3.4.24.45	Atrolysin F.
3.4.23.35	Barrierpepsin.	3.4.24.46	Adamalysin.
3.4.23.36	Signal peptidase II.	3.4.24.47	Horrolysin.
3.4.23.38	Plasmepsin I.	3.4.24.48	Ruberlysin.
3.4.23.39	Plasmepsin II.	3.4.24.49	Bothropasin.
3.4.23.40	Phytepsin.	3.4.24.50	Bothrolysin.
3.4.23.41	Yapsin 1.	3.4.24.51	Ophiolysin.
3.4.23.42	Thermopsin.	3.4.24.52	Trimerelysin I.
3.4.23.43	Prepilin peptidase.	3.4.24.53	Trimerelysin II.

3.4.24.54	Mucrolysin.	3.5.1.16	Acetylornithine deacetylase.
3.4.24.55	Pitrilysin.	3.5.1.17	Acyl-lysine deacylase.
3.4.24.56	Insulysin.	3.5.1.18	Succinyl-diaminopimelate desuccinylase.
3.4.24.57	O-sialoglycoprotein endopeptidase.	3.5.1.19	Nicotinamidase.
3.4.24.58	Russellysin.	3.5.1.20	Citrullinase.
3.4.24.59	Mitochondrial intermediate peptidase.	3.5.1.21	N-acetyl-beta-alanine deacetylase.
3.4.24.60	Dactylisin.	3.5.1.22	Pantothenase.
3.4.24.61	Nardilysin.	3.5.1.23	Ceramidase.
3.4.24.62	Magnolysin.	3.5.1.24	Choloylglycine hydrolase.
3.4.24.63	Mepirin B.	3.5.1.25	N-acetylglucosamine-6-phosphate deacetylase.
3.4.24.64	Mitochondrial processing peptidase.	3.5.1.26	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase.
3.4.24.65	Macrophage elastase.	3.5.1.27	N-formylmethionylaminoacyl-tRNA deformylase.
3.4.24.66	Choriolysin L.	3.5.1.28	N-acetylmuramoyl-L-alanine amidase.

3.4.24.67	Choriolysin H.	3.5.1.29	2-(acetamidomethylene)succinate hydrolase.
3.4.24.68	Tentoxilysin.	3.5.1.30	5-aminopentanamidase.
3.4.24.69	Bontoxilysin.	3.5.1.31	Formylmethionine deformylase.
3.4.24.70	Oligopeptidase A.	3.5.1.32	Hippurate hydrolase.
3.4.24.71	Endothelin-converting enzyme 1.	3.5.1.33	N-acetylglucosamine deacetylase.
3.4.24.72	Fibrolase.	3.5.1.35	D-glutaminase.
3.4.24.73	Jararhagin.	3.5.1.36	N-methyl-2-oxoglutaramate hydrolase.
3.4.24.74	Fragilysin.	3.5.1.38	Glutamin-(asparagin-)ase.
3.4.24.75	Lysostaphin.	3.5.1.39	Alkylamidase.
3.4.24.76	Flavastacin.	3.5.1.40	Acylagmatine amidase.
3.4.24.77	Snapalysin.	3.5.1.41	Chitin deacetylase.
3.4.24.78	GPR endopeptidase.	3.5.1.42	Nicotinamide-nucleotide amidase.
3.4.24.79	Pappalysin-1.	3.5.1.43	Peptidyl-glutaminase.
3.4.24.80	Membrane-type matrix metalloproteinase-1.	3.5.1.44	Protein-glutamine glutaminase.
3.4.24.81	ADAM10 endopeptidase.	3.5.1.46	6-aminohexanoate-dimer hydrolase.
3.4.24.82	ADAMTS-4 endopeptidase.	3.5.1.47	N-acetyldiaminopimelate deacetylase.
3.4.24.83	Anthrax lethal factor endopeptidase.	3.5.1.48	Acetylspermidine deacetylase.
3.4.24.84	Ste24 endopeptidase.	3.5.1.49	Formamidase.
3.4.24.85	S2P endopeptidase.	3.5.1.50	Pentanamidase.
3.4.24.86	ADAM 17 endopeptidase.	3.5.1.51	4-acetamidobutyryl-CoA deacetylase.
3.4.25.1	Proteasome endopeptidase complex.	3.5.1.52	Peptide-N(4)-(N-acetyl-beta-glucosaminy)asparagine amidase.
3.5.1.1	Asparaginase.	3.5.1.53	N-carbamoylputrescine amidase.
3.5.1.2	Glutaminase.	3.5.1.54	Allophanate hydrolase.
3.5.1.3	Omega-amidase.	3.5.1.55	Long-chain-fatty-acyl-glutamate deacylase.
3.5.1.4	Amidase.	3.5.1.56	N,N-dimethylformamidase.
3.5.1.5	Urease.	3.5.1.57	Tryptophanamidase.
3.5.1.6	Beta-ureidopropionase.	3.5.1.58	N-benzoyloxycarbonylglycine hydrolase.
3.5.1.7	Ureidosuccinase.	3.5.1.59	N-carbamoylsarcosine amidase.
3.5.1.8	Formylaspartate deformylase.	3.5.1.60	N-(long-chain-acyl)ethanolamine deacylase.
3.5.1.9	Arylformamidase.	3.5.1.61	Mimosinase.
3.5.1.10	Formyltetrahydrofolate deformylase.	3.5.1.62	Acetylputrescine deacetylase.
3.5.1.11	Penicillin amidase.	3.5.1.63	4-acetamidobutyrate deacetylase.
3.5.1.12	Biotinidase.	3.5.1.64	N(alpha)-benzoyloxycarbonylleucine hydrolase.
3.5.1.13	Aryl-acylamidase.	3.5.1.65	Theanine hydrolase.
3.5.1.14	Aminoacylase.	3.5.1.66	2-(hydroxymethyl)-3-(acetamidomethylene)succinate hydrolase.
3.5.1.15	Aspartoacylase.	3.5.1.67	4-methyleneglutaminase.

3.5.1.68	N-formylglutamate deformylase.	3.5.3.9	Allantoate deiminase.
3.5.1.69	Glycosphingolipid deacylase.	3.5.3.10	D-arginase.
3.5.1.70	Aculeacin-A deacylase.	3.5.3.11	Agmatinase.
3.5.1.71	N-feruloylglycine deacylase.	3.5.3.12	Agmatine deiminase.
3.5.1.72	D-benzoylarginine-4-nitroanilide amidase.	3.5.3.13	Formimidoylglutamate deiminase.
3.5.1.73	Carnitinamidase.	3.5.3.14	Amidinoaspartase.
3.5.1.74	Chenodeoxycholytaurine hydrolase.	3.5.3.15	Protein-arginine deiminase.
3.5.1.75	Urethanase.	3.5.3.16	Methylguanidinase.
3.5.1.76	Arylalkyl acylamidase.	3.5.3.17	Guanidinopropionase.
3.5.1.77	N-carbamoyl-D-amino acid hydrolase.	3.5.3.18	Dimethylargininase.
3.5.1.78	Glutathionylspermidine amidase.	3.5.3.19	Ureidoglycolate hydrolase.

3.5.1.79	Phthalyl amidase.	3.5.3.20	Diguanidinobutanase.
3.5.1.81	N-acyl-D-amino-acid deacylase.	3.5.3.21	Methylenediurea deaminase.
3.5.1.82	N-acyl-D-glutamate deacylase.	3.5.3.22	Proclavamate amidohydrolase.
3.5.1.83	N-acyl-D-aspartate deacylase.	3.5.4.1	Cytosine deaminase.
3.5.1.84	Biuret amidohydrolase.	3.5.4.2	Adenine deaminase.
3.5.1.85	(S)-N-acetyl-1-phenylethylamine hydrolase.	3.5.4.3	Guanine deaminase.
3.5.1.86	Mandelamide amidase.	3.5.4.4	Adenosine deaminase.
3.5.1.87	N-carbamoyl-L-amino-acid hydrolase.	3.5.4.5	Cytidine deaminase.
3.5.1.88	Peptide deformylase.	3.5.4.6	AMP deaminase.
3.5.1.89	N-acetylglucosaminylphosphatidylinositol deacetylase.	3.5.4.7	ADP deaminase.
3.5.1.90	Adenosylcobinamide hydrolase.	3.5.4.8	Aminoimidazole.
3.5.2.1	Barbiturase.	3.5.4.9	Methenyltetrahydrofolate cyclohydrolase.
3.5.2.2	Dihydropyrimidinase.	3.5.4.10	IMP cyclohydrolase.
3.5.2.3	Dihydroorotase.	3.5.4.11	Pterin deaminase.
3.5.2.4	Carboxymethylhydantoinase.	3.5.4.12	dCMP deaminase.
3.5.2.5	Allantoinase.	3.5.4.13	dCTP deaminase.
3.5.2.6	Beta-lactamase.	3.5.4.14	Deoxycytidine deaminase.
3.5.2.7	Imidazolonepropionase.	3.5.4.15	Guanosine deaminase.
3.5.2.9	5-oxoprolinase (ATP-hydrolyzing).	3.5.4.16	GTP cyclohydrolase I.
3.5.2.10	Creatininase.	3.5.4.17	Adenosine-phosphate deaminase.
3.5.2.11	L-lysine-lactamase.	3.5.4.18	ATP deaminase.
3.5.2.12	6-aminohexanoate-cyclic-dimer hydrolase.	3.5.4.19	Phosphoribosyl-AMP cyclohydrolase.
3.5.2.13	2,5-dioxopiperazine hydrolase.	3.5.4.20	Pyriithamine deaminase.
3.5.2.14	N-methylhydantoinase (ATP-hydrolyzing).	3.5.4.21	Creatinine deaminase.
3.5.2.15	Cyanuric acid amidohydrolase.	3.5.4.22	1-pyrroline-4-hydroxy-2-carboxylate deaminase.
3.5.2.16	Maleimide hydrolase.	3.5.4.23	Blasticidin-S deaminase.
3.5.2.17	Hydroxyisourate hydrolase.	3.5.4.24	Sepiapterin deaminase.
3.5.3.1	Arginase.	3.5.4.25	GTP cyclohydrolase II.
3.5.3.2	Guanidinoacetase.	3.5.4.26	Diaminohydroxyphosphoribosylaminopyrimidine deaminase.
3.5.3.3	Creatinase.	3.5.4.27	Methenyltetrahydromethanopterin cyclohydrolase.
3.5.3.4	Allantoicase.	3.5.4.28	S-adenosylhomocysteine deaminase.
3.5.3.5	Formimidoylaspartate deiminase.	3.5.4.29	GTP cyclohydrolase IIa.
3.5.3.6	Arginine deiminase.	3.5.4.30	dCTP deaminase (dUMP-forming).
3.5.3.7	Guanidinobutyrase.	3.5.5.1	Nitrilase.
3.5.3.8	Formimidoylglutamase.	3.5.5.2	Ricinine nitrilase.

3.5.5.4	Cyanoalanine nitrilase.	3.6.1.40	Guanosine-5'-triphosphate,3'-diphosphate diphosphatase.
3.5.5.5	Arylacetonitrilase.	3.6.1.41	Bis(5'-nucleosyl)-tetraphosphatase (symmetrical).
3.5.5.6	Bromoxynil nitrilase.	3.6.1.42	Guanosine-diphosphatase.
3.5.5.7	Aliphatic nitrilase.	3.6.1.43	Dolichyldiphosphatase.
3.5.5.8	Thiocyanate hydrolase.	3.6.1.44	Oligosaccharide-diphosphodolichol diphosphatase.
3.5.99.1	Riboflavinase.	3.6.1.45	UDP-sugar diphosphatase.

3.5.99.2 Thiaminase.	3.6.1.52 Diphosphoinositol-polyphosphate diphosphatase.
3.5.99.3 Hydroxydechloroatrazine ethylaminohydrolase.	3.6.2.1 Adenylylsulfatase.
3.5.99.4 N-isopropylammelide isopropylaminohydrolase.	3.6.2.2 Phosphoadenylylsulfatase.
3.5.99.5 2-aminomuconate deaminase.	3.6.3.1 Phospholipid-translocating ATPase.
3.5.99.6 Glucosamine-6-phosphate deaminase.	3.6.3.2 Magnesium-importing ATPase.
3.5.99.7 1-aminocyclopropane-1-carboxylate deaminase.	3.6.3.3 Cadmium-exporting ATPase.
3.6.1.1 Inorganic diphosphatase.	3.6.3.4 Copper-exporting ATPase.
3.6.1.2 Trimetaphosphatase.	3.6.3.5 Zinc-exporting ATPase.
3.6.1.3 Adenosinetriphosphatase.	3.6.3.6 Proton-exporting ATPase.
3.6.1.5 Apyrase.	3.6.3.7 Sodium-exporting ATPase.
3.6.1.6 Nucleoside-diphosphatase.	3.6.3.8 Calcium-transporting ATPase.
3.6.1.7 Acylphosphatase.	3.6.3.9 Sodium/potassium-exchanging ATPase.
3.6.1.8 ATP diphosphatase.	3.6.3.10 Hydrogen/potassium-exchanging ATPase.
3.6.1.9 Nucleotide diphosphatase.	3.6.3.11 Chloride-transporting ATPase.
3.6.1.10 Endopolyphosphatase.	3.6.3.12 Potassium-transporting ATPase.
3.6.1.11 Exopolyphosphatase.	3.6.3.14 H(+)-transporting two-sector ATPase.
3.6.1.12 dCTP diphosphatase.	3.6.3.15 Sodium-transporting two-sector ATPase.
3.6.1.13 ADP-ribose diphosphatase.	3.6.3.16 Arsenite-transporting ATPase.
3.6.1.14 Adenosine-tetraphosphatase.	3.6.3.17 Monosaccharide-transporting ATPase.
3.6.1.15 Nucleoside-triphosphatase.	3.6.3.18 Oligosaccharide-transporting ATPase.
3.6.1.16 CDP-glycerol diphosphatase.	3.6.3.19 Maltose-transporting ATPase.
3.6.1.17 Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical).	3.6.3.20 Glycerol-3-phosphate-transporting ATPase.
3.6.1.18 FAD diphosphatase.	3.6.3.21 Polar-amino-acid-transporting ATPase.
3.6.1.19 Nucleoside-triphosphate diphosphatase.	3.6.3.22 Nonpolar-amino-acid-transporting ATPase.
3.6.1.20 5'-acylphosphoadenosine hydrolase.	3.6.3.23 Oligopeptide-transporting ATPase.
3.6.1.21 ADP-sugar diphosphatase.	3.6.3.24 Nickel-transporting ATPase.
3.6.1.22 NAD ⁺ diphosphatase.	3.6.3.25 Sulfate-transporting ATPase.
3.6.1.23 dUTP diphosphatase.	3.6.3.26 Nitrate-transporting ATPase.
3.6.1.24 Nucleoside phosphoacylhydrolase.	3.6.3.27 Phosphate-transporting ATPase.
3.6.1.25 Triphosphatase.	3.6.3.28 Phosphonate-transporting ATPase.
3.6.1.26 CDP-diacylglycerol diphosphatase.	3.6.3.29 Molybdate-transporting ATPase.
3.6.1.27 Undecaprenyl-diphosphatase.	3.6.3.30 Fe(3+)-transporting ATPase.
3.6.1.28 Thiamine-triphosphatase.	3.6.3.31 Polyamine-transporting ATPase.
3.6.1.29 Bis(5'-adenosyl)-triphosphatase.	3.6.3.32 Quaternary-amine-transporting ATPase.
3.6.1.30 M(7)G(5')pppN diphosphatase.	3.6.3.33 Vitamin B12-transporting ATPase.
3.6.1.31 Phosphoribosyl-ATP diphosphatase.	3.6.3.34 Iron-chelate-transporting ATPase.
3.6.1.39 Thymidine-triphosphatase.	3.6.3.35 Manganese-transporting ATPase.

3.6.3.36 Taurine-transporting ATPase.	3.8.1.1 Alkylhalidase.
3.6.3.37 Guanine-transporting ATPase.	3.8.1.2 (S)-2-haloacid dehalogenase.
3.6.3.38 Capsular-polysaccharide-transporting ATPase.	3.8.1.3 Haloacetate dehalogenase.
3.6.3.39 Lipopolysaccharide-transporting	3.8.1.5 Haloalkane dehalogenase.

ATPase.	
3.6.3.40 Teichoic-acid-transporting ATPase.	3.8.1.6 4-chlorobenzoate dehalogenase.
3.6.3.41 Heme-transporting ATPase.	3.8.1.7 4-chlorobenzoyl-CoA dehalogenase.
3.6.3.42 Beta-glucan-transporting ATPase.	3.8.1.8 Atrazine chlorohydrolase.
3.6.3.43 Peptide-transporting ATPase.	3.8.1.9 (R)-2-haloacid dehalogenase.
3.6.3.44 Xenobiotic-transporting ATPase.	3.8.1.10 2-haloacid dehalogenase (configuration-inverting).
3.6.3.45 Stéroid-transporting ATPase.	3.8.1.11 2-haloacid dehalogenase (configuration-retaining).
3.6.3.46 Cadmium-transporting ATPase.	3.9.1.1 Phosphoamidase.
3.6.3.47 Fatty-acyl-CoA-transporting ATPase.	3.10.1.1 N-sulfoglucosamine sulfohydrolase.
3.6.3.48 Alpha-factor-transporting ATPase.	3.10.1.2 Cyclamate sulfohydrolase.
3.6.3.49 Channel-conductance-controlling ATPase.	3.11.1.1 Phosphonoacetaldehyde hydrolase.
3.6.3.50 Protein-secreting ATPase.	3.11.1.2 Phosphonoacetate hydrolase.
3.6.3.51 Mitochondrial protein-transporting ATPase.	3.12.1.1 Trithionate hydrolase.
3.6.3.52 Chloroplast protein-transporting ATPase.	3.13.1.1 UDP-sulfoquinovose synthase.
3.6.3.53 Ag(+)-exporting ATPase.	
3.6.4.1 Myosin ATPase.	ENZYME: 4.-.-.-
3.6.4.2 Dynein ATPase.	4.1.1.1 Pyruvate decarboxylase.
3.6.4.3 Microtubule-severing ATPase.	4.1.1.2 Oxalate decarboxylase.
3.6.4.4 Plus-end-directed kinesin ATPase.	4.1.1.3 Oxaloacetate decarboxylase.
3.6.4.5 Minus-end-directed kinesin ATPase.	4.1.1.4 Acetoacetate decarboxylase.
3.6.4.6 Vesicle-fusing ATPase.	4.1.1.5 Acetolactate decarboxylase.
3.6.4.7 Peroxisome-assembly ATPase.	4.1.1.6 Aconitate decarboxylase.
3.6.4.8 Proteasome ATPase.	4.1.1.7 Benzoylformate decarboxylase.
3.6.4.9 Chaperonin ATPase.	4.1.1.8 Oxalyl-CoA decarboxylase.
3.6.4.10 Non-chaperonin molecular chaperone ATPase.	4.1.1.9 Malonyl-CoA decarboxylase.
3.6.4.11 Nucleoplasmin ATPase.	4.1.1.11 Aspartate 1-decarboxylase.
3.6.5.1 Heterotrimeric G-protein GTPase.	4.1.1.12 Aspartate 4-decarboxylase.
3.6.5.2 Small monomeric GTPase.	4.1.1.14 Valine decarboxylase.
3.6.5.3 Protein-synthesizing GTPase.	4.1.1.15 Glutamate decarboxylase.
3.6.5.4 Signal-recognition-particle GTPase.	4.1.1.16 Hydroxyglutamate decarboxylase.
3.6.5.5 Dynammin GTPase.	4.1.1.17 Ornithine decarboxylase.
3.6.5.6 Tubulin GTPase.	4.1.1.18 Lysine decarboxylase.
3.7.1.1 Oxaloacetase.	4.1.1.19 Arginine decarboxylase.
3.7.1.2 Fumarylacetoacetase.	4.1.1.20 Diaminopimelate decarboxylase.
3.7.1.3 Kynureninase.	4.1.1.21 Phosphoribosylaminoimidazole carboxylase.
3.7.1.4 Phloretin hydrolase.	4.1.1.22 Histidine decarboxylase.
3.7.1.5 Acylpyruvate hydrolase.	4.1.1.23 Orotidine-5'-phosphate decarboxylase.
3.7.1.6 Acetylpyruvate hydrolase.	4.1.1.24 Aminobenzoate decarboxylase.
3.7.1.7 Beta-diketone hydrolase.	4.1.1.25 Tyrosine decarboxylase.
3.7.1.8 2,6-dioxo-6-phenylhexa-3-enoate hydrolase.	4.1.1.28 Aromatic-L-amino-acid decarboxylase.
3.7.1.9 2-hydroxymuconate-semialdehyde hydrolase.	4.1.1.29 Sulfinolalanine decarboxylase.
3.7.1.10 Cyclohexane-1,3-dione hydrolase.	4.1.1.30 Pantothenoylcysteine decarboxylase.
4.1.1.31 Phosphoenolpyruvate carboxylase.	4.1.1.74 Indolepyruvate decarboxylase.

4.1.1.32 Phosphoenolpyruvate carboxykinase (GTP).	4.1.1.75 5-guanidino-2-oxopentanoate decarboxylase.
4.1.1.33 Diphosphomevalonate decarboxylase.	4.1.1.76 Arylmalonate decarboxylase.
4.1.1.34 Dehydro-L-gulonate decarboxylase.	4.1.1.77 4-oxalocrotonate decarboxylase.
4.1.1.35 UDP-glucuronate decarboxylase.	4.1.1.78 Acetylenedicarboxylate decarboxylase.
4.1.1.36 Phosphopantothenoylcysteine decarboxylase.	4.1.1.79 Sulfopyruvate decarboxylase.
4.1.1.37 Uroporphyrinogen decarboxylase.	4.1.1.80 4-hydroxyphenylpyruvate decarboxylase.
4.1.1.38 Phosphoenolpyruvate carboxykinase (diphosphate).	4.1.1.81 Threonine-phosphate decarboxylase.
4.1.1.39 Ribulose-bisphosphate carboxylase.	4.1.2.2 Ketotetrose-phosphate aldolase.
4.1.1.40 Hydroxypyruvate decarboxylase.	4.1.2.4 Deoxyribose-phosphate aldolase.
4.1.1.41 Methylmalonyl-CoA decarboxylase.	4.1.2.5 Threonine aldolase.
4.1.1.42 Carnitine decarboxylase.	4.1.2.9 Phosphoketolase.
4.1.1.43 Phenylpyruvate decarboxylase.	4.1.2.10 Mandelonitrile lyase.
4.1.1.44 4-carboxymuconolactone decarboxylase.	4.1.2.11 Hydroxymandelonitrile lyase.
4.1.1.45 Aminocarboxymuconate-semialdehyde decarboxylase.	4.1.2.12 2-dehydropantoate aldolase.
4.1.1.46 O-pyrocatechuate decarboxylase.	4.1.2.13 Fructose-bisphosphate aldolase.
4.1.1.47 Tartronate-semialdehyde synthase.	4.1.2.14 2-dehydro-3-deoxy-phosphogluconate aldolase.
4.1.1.48 Indole-3-glycerol-phosphate synthase.	4.1.2.17 L-fucose-phosphate aldolase.
4.1.1.49 Phosphoenolpyruvate carboxykinase (ATP).	4.1.2.18 2-dehydro-3-deoxy-L-pentionate aldolase.
4.1.1.50 Adenosylmethionine decarboxylase.	4.1.2.19 Rhamnulose-1-phosphate aldolase.
4.1.1.51 3-hydroxy-2-methylpyridine-4,5-dicarboxylate 4-decarboxylase.	4.1.2.20 2-dehydro-3-deoxyglucarate aldolase.
4.1.1.52 6-methylsalicylate decarboxylase.	4.1.2.21 2-dehydro-3-deoxy-6-phosphogalactonate aldolase.
4.1.1.53 Phenylalanine decarboxylase.	4.1.2.22 Fructose-6-phosphate phosphoketolase.
4.1.1.54 Dihydroxyfumarate decarboxylase.	4.1.2.23 3-deoxy-D-manno-octulosonate aldolase.
4.1.1.55 4,5-dihydroxyphthalate decarboxylase.	4.1.2.24 Dimethylaniline-N-oxide aldolase.
4.1.1.56 3-oxolaurate decarboxylase.	4.1.2.25 Dihydroneopterin aldolase.
4.1.1.57 Methionine decarboxylase.	4.1.2.26 Phenylserine aldolase.
4.1.1.58 Orsellinate decarboxylase.	4.1.2.27 Sphinganine-1-phosphate aldolase.
4.1.1.59 Gallate decarboxylase.	4.1.2.28 2-dehydro-3-deoxy-D-pentionate aldolase.
4.1.1.60 Stipitatonate decarboxylase.	4.1.2.29 5-dehydro-2-deoxyphosphogluconate aldolase.
4.1.1.61 4-hydroxybenzoate decarboxylase.	4.1.2.30 17-alpha-hydroxyprogesterone aldolase.
4.1.1.62 Gentisate decarboxylase.	4.1.2.32 Trimethylamine-oxide aldolase.
4.1.1.63 Protocatechuate decarboxylase.	4.1.2.33 Fucosterol-epoxide lyase.
4.1.1.64 2,2-dialkylglycine decarboxylase (pyruvate).	4.1.2.34 4-(2-carboxyphenyl)-2-oxobut-3-enoate aldolase.
4.1.1.65 Phosphatidylserine decarboxylase.	4.1.2.35 Propioin synthase.
4.1.1.66 Uracil-5-carboxylate decarboxylase.	4.1.2.36 Lactate aldolase.
4.1.1.67 UDP-galacturonate decarboxylase.	4.1.2.37 Acetone-cyanohydrin lyase.
4.1.1.68 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase.	4.1.2.38 Benzoin aldolase.
4.1.1.69 3,4-dihydroxyphthalate decarboxylase.	4.1.2.39 Hydroxynitrilase.
4.1.1.70 Glutaconyl-CoA decarboxylase.	4.1.2.40 Tagatose-bisphosphate aldolase.
4.1.1.71 2-oxoglutarate decarboxylase.	4.1.2.41 Vanillin synthase.
4.1.1.72 Branched-chain-2-oxoacid decarboxylase.	4.1.3.1 Isocitrate lyase.

4.1.1.73 Tartrate decarboxylase.	4.1.3.3 N-acetylneuraminate lyase.
4.1.3.4 Hydroxymethylglutaryl-CoA lyase.	4.2.1.32 L(+)-tartrate dehydratase.
4.1.3.6 Citrate (pro-3S)-lyase.	4.2.1.33 3-isopropylmalate dehydratase.
4.1.3.13 Oxalomalate lyase.	4.2.1.34 (S)-2-methylmalate dehydratase.
4.1.3.14 3-hydroxyaspartate aldolase.	4.2.1.35 (R)-2-methylmalate dehydratase.
4.1.3.16 4-hydroxy-2-oxoglutarate aldolase.	4.2.1.36 Homoaconitate hydratase.
4.1.3.17 4-hydroxy-4-methyl-2-oxoglutarate aldolase.	4.2.1.39 Gluconate dehydratase.
4.1.3.22 Citramalate lyase.	4.2.1.40 Glucarate dehydratase.
4.1.3.24 Maltol-CoA lyase.	4.2.1.41 5-dehydro-4-deoxyglucarate dehydratase.
4.1.3.25 Citramalyl-CoA lyase.	4.2.1.42 Galactarate dehydratase.
4.1.3.26 3-hydroxy-3-isohexenylglutaryl-CoA lyase.	4.2.1.43 2-dehydro-3-deoxy-L-arabinonate dehydratase.
4.1.3.27 Anthranilate synthase.	4.2.1.44 Myo-inosose-2 dehydratase.
4.1.3.30 Methylisocitrate lyase.	4.2.1.45 CDP-glucose 4,6-dehydratase.
4.1.3.32 2,3-dimethylmalate lyase.	4.2.1.46 dTDP-glucose 4,6-dehydratase.
4.1.3.34 Citryl-CoA lyase.	4.2.1.47 GDP-mannose 4,6-dehydratase.
4.1.3.35 (1-hydroxycyclohexan-1-yl)acetyl-CoA lyase.	4.2.1.48 D-glutamate cyclase.
4.1.3.36 Naphthoate synthase.	4.2.1.49 Urocanate hydratase.
4.1.3.38 Aminodeoxychorismate lyase.	4.2.1.50 Pyrazolylalanine synthase.
4.1.99.1 Tryptophanase.	4.2.1.51 Prephenate dehydratase.
4.1.99.2 Tyrosine phenol-lyase.	4.2.1.52 Dihydrodipicolinate synthase.
4.1.99.3 Deoxyribodipyrimidine photo-lyase.	4.2.1.53 Oleate hydratase.
4.1.99.5 Octadecanal decarbonylase.	4.2.1.54 Lactoyl-CoA dehydratase.
4.1.99.11 Benzylsuccinate synthase.	4.2.1.55 3-hydroxybutyryl-CoA dehydratase.
4.2.1.1 Carbonate dehydratase.	4.2.1.56 Itaconyl-CoA hydratase.
4.2.1.2 Fumarate hydratase.	4.2.1.57 Isohexenylglutaconyl-CoA hydratase.
4.2.1.3 Aconitate hydratase.	4.2.1.58 Crotonoyl-[acyl-carrier-protein] hydratase.
4.2.1.4 Citrate dehydratase.	4.2.1.59 3-hydroxyoctanoyl-[acyl-carrier-protein] dehydratase.
4.2.1.5 Arabinonate dehydratase.	4.2.1.60 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase.
4.2.1.6 Galactonate dehydratase.	4.2.1.61 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase.
4.2.1.7 Altronate dehydratase.	4.2.1.62 5-alpha-hydroxysteroid dehydratase.
4.2.1.8 Mannonate dehydratase.	4.2.1.65 3-cyanoalanine hydratase.
4.2.1.9 Dihydroxy-acid dehydratase.	4.2.1.66 Cyanide hydratase.
4.2.1.10 3-dehydroquinone dehydratase.	4.2.1.67 D-fuconate dehydratase.
4.2.1.11 Phosphopyruvate hydratase.	4.2.1.68 L-fuconate dehydratase.
4.2.1.12 Phosphogluconate dehydratase.	4.2.1.69 Cyanamide hydratase.
4.2.1.17 Enoyl-CoA hydratase.	4.2.1.70 Pseudouridylyl synthase.
4.2.1.18 Methylglutaconyl-CoA hydratase.	4.2.1.73 Protoaphin-aglucone dehydratase (cyclizing).
4.2.1.19 Imidazoleglycerol-phosphate dehydratase.	4.2.1.74 Long-chain-enoil-CoA hydratase.
4.2.1.20 Tryptophan synthase.	4.2.1.75 Uroporphyrinogen-III synthase.
4.2.1.22 Cystathionine beta-synthase.	4.2.1.76 UDP-glucose 4,6-dehydratase.
4.2.1.24 Porphobilinogen synthase.	4.2.1.77 Trans-L-3-hydroxyproline dehydratase.
4.2.1.25 L-arabinonate dehydratase.	4.2.1.78 (S)-norcoclaurine synthase.

4.2.1.27	Acetylenecarboxylate hydratase.	4.2.1.79	2-methylcitrate dehydratase.
4.2.1.28	Propanediol dehydratase.	4.2.1.80	2-oxopent-4-enoate hydratase.
4.2.1.30	Glycerol dehydratase.	4.2.1.81	D(-)-tartrate dehydratase.
4.2.1.31	Maleate hydratase.	4.2.1.82	Xylionate dehydratase.

4.2.1.83	4-oxalmesaconate hydratase.	4.2.3.6	Trichodiene synthase.
4.2.1.84	Nitrile hydratase.	4.2.3.7	Pentalenene synthase.
4.2.1.85	Dimethylmaleate hydratase.	4.2.3.8	Casbene synthase.
4.2.1.86	16-dehydropregesterone hydratase.	4.2.3.9	Aristolochene synthase.
4.2.1.87	Octopamine dehydratase.	4.2.3.10	(-)-endo-fenchol synthase.
4.2.1.88	Synephrine dehydratase.	4.2.3.11	Sabinene-hydrate synthase.
4.2.1.89	Carnitine dehydratase.	4.2.3.12	6-pyruvoyltetrahydropterin synthase.
4.2.1.90	L-rhamnonate dehydratase.	4.2.3.13	(+)-delta-cadinene synthase.
4.2.1.91	Carboxycyclohexadienyl dehydratase.	4.2.3.14	Pinene synthase.
4.2.1.92	Hydroperoxide dehydratase.	4.2.3.15	Myrcene synthase.
4.2.1.93	ATP-dependent NAD(P)H-hydrate dehydratase.	4.2.3.16	(4S)-limonene synthase.
4.2.1.94	Scytalone dehydratase.	4.2.3.17	Taxadiene synthase.
4.2.1.95	Kievitone hydratase.	4.2.3.18	Abietadiene synthase.
4.2.1.96	4a-hydroxytetrahydrobiopterin dehydratase.	4.2.3.19	Ent-kaurene synthase.
4.2.1.97	Phaseollidin hydratase.	4.2.3.20	(+)-limonene synthase.
4.2.1.98	16-alpha-hydroxyprogesterone dehydratase.	4.2.3.21	Vetispiradiene synthase.
4.2.1.99	2-methylisocitrate dehydratase.	4.2.99.12	Carboxymethyloxysuccinate lyase.
4.2.1.100	Cyclohexa-1,5-dienecarbonyl-CoA hydratase.	4.2.99.18	DNA-(apurinic or apyrimidinic site) lyase.
4.2.1.101	Trans-feruloyl-CoA hydratase.	4.2.99.19	2-hydroxypropyl-CoM lyase.
4.2.1.103	Cyclohexyl-isocyanide hydratase.	4.3.1.1	Aspartate ammonia-lyase.
4.2.1.104	Cyanate hydratase.	4.3.1.2	Methylaspartate ammonia-lyase.
4.2.2.1	Hyaluronate lyase.	4.3.1.3	Histidine ammonia-lyase.
4.2.2.2	Pectate lyase.	4.3.1.4	Formimidoyltetrahydrofolate cyclodeaminase.
4.2.2.3	Poly(beta-D-mannuronate) lyase.	4.3.1.5	Phenylalanine ammonia-lyase.
4.2.2.4	Chondroitin ABC lyase.	4.3.1.6	Beta-alanyl-CoA ammonia-lyase.
4.2.2.5	Chondroitin AC lyase.	4.3.1.7	Ethanolamine ammonia-lyase.
4.2.2.6	Oligogalacturonide lyase.	4.3.1.9	Glucosaminase ammonia-lyase.
4.2.2.7	Heparin lyase.	4.3.1.10	Serine-sulfate ammonia-lyase.
4.2.2.8	Heparin-sulfate lyase.	4.3.1.11	Dihydroxyphenylalanine ammonia-lyase.
4.2.2.9	Pectate disaccharide-lyase.	4.3.1.12	Ornithine cyclodeaminase.
4.2.2.10	Pectin lyase.	4.3.1.13	Carbamoyl-serine ammonia-lyase.
4.2.2.11	Poly(alpha-L-guluronate) lyase.	4.3.1.14	3-aminobutyryl-CoA ammonia-lyase.
4.2.2.12	Xanthan lyase.	4.3.1.15	Diaminopropionate ammonia-lyase.
4.2.2.13	Exo-(1->4)-alpha-D-glucan lyase.	4.3.1.16	Threo-3-hydroxyaspartate ammonia-lyase.
4.2.2.14	Glucuronan lyase.	4.3.1.17	L-serine ammonia-lyase.
4.2.2.15	Anhydrosialidase.	4.3.1.18	D-serine ammonia-lyase.
4.2.2.16	Levan fructotransferase (DFA-IV-forming).	4.3.1.19	Threonine ammonia-lyase.
4.2.2.17	Inulin fructotransferase (DFA-I-forming).	4.3.1.20	Erythro-3-hydroxyaspartate ammonia-lyase.

4.2.2.18	Inulin fructotransferase (DFA-III-forming).	4.3.2.1	Argininosuccinate lyase.
4.2.3.1	Threonine synthase.	4.3.2.2	Adenylosuccinate lyase.
4.2.3.2	Ethanolamine-phosphate phospho-lyase.	4.3.2.3	Ureidoglycolate lyase.
4.2.3.3	Methylglyoxal synthase.	4.3.2.4	Purine imidazole-ring cyclase.
4.2.3.4	3-dehydroquininate synthase.	4.3.2.5	Peptidylamidoglycolate lyase.
4.2.3.5	Chorismate synthase.	4.3.3.1	3-ketovalidoxylamine C-N-lyase.

4.3.3.2	Strictosidine synthase.	5.1.1.7	Diaminopimelate epimerase.
4.3.3.3	Deacetylisopecoside synthase.	5.1.1.8	4-hydroxyproline epimerase.
4.3.3.4	Deacetylpecoside synthase.	5.1.1.9	Arginine racemase.
4.4.1.1	Cystathionine gamma-lyase.	5.1.1.10	Amino-acid racemase.
4.4.1.2	Homocysteine desulfhydrase.	5.1.1.11	Phenylalanine racemase (ATP-hydrolyzing).
4.4.1.3	Dimethylpropiothetin dethiomethylase.	5.1.1.12	Ornithine racemase.
4.4.1.4	Alliin lyase.	5.1.1.13	Aspartate racemase.
4.4.1.5	Lactoylglutathione lyase.	5.1.1.14	Nocardicin-A epimerase.
4.4.1.6	S-alkylcysteine lyase.	5.1.1.15	2-aminohexano-6-lactam racemase.
4.4.1.8	Cystathionine beta-lyase.	5.1.1.16	Protein-serine epimerase.
4.4.1.9	L-3-cyanoalanine synthase.	5.1.1.17	Isopenicillin-N epimerase.
4.4.1.10	Cysteine lyase.	5.1.2.1	Lactate racemase.
4.4.1.11	Methionine gamma-lyase.	5.1.2.2	Mandelate racemase.
4.4.1.13	Cysteine-S-conjugate beta-lyase.	5.1.2.3	3-hydroxybutyryl-CoA epimerase.
4.4.1.14	1-aminocyclopropane-1-carboxylate synthase.	5.1.2.4	Acetoin racemase.
4.4.1.15	D-cysteine desulfhydrase.	5.1.2.5	Tartrate epimerase.
4.4.1.16	Selenocysteine lyase.	5.1.2.6	Isocitrate epimerase.
4.4.1.17	Holocytochrome-c synthase.	5.1.3.1	Ribulose-phosphate 3-epimerase.
4.4.1.19	Phosphosulfolactate synthase.	5.1.3.2	UDP-glucose 4-epimerase.
4.4.1.20	Leukotriene-C(4) synthase.	5.1.3.3	Aldose 1-epimerase.
4.5.1.1	DDT-dehydrochlorinase.	5.1.3.4	L-ribulose-phosphate 4-epimerase.
4.5.1.2	3-chloro-D-alanine dehydrochlorinase.	5.1.3.5	UDP-arabinose 4-epimerase.
4.5.1.3	Dichloromethane dehalogenase.	5.1.3.6	UDP-glucuronate 4-epimerase.
4.5.1.4	L-2-amino-4-chloropent-4-enoate dehydrochlorinase.	5.1.3.7	UDP-N-acetylglucosamine 4-epimerase.
4.5.1.5	S-carboxymethylcysteine synthase.	5.1.3.8	N-acylglucosamine 2-epimerase.
4.6.1.1	Adenylate cyclase.	5.1.3.9	N-acylglucosamine-6-phosphate 2-epimerase.
4.6.1.2	Guanylate cyclase.	5.1.3.10	CDP-abequose epimerase.
4.6.1.6	Cytidylate cyclase.	5.1.3.11	Cellobiose epimerase.
4.6.1.12	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase.	5.1.3.12	UDP-glucuronate 5'-epimerase.
4.6.1.13	Phosphatidylinositol diacylglycerol-lyase.	5.1.3.13	dTDP-4-dehydrorhamnose 3,5-epimerase.
4.6.1.14	Glycosylphosphatidylinositol diacylglycerol-lyase.	5.1.3.14	UDP-N-acetylglucosamine 2-epimerase.
4.6.1.15	FAD-AMP lyase (cyclizing).	5.1.3.15	Glucose-6-phosphate 1-epimerase.
4.99.1.1	Ferrochelataase.	5.1.3.16	UDP-glucosamine 4-epimerase.
4.99.1.2	Alkylmercury lyase.	5.1.3.17	Heparosan-N-sulfate-glucuronate 5-epimerase.
4.99.1.3	Sirohydrochlorin cobaltochelataase.	5.1.3.18	GDP-mannose 3,5-epimerase.
4.99.1.4	Sirohydrochlorin ferrochelataase.	5.1.3.19	Chondroitin-glucuronate 5-epimerase.
4.99.1.5	Aliphatic aldoxime dehydratase.	5.1.3.20	ADP-glyceromanno-heptose 6-epimerase.

4.99.1.6	Indoleacetaldoxime dehydratase.	5.1.3.21	Maltose epimerase.
ENZYME: 5.-.-.-		5.1.99.1	Methylmalonyl-CoA epimerase.
5.1.1.1	Alanine racemase.	5.1.99.2	16-hydroxysteroid epimerase.
5.1.1.2	Methionine racemase.	5.1.99.3	Allantoin racemase.
5.1.1.3	Glutamate racemase.	5.1.99.4	Alpha-methylacyl-CoA racemase.
5.1.1.4	Proline racemase.	5.2.1.1	Maleate isomerase.
5.1.1.5	Lysine racemase.	5.2.1.2	Maleylacetoacetate isomerase.
5.1.1.6	Threonine racemase.	5.2.1.3	Retinal isomerase.
		5.2.1.4	Maleylpyruvate isomerase.

5.2.1.5	Linoleate isomerase.	5.3.4.1	Protein disulfide-isomerase.
5.2.1.6	Furylfuramide isomerase.	5.3.99.2	Prostaglandin-D synthase.
5.2.1.7	Retinol isomerase.	5.3.99.3	Prostaglandin-E synthase.
5.2.1.8	Peptidylprolyl isomerase.	5.3.99.4	Prostaglandin-I synthase.
5.2.1.9	Farnesol 2-isomerase.	5.3.99.5	Thromboxane-A synthase.
5.2.1.10	2-chloro-4-carboxymethylenebut-2-en-1,4-olide isomerase.	5.3.99.6	Allene-oxide cyclase.
5.2.1.11	4-hydroxyphenylacetaldehyde-oxime isomerase.	5.3.99.7	Styrene-oxide isomerase.
5.3.1.1	Triose-phosphate isomerase.	5.4.1.1	Lysolecithin acylmutase.
5.3.1.3	Arabinose isomerase.	5.4.1.2	Precorrin-8X methylmutase.
5.3.1.4	L-arabinose isomerase.	5.4.2.1	Phosphoglycerate mutase.
5.3.1.5	Xylose isomerase.	5.4.2.2	Phosphoglucomutase.
5.3.1.6	Ribose-5-phosphate isomerase.	5.4.2.3	Phosphoacetylglucosamine mutase.
5.3.1.7	Mannose isomerase.	5.4.2.4	Bisphosphoglycerate mutase.
5.3.1.8	Mannose-6-phosphate isomerase.	5.4.2.5	Phosphoglucomutase (glucose-cofactor).
5.3.1.9	Glucose-6-phosphate isomerase.	5.4.2.6	Beta-phosphoglucomutase.
5.3.1.12	Glucuronate isomerase.	5.4.2.7	Phosphopentomutase.
5.3.1.13	Arabinose-5-phosphate isomerase.	5.4.2.8	Phosphomannomutase.
5.3.1.14	L-rhamnose isomerase.	5.4.2.9	Phosphoenolpyruvate mutase.
5.3.1.15	D-lyxose ketol-isomerase.	5.4.2.10	Phosphoglucosamine mutase.
5.3.1.16	1-(5-phosphoribosyl)-5-((5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase.	5.4.3.2	Lysine 2,3-aminomutase.
5.3.1.17	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase.	5.4.3.3	Beta-lysine 5,6-aminomutase.
5.3.1.20	Ribose isomerase.	5.4.3.4	D-lysine 5,6-aminomutase.
5.3.1.21	Corticosteroid side-chain-isomerase.	5.4.3.5	D-ornithine 4,5-aminomutase.
5.3.1.22	Hydroxypyruvate isomerase.	5.4.3.6	Tyrosine 2,3-aminomutase.
5.3.1.23	S-methyl-5-thioribose-1-phosphate isomerase.	5.4.3.7	Leucine 2,3-aminomutase.
5.3.1.24	Phosphoribosylanthranilate isomerase.	5.4.3.8	Glutamate-1-semialdehyde 2,1-aminomutase.
5.3.1.25	L-fucose isomerase.	5.4.4.1	(Hydroxyamino)benzene mutase.
5.3.1.26	Galactose-6-phosphate isomerase.	5.4.4.2	Isochorismate synthase.
5.3.2.1	Phenylpyruvate tautomerase.	5.4.4.3	3-(hydroxyamino)phenol mutase.
5.3.2.2	Oxaloacetate tautomerase.	5.4.99.1	Methylaspartate mutase.
5.3.3.1	Steroid delta-isomerase.	5.4.99.2	Methylmalonyl-CoA mutase.
5.3.3.2	Isopentenyl-diphosphate delta-isomerase.	5.4.99.3	2-acetolactate mutase.
5.3.3.3	Vinylacetyl-CoA delta-isomerase.	5.4.99.4	2-methyleneglutarate mutase.
5.3.3.4	Muconolactone delta-isomerase.	5.4.99.5	Chorismate mutase.
5.3.3.5	Cholestenol delta-isomerase.	5.4.99.7	Lanosterol synthase.
5.3.3.6	Methylitaconate delta-isomerase.	5.4.99.8	Cycloartenol synthase.

5.3.3.7 Aconitate delta-isomerase.	5.4.99.9 UDP-galactopyranose mutase.
5.3.3.8 Dodecenoyl-CoA delta-isomerase.	5.4.99.11 Isomaltulose synthase.
5.3.3.9 Prostaglandin-A(1) delta-isomerase.	5.4.99.12 tRNA-pseudouridine synthase I.
5.3.3.10 5-carboxymethyl-2-hydroxymuconate delta-isomerase.	5.4.99.13 Isobutyryl-CoA mutase.
5.3.3.11 Isopiperitenone delta-isomerase.	5.4.99.14 4-carboxymethyl-4-methylbutenolide mutase.
5.3.3.12 Dopachrome isomerase.	5.4.99.15 (1->4)-alpha-D-glucan 1-alpha-D-glucosylmutase.
5.3.3.13 Polyenoic fatty acid isomerase.	5.4.99.16 Maltose alpha-D-glucosyltransferase.

5.4.99.17 Squalene--hopene cyclase.	6.2.1.5 Succinate--CoA ligase (ADP-forming).
5.5.1.1 Muconate cycloisomerase.	6.2.1.6 Glutarate--CoA ligase.
5.5.1.2 3-carboxy-cis,cis-muconate cycloisomerase.	6.2.1.7 Cholate--CoA ligase.
5.5.1.3 Tetrahydroxypteridine cycloisomerase.	6.2.1.8 Oxalate--CoA ligase.
5.5.1.4 Inositol-3-phosphate synthase.	6.2.1.9 Malate--CoA ligase.
5.5.1.5 Carboxy-cis,cis-muconate cyclase.	6.2.1.10 Acid--CoA ligase (GDP-forming).
5.5.1.6 Chalcone isomerase.	6.2.1.11 Biotin--CoA ligase.
5.5.1.7 Chloromuconate cycloisomerase.	6.2.1.12 4-coumarate--CoA ligase.
5.5.1.8 Geranyl-diphosphate cyclase.	6.2.1.13 Acetate--CoA ligase (ADP-forming).
5.5.1.9 Cycloeucalenol cycloisomerase.	6.2.1.14 6-carboxyhexanoate--CoA ligase.
5.5.1.10 Alpha-pinene-oxide decyclase.	6.2.1.15 Arachidonate--CoA ligase.
5.5.1.11 Dichloromuconate cycloisomerase.	6.2.1.16 Acetoacetate--CoA ligase.
5.5.1.12 Copalyl diphosphate synthase.	6.2.1.17 Propionate--CoA ligase.
5.5.1.13 Ent-copalyl diphosphate synthase.	6.2.1.18 Citrate--CoA ligase.
5.99.1.1 Thiocyanate isomerase.	6.2.1.19 Long-chain-fatty-acid--luciferin-component ligase.
5.99.1.2 DNA topoisomerase.	6.2.1.20 Long-chain-fatty-acid--[acyl-carrier-protein] ligase.
5.99.1.3 DNA topoisomerase (ATP-hydrolyzing).	6.2.1.22 [Citrate (pro-3S)-lyase] ligase.
ENZYME: 6.-.-.	6.2.1.23 Dicarboxylate--CoA ligase.
6.1.1.1 Tyrosine--tRNA ligase.	6.2.1.24 Phytanate--CoA ligase.
6.1.1.2 Tryptophan--tRNA ligase.	6.2.1.25 Benzoate--CoA ligase.
6.1.1.3 Threonine--tRNA ligase.	6.2.1.26 O-succinylbenzoate--CoA ligase.
6.1.1.4 Leucine--tRNA ligase.	6.2.1.27 4-hydroxybenzoate--CoA ligase.
6.1.1.5 Isoleucine--tRNA ligase.	6.2.1.28 3-alpha,7-alpha-dihydroxy-5-beta-cholestanate--CoA ligase.
6.1.1.6 Lysine--tRNA ligase.	6.2.1.29 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanate--CoA ligase.
6.1.1.7 Alanine--tRNA ligase.	6.2.1.30 Phenylacetate--CoA ligase.
6.1.1.9 Valine--tRNA ligase.	6.2.1.31 2-furoate--CoA ligase.
6.1.1.10 Methionine--tRNA ligase.	6.2.1.32 Anthranilate--CoA ligase.
6.1.1.11 Serine--tRNA ligase.	6.2.1.33 4-chlorobenzoate--CoA ligase.
6.1.1.12 Aspartate--tRNA ligase.	6.2.1.34 Trans-feruloyl--CoA synthase.
6.1.1.13 D-alanine--poly(phosphoribitol) ligase.	6.3.1.1 Aspartate--ammonia ligase.
6.1.1.14 Glycine--tRNA ligase.	6.3.1.2 Glutamate--ammonia ligase.
6.1.1.15 Proline--tRNA ligase.	6.3.1.4 Aspartate--ammonia ligase (ADP-forming).
6.1.1.16 Cysteine--tRNA ligase.	6.3.1.5 NAD(+) synthase.
6.1.1.17 Glutamate--tRNA ligase.	6.3.1.6 Glutamate--ethylamine ligase.
6.1.1.18 Glutamine--tRNA ligase.	6.3.1.7 4-methyleneglutamate--ammonia

	ligase.
6.1.1.19 Arginine--tRNA ligase.	6.3.1.8 Glutathionylspermidine synthase.
6.1.1.20 Phenylalanine--tRNA ligase.	6.3.1.9 Trypanothione synthase.
6.1.1.21 Histidine--tRNA ligase.	6.3.1.10 Adenosylcobinamide-phosphate synthase.
6.1.1.22 Asparagine--tRNA ligase.	6.3.2.1 Pantoate--beta-alanine ligase.
6.1.1.23 Aspartate--tRNA(Asn) ligase.	6.3.2.2 Glutamate--cysteine ligase.
6.1.1.24 Glutamate--tRNA(Gln) ligase.	6.3.2.3 Glutathione synthase.
6.1.1.25 Lysine--tRNA(Pyl) ligase.	6.3.2.4 D-alanine--D-alanine ligase.
6.2.1.1 Acetate--CoA ligase.	6.3.2.5 Phosphopantothenate--cysteine ligase.
6.2.1.2 Butyrate--CoA ligase.	6.3.2.6 Phosphoribosylaminoimidazolesuccinocarboxamide synthase.
6.2.1.3 Long-chain-fatty-acid--CoA ligase.	6.3.2.7 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--L-lysine ligase.
6.2.1.4 Succinate--CoA ligase (GDP-forming).	6.3.2.8 UDP-N-acetylmuramate--L-alanine ligase.

6.3.2.9 UDP-N-acetylmuramoylalanine--D-glutamate ligase.	6.3.4.14 Biotin carboxylase.
6.3.2.10 UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase.	6.3.4.15 Biotin--[acetyl-CoA-carboxylase] ligase.
6.3.2.11 Carnosine synthase.	6.3.4.16 Carbamoyl-phosphate synthase (ammonia).
6.3.2.12 Dihydrofolate synthase.	6.3.4.17 Formate--dihydrofolate ligase.
6.3.2.13 UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase.	6.3.5.1 NAD(+) synthase (glutamine-hydrolyzing).
6.3.2.14 2,3-dihydroxybenzoate--serine ligase.	6.3.5.2 GMP synthase (glutamine-hydrolyzing).
6.3.2.16 D-alanine--alanyl-poly(glycerolphosphate) ligase.	6.3.5.3 Phosphoribosylformylglycinamidine synthase.
6.3.2.17 Tetrahydrofolylpolyglutamate synthase.	6.3.5.4 Asparagine synthase (glutamine-hydrolyzing).
6.3.2.18 Gamma-glutamylhistamine synthase.	6.3.5.5 Carbamoyl-phosphate synthase (glutamine-hydrolyzing).
6.3.2.19 Ubiquitin--protein ligase.	6.3.5.6 Asparaginyl-tRNA synthase (glutamine-hydrolyzing).
6.3.2.20 Indoleacetate-lysine synthetase.	6.3.5.7 Glutaminyl-tRNA synthase (glutamine-hydrolyzing).
6.3.2.21 Ubiquitin--calmodulin ligase.	6.3.5.8 Aminodeoxychorismate synthase.
6.3.2.22 Diphthine--ammonia ligase.	6.3.5.9 Hydrogenobyrinic acid a,c-diamide synthase (glutamine-hydrolyzing).
6.3.2.23 Homoglutathione synthase.	6.3.5.10 Adenosylcobyric acid synthase (glutamine-hydrolyzing).
6.3.2.24 Tyrosine--arginine ligase.	6.4.1.1 Pyruvate carboxylase.
6.3.2.25 Tubulin--tyrosine ligase.	6.4.1.2 Acetyl-CoA carboxylase.
6.3.2.26 N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase.	6.4.1.3 Propionyl-CoA carboxylase.
6.3.2.27 Aerobactin synthase.	6.4.1.4 Methylcrotonoyl-CoA carboxylase.
6.3.3.1 Phosphoribosylformylglycinamidine cyclo-ligase.	6.4.1.5 Geranoyl-CoA carboxylase.
6.3.3.2 5-formyltetrahydrofolate cyclo-ligase.	6.4.1.6 Acetone carboxylase.
6.3.3.3 Dethiobiotin synthase.	6.5.1.1 DNA ligase (ATP).

6.3.3.4 (Carboxyethyl)arginine beta-lactam-synthase.	6.5.1.2 DNA ligase (NAD+).
6.3.4.1 GMP synthase.	6.5.1.3 RNA ligase (ATP).
6.3.4.2 CTP synthase.	6.5.1.4 RNA-3'-phosphate cyclase.
6.3.4.3 Formate--tetrahydrofolate ligase.	6.6.1.1 Magnesium chelatase.
6.3.4.4 Adenylosuccinate synthase.	6.6.1.2 Cobaltochelataase.
6.3.4.5 Argininosuccinate synthase.	6.3.4.17 Formate--dihydrofolate ligase.
6.3.4.6 Urea carboxylase.	6.3.5.1 NAD(+) synthase (glutamine-hydrolyzing).
6.3.4.7 Ribose-5-phosphate--ammonia ligase.	6.3.5.2 GMP synthase (glutamine-hydrolyzing).
6.3.4.8 Imidazoleacetate--phosphoribosyldiphosphate ligase.	6.3.5.3 Phosphoribosylformylglycinamide synthase.
6.3.4.9 Biotin--[methylmalonyl-CoA-carboxytransferase] ligase.	6.3.5.4 Asparagine synthase (glutamine-hydrolyzing).
6.3.4.10 Biotin--[propionyl-CoA-carboxylase (ATP-hydrolyzing)] ligase.	6.3.5.5 Carbamoyl-phosphate synthase (glutamine-hydrolyzing).
6.3.4.11 Biotin--[methylcrotonoyl-CoA-carboxylase] ligase.	6.3.5.6 Asparaginyl-tRNA synthase (glutamine-hydrolyzing).
6.3.4.12 Glutamate--methylamine ligase.	6.3.5.7 Glutaminyl-tRNA synthase (glutamine-hydrolyzing).
6.3.4.13 Phosphoribosylamine- glycine ligase.	6.3.5.8 Aminodeoxychorismate synthase.

6.3.5.9 Hydrogenobyrinic acid a,c-diamide synthase (glutamine-hydrolyzing).	6.4.1.6 Acetone carboxylase.
6.3.5.10 Adenosylcobyrinic acid synthase (glutamine-hydrolyzing).	6.5.1.1 DNA ligase (ATP).
6.4.1.1 Pyruvate carboxylase.	6.5.1.2 DNA ligase (NAD+).
6.4.1.2 Acetyl-CoA carboxylase.	6.5.1.3 RNA ligase (ATP).
6.4.1.3 Propionyl-CoA carboxylase.	6.5.1.4 RNA-3'-phosphate cyclase.
6.4.1.4 Methylcrotonoyl-CoA carboxylase.	6.6.1.1 Magnesium chelatase.
6.4.1.5 Geranoyl-CoA carboxylase.	6.6.1.2 Cobaltochelataase.

Table 3 summarizes exemplary functions of exemplary enzymes of the invention; these enzyme functions were determined using sequence identity comparison analysis using closest BLAST hits to the exemplary polypeptides and polynucleotides of the invention.

The invention also provides isolated and recombinant nucleic acids encoding polypeptides, e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, etc., and all additional nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897 (the exemplary polynucleotides of the invention). The invention also provides isolated and recombinant polypeptides, SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc., and all polypeptides disclosed in the SEQ ID listing, which include

all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898 (the exemplary polypeptides of the invention).

In another embodiment, the polypeptides of the invention can be expressed in any expression system, in vitro or in vivo, e.g., any microorganism or other cell system (e.g., eukaryotic, such as yeast or mammalian cells) using procedures known in the art. In other aspects, the polypeptides of the invention can be immobilized on a solid support prior to use in the methods of the invention. Methods for immobilizing enzymes on solid supports are commonly known in the art, for example J. Mol. Cat. B: Enzymatic 6 (1999) 29-39; Chivata et al. Biocatalysis: Immobilized cells and enzymes, J Mol. Cat. 37 (1986) 1-24; Sharma et al., Immobilized Biomaterials Techniques and Applications, Angew. Chem. Int. Ed. Engl. 21 (1982) 837-54; Laskin (Ed.), Enzymes and Immobilized Cells in Biotechnology.

Definitions

A "coding sequence of" or a "sequence encodes" a particular polypeptide or protein, is a nucleic acid sequence which is transcribed and translated into a polypeptide or protein when placed under the control of appropriate regulatory sequences.

A promoter sequence is "operably linked to" a coding sequence when RNA polymerase which initiates transcription at the promoter will transcribe the coding sequence into mRNA.

The phrase "substantially identical" in the context of two nucleic acids or polypeptides, refers to two or more sequences that have, e.g., at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more nucleotide or amino acid residue (sequence) identity, when compared and aligned for maximum correspondence, as measured using one of the known sequence comparison algorithms or by visual inspection. In alternative aspects, the substantial identity exists over a region of at least about 100 or more residues and most commonly the sequences are substantially identical over at least about 150 to 200 or more residues. In some aspects, the sequences are substantially identical over the entire length of the coding regions.

Additionally a "substantially identical" amino acid sequence is a sequence that differs from a reference sequence by one or more conservative or non-conservative amino acid substitutions, deletions, or insertions. In one aspect, the substitution occurs at

a site that is not the active site of the molecule, or, alternatively the substitution occurs at a site that is the active site of the molecule, provided that the polypeptide essentially retains its functional (enzymatic) properties. A conservative amino acid substitution, for example, substitutes one amino acid for another of the same class (e.g., substitution of one hydrophobic amino acid, such as isoleucine, valine, leucine, or methionine, for another, or substitution of one polar amino acid for another, such as substitution of arginine for lysine, glutamic acid for aspartic acid or glutamine for asparagine). One or more amino acids can be deleted, for example, from a polypeptide, resulting in modification of the structure of the polypeptide, without significantly altering its biological activity. For example, amino- or carboxyl-terminal amino acids that are not required for a polypeptide, enzyme, protein, e.g. structural or binding protein, biological activity can be removed. Modified polypeptide sequences of the invention can be assayed for enzyme, structural or binding activity by any number of methods, including contacting the modified polypeptide sequence with a substrate and determining whether the modified polypeptide decreases the amount of specific substrate in the assay or increases the bioproducts of the reaction of a functional polypeptide, enzyme, protein, e.g. structural or binding protein, with the substrate. Assays for enzyme activity are well known in the art.

“Fragments” as used herein are a portion of a naturally occurring protein which can exist in at least two different conformations. Fragments can have the same or substantially the same amino acid sequence as the naturally occurring protein. Fragments which have different three dimensional structures as the naturally occurring protein are also included. An example of this, is a “pro-form” molecule, such as a low activity proprotein that can be modified by cleavage to produce a mature enzyme with significantly higher activity.

The term “variant” refers to polynucleotides or polypeptides of the invention modified at one or more base pairs, codons, introns, exons, or amino acid residues (respectively) yet still retain the biological activity of a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention. Variants can be produced by any number of means included methods such as, for example, error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, GSSM and any combination thereof.

The term "saturation mutagenesis", Gene Site Saturation Mutagenesis, or "GSSM" includes a method that uses degenerate oligonucleotide primers to introduce point mutations into a polynucleotide, as described in detail, below.

The term "optimized directed evolution system" or "optimized directed evolution" includes a method for reassembling fragments of related nucleic acid sequences, e.g., related genes, and explained in detail, below.

The term "synthetic ligation reassembly" or "SLR" includes a method of ligating oligonucleotide fragments in a non-stochastic fashion, and explained in detail, below.

Nucleic Acids

The invention provides nucleic acids (e.g., the exemplary SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, etc., including all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897), including expression cassettes such as expression vectors, encoding polypeptides (e.g., enzymes) of the invention. The invention also includes methods for discovering new polypeptide (e.g., enzyme) sequences using the nucleic acids of the invention. The invention also includes methods for inhibiting the expression of enzymes, genes, transcripts and polypeptides using the nucleic acids of the invention. Also provided are methods for modifying the nucleic acids of the invention by, e.g., synthetic ligation reassembly, optimized directed evolution system and/or saturation mutagenesis.

The nucleic acids of the invention can be made, isolated and/or manipulated by, e.g., cloning and expression of cDNA libraries, amplification of message or genomic DNA by PCR, and the like. For example, exemplary sequences of the invention were initially derived from environmental sources.

In one aspect, the invention provides nucleic acids, and the polypeptides encoded by them, with a common novelty in that they are derived from a common source, e.g., an environmental or a bacterial source.

In practicing the methods of the invention, homologous genes can be modified by manipulating a template nucleic acid, as described herein. The invention can be practiced in conjunction with any method or protocol or device known in the art, which are well described in the scientific and patent literature.

The phrases "nucleic acid" or "nucleic acid sequence" as used herein refer to an oligonucleotide, nucleotide, polynucleotide, or to a fragment of any of these, to DNA or

RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent a sense or antisense (complementary) strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material, natural or synthetic in origin. The phrases "nucleic acid" or "nucleic acid sequence" includes oligonucleotide, nucleotide, polynucleotide, or to a fragment of any of these, to DNA or RNA (e.g., mRNA, rRNA, tRNA, iRNA) of genomic or synthetic origin which may be single-stranded or double-stranded and may represent a sense or antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material, natural or synthetic in origin, including, e.g., iRNA, ribonucleoproteins (e.g., e.g., double stranded iRNAs, e.g., iRNPs). The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogues of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones, see e.g., Mata (1997) *Toxicol. Appl. Pharmacol.* 144:189-197; Strauss-Soukup (1997) *Biochemistry* 36:8692-8698; Samstag (1996) *Antisense Nucleic Acid Drug Dev* 6:153-156. "Oligonucleotide" includes either a single stranded polydeoxynucleotide or two complementary polydeoxynucleotide strands which may be chemically synthesized. Such synthetic oligonucleotides have no 5' phosphate and thus will not ligate to another oligonucleotide without adding a phosphate with an ATP in the presence of a kinase. A synthetic oligonucleotide can ligate to a fragment that has not been dephosphorylated.

A "coding sequence of" or a "nucleotide sequence encoding" a particular polypeptide or protein, is a nucleic acid sequence which is transcribed and translated into a polypeptide or protein when placed under the control of appropriate regulatory sequences. The term "gene" means the segment of DNA involved in producing a polypeptide chain; it includes regions preceding and following the coding region (leader and trailer) as well as, where applicable, intervening sequences (introns) between individual coding segments (exons). "Operably linked" as used herein refers to a functional relationship between two or more nucleic acid (e.g., DNA) segments. Typically, it refers to the functional relationship of transcriptional regulatory sequence to a transcribed sequence. For example, a promoter is operably linked to a coding sequence, such as a nucleic acid of the invention, if it stimulates or modulates the transcription of the coding sequence in an appropriate host cell or other expression system. Generally, promoter transcriptional regulatory sequences that are operably linked to a transcribed sequence are physically contiguous to the transcribed sequence, i.e., they are cis-acting. However, some transcriptional regulatory sequences, such as enhancers, need not be

physically contiguous or located in close proximity to the coding sequences whose transcription they enhance.

As used herein, the term "promoter" includes all sequences capable of driving transcription of a coding sequence in a cell, e.g., a plant cell. Thus, promoters used in the constructs of the invention include *cis*-acting transcriptional control elements and regulatory sequences that are involved in regulating or modulating the timing and/or rate of transcription of a gene. For example, a promoter can be a *cis*-acting transcriptional control element, including an enhancer, a promoter, a transcription terminator, an origin of replication, a chromosomal integration sequence, 5' and 3' untranslated regions, or an intronic sequence, which are involved in transcriptional regulation. These *cis*-acting sequences typically interact with proteins or other biomolecules to carry out (turn on/off, regulate, modulate, etc.) transcription. "Constitutive" promoters are those that drive expression continuously under most environmental conditions and states of development or cell differentiation. "Inducible" or "regulatable" promoters direct expression of the nucleic acid of the invention under the influence of environmental conditions or developmental conditions. Examples of environmental conditions that may affect transcription by inducible promoters include anaerobic conditions, elevated temperature, drought, or the presence of light.

"Plasmids" can be commercially available, publicly available on an unrestricted basis, or can be constructed from available plasmids in accord with published procedures. Equivalent plasmids to those described herein are known in the art and will be apparent to the ordinarily skilled artisan.

In one aspect, the term "recombinant" means that the nucleic acid is adjacent to a "backbone" nucleic acid to which it is not adjacent in its natural environment. Additionally, to be "enriched" the nucleic acids will represent 5% or more of the number of nucleic acid inserts in a population of nucleic acid backbone molecules. Backbone molecules according to the invention include nucleic acids such as expression vectors, self-replicating nucleic acids, viruses, integrating nucleic acids and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. Typically, the enriched nucleic acids represent 15% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. More typically, the enriched nucleic acids represent 50% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. In a one aspect, the enriched nucleic acids represent 90% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules.

One aspect of the invention is an isolated nucleic acid comprising one of the sequences of the invention, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 or more consecutive bases of a nucleic acid of the invention. The isolated, nucleic acids may comprise DNA, including cDNA, genomic DNA and synthetic DNA. The DNA may be double-stranded or single-stranded and if single stranded may be the coding strand or non-coding (anti-sense) strand. Alternatively, the isolated nucleic acids may comprise RNA.

The isolated nucleic acids of the invention may be used to prepare one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids of one of the polypeptides of the invention. Accordingly, another aspect of the invention is an isolated nucleic acid which encodes one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids of one of the polypeptides of the invention. The coding sequences of these nucleic acids may be identical to one of the coding sequences of one of the nucleic acids of the invention or may be different coding sequences which encode one of the of the invention having at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids of one of the polypeptides of the invention, as a result of the redundancy or degeneracy of the genetic code. The genetic code is well known to those of skill in the art and can be obtained, e.g., on page 214 of B. Lewin, *Genes VI*, Oxford University Press, 1997.

The isolated nucleic acid which encodes one of the polypeptides of the invention, but is not limited to: only the coding sequence of a nucleic acid of the invention and additional coding sequences, such as leader sequences or proprotein sequences and non-coding sequences, such as introns or non-coding sequences 5' and/or 3' of the coding sequence. Thus, as used herein, the term "polynucleotide encoding a polypeptide" encompasses a polynucleotide which includes only the coding sequence for the polypeptide as well as a polynucleotide which includes additional coding and/or non-coding sequence.

Alternatively, the nucleic acid sequences of the invention, may be mutagenized using conventional techniques, such as site directed mutagenesis, or other techniques familiar to those skilled in the art, to introduce silent changes into the polynucleotides of the invention. As used herein, "silent changes" include, for example, changes which do not alter the amino acid sequence encoded by the polynucleotide. Such changes may be desirable in order to increase the level of the

polypeptide produced by host cells containing a vector encoding the polypeptide by introducing codons or codon pairs which occur frequently in the host organism.

The invention also relates to polynucleotides which have nucleotide changes which result in amino acid substitutions, additions, deletions, fusions and truncations in the polypeptides of the invention. Such nucleotide changes may be introduced using techniques such as site directed mutagenesis, random chemical mutagenesis, exonuclease III deletion and other recombinant DNA techniques. Alternatively, such nucleotide changes may be naturally occurring allelic variants which are isolated by identifying nucleic acids which specifically hybridize to probes comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of the invention (or the sequences complementary thereto) under conditions of high, moderate, or low stringency as provided herein.

General Techniques

The nucleic acids used to practice this invention, whether RNA, iRNA, antisense nucleic acid, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed/generated recombinantly. Recombinant polypeptides generated from these nucleic acids can be individually isolated or cloned and tested for a desired activity. Any recombinant expression system can be used, including bacterial, mammalian, yeast, insect or plant cell expression systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, e.g., Adams (1983) J. Am. Chem. Soc. 105:661; Belousov (1997) Nucleic Acids Res. 25:3440-3444; Frenkel (1995) Free Radic. Biol. Med. 19:373-380; Blommers (1994) Biochemistry 33:7886-7896; Narang (1979) Meth. Enzymol. 68:90; Brown (1979) Meth. Enzymol. 68:109; Beaucage (1981) Tetra. Lett. 22:1859; U.S. Patent No. 4,458,066.

Techniques for the manipulation of nucleic acids, such as, e.g., subcloning, labeling probes (e.g., random-primer labeling using Klenow polymerase, nick translation, amplification), sequencing, hybridization and the like are well described in the scientific and patent literature, see, e.g., Sambrook, ed., MOLECULAR CLONING: A LABORATORY MANUAL (2ND ED.), Vols. 1-3, Cold Spring Harbor Laboratory, (1989); CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); LABORATORY TECHNIQUES IN

BIOCHEMISTRY AND MOLECULAR BIOLOGY: HYBRIDIZATION WITH NUCLEIC ACID PROBES, Part I. Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Another useful means of obtaining and manipulating nucleic acids used to practice the methods of the invention is to clone from genomic samples, and, if desired, screen and re-clone inserts isolated or amplified from, e.g., genomic clones or cDNA clones. Sources of nucleic acid used in the methods of the invention include genomic or cDNA libraries contained in, e.g., mammalian artificial chromosomes (MACs), see, e.g., U.S. Patent Nos. 5,721,118; 6,025,155; human artificial chromosomes, see, e.g., Rosenfeld (1997) *Nat. Genet.* 15:333-335; yeast artificial chromosomes (YAC); bacterial artificial chromosomes (BAC); P1 artificial chromosomes, see, e.g., Woon (1998) *Genomics* 50:306-316; P1-derived vectors (PACs), see, e.g., Kern (1997) *Biotechniques* 23:120-124; cosmids, recombinant viruses, phages or plasmids.

In one aspect, a nucleic acid encoding a polypeptide of the invention is assembled in appropriate phase with a leader sequence capable of directing secretion of the translated polypeptide or fragment thereof.

The invention provides fusion proteins and nucleic acids encoding them. A polypeptide of the invention can be fused to a heterologous peptide or polypeptide, such as N-terminal identification peptides which impart desired characteristics, such as increased stability or simplified purification. Peptides and polypeptides of the invention can also be synthesized and expressed as fusion proteins with one or more additional domains linked thereto for, e.g., producing a more immunogenic peptide, to more readily isolate a recombinantly synthesized peptide, to identify and isolate antibodies and antibody-expressing B cells, and the like. Detection and purification facilitating domains include, e.g., metal chelating peptides such as polyhistidine tracts and histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA). The inclusion of a cleavable linker sequences such as Factor Xa or enterokinase (Invitrogen, San Diego CA) between a purification domain and the motif-comprising peptide or polypeptide to facilitate purification. For example, an expression vector can include an epitope-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin and an enterokinase cleavage site (see e.g., Williams (1995) *Biochemistry* 34:1787-1797; Dobeli (1998) *Protein Expr. Purif.* 12:404-414). The histidine residues

facilitate detection and purification while the enterokinase cleavage site provides a means for purifying the epitope from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature, see e.g., Kroll (1993) *DNA Cell. Biol.*, 12:441-53.

Transcriptional and translational control sequences

The invention provides nucleic acid (e.g., DNA) sequences of the invention operatively linked to expression (e.g., transcriptional or translational) control sequence(s), e.g., promoters or enhancers, to direct or modulate RNA synthesis/expression. The expression control sequence can be in an expression vector. Exemplary bacterial promoters include *lacI*, *lacZ*, T3, T7, *gpt*, lambda PR, PL and *trp*. Exemplary eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein I.

Promoters suitable for expressing a polypeptide in bacteria include the *E. coli lac* or *trp* promoters, the *lacI* promoter, the *lacZ* promoter, the T3 promoter, the T7 promoter, the *gpt* promoter, the lambda PR promoter, the lambda PL promoter, promoters from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK), and the acid phosphatase promoter. Eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, heat shock promoters, the early and late SV40 promoter, LTRs from retroviruses, and the mouse metallothionein-I promoter. Other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses may also be used. Promoters suitable for expressing the polypeptide or fragment thereof in bacteria include the *E. coli lac* or *trp* promoters, the *lacI* promoter, the *lacZ* promoter, the T3 promoter, the T7 promoter, the *gpt* promoter, the lambda PR promoter, the lambda PL promoter, promoters from operons encoding glycolytic enzymes such as 3-phosphoglycerate kinase (PGK) and the acid phosphatase promoter. Fungal promoters include the α -factor promoter. Eukaryotic promoters include the CMV immediate early promoter, the HSV thymidine kinase promoter, heat shock promoters, the early and late SV40 promoter, LTRs from retroviruses and the mouse metallothionein-I promoter. Other promoters known to control expression of genes in prokaryotic or eukaryotic cells or their viruses may also be used.

Tissue-Specific Promoters

The invention provides expression cassettes that can be expressed in a tissue-specific manner, e.g., that can express a polypeptide, enzyme, protein, e.g. structural or

binding protein, of the invention in a tissue-specific manner. The invention also provides plants or seeds that express a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention in a tissue-specific manner. The tissue-specificity can be seed specific, stem specific, leaf specific, root specific, fruit specific and the like.

The term "expression cassette" as used herein refers to a nucleotide sequence which is capable of affecting expression of a structural gene (i.e., a protein coding sequence, such as a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention) in a host compatible with such sequences. Expression cassettes include at least a promoter operably linked with the polypeptide coding sequence; and, optionally, with other sequences, e.g., transcription termination signals. Additional factors necessary or helpful in effecting expression may also be used, e.g., enhancers, alpha-factors. Thus, expression cassettes also include plasmids, expression vectors, recombinant viruses, any form of recombinant "naked DNA" vector, and the like. A "vector" comprises a nucleic acid which can infect, transfect, transiently or permanently transduce a cell. It will be recognized that a vector can be a naked nucleic acid, or a nucleic acid complexed with protein or lipid. The vector optionally comprises viral or bacterial nucleic acids and/or proteins, and/or membranes (e.g., a cell membrane, a viral lipid envelope, etc.). Vectors include, but are not limited to replicons (e.g., RNA replicons, bacteriophages) to which fragments of DNA may be attached and become replicated. Vectors thus include, but are not limited to RNA, autonomous self-replicating circular or linear DNA or RNA (e.g., plasmids, viruses, and the like, see, e.g., U.S. Patent No. 5,217,879), and include both the expression and non-expression plasmids. Where a recombinant microorganism or cell culture is described as hosting an "expression vector" this includes both extra-chromosomal circular and linear DNA and DNA that has been incorporated into the host chromosome(s). Where a vector is being maintained by a host cell, the vector may either be stably replicated by the cells during mitosis as an autonomous structure, or is incorporated within the host's genome.

"Tissue-specific" promoters are transcriptional control elements that are only active in particular cells or tissues or organs, e.g., in plants or animals. Tissue-specific regulation may be achieved by certain intrinsic factors which ensure that genes encoding proteins specific to a given tissue are expressed. Such factors are known to exist in mammals and plants so as to allow for specific tissues to develop.

The term "plant" includes whole plants, plant parts (e.g., leaves, stems, flowers, roots, etc.), plant protoplasts, seeds and plant cells and progeny of same. The class of

plants which can be used in the method of the invention is generally as broad as the class of higher plants amenable to transformation techniques, including angiosperms (monocotyledonous and dicotyledonous plants), as well as gymnosperms. It includes plants of a variety of ploidy levels, including polyploid, diploid, haploid and hemizygous states. As used herein, the term "transgenic plant" includes plants or plant cells into which a heterologous nucleic acid sequence has been inserted, e.g., the nucleic acids and various recombinant constructs (e.g., expression cassettes) of the invention.

In one aspect, a constitutive promoter such as the CaMV 35S promoter can be used for expression in specific parts of the plant or seed or throughout the plant. For example, for overexpression, a plant promoter fragment can be employed which will direct expression of a nucleic acid in some or all tissues of a plant, e.g., a regenerated plant. Such promoters are referred to herein as "constitutive" promoters and are active under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35S transcription initiation region, the 1'- or 2'- promoter derived from T-DNA of *Agrobacterium tumefaciens*, and other transcription initiation regions from various plant genes known to those of skill. Such genes include, e.g., *ACT11* from *Arabidopsis* (Huang (1996) *Plant Mol. Biol.* 33:125-139); *Cat3* from *Arabidopsis* (GenBank No. U43147, Zhong (1996) *Mol. Gen. Genet.* 251:196-203); the gene encoding stearyl-acyl carrier protein desaturase from *Brassica napus* (Genbank No. X74782, Solcombe (1994) *Plant Physiol.* 104:1167-1176); *GPc1* from maize (GenBank No. X15596; Martinez (1989) *J. Mol. Biol.* 208:551-565); the *Gpc2* from maize (GenBank No. U45855, Manjunath (1997) *Plant Mol. Biol.* 33:97-112); plant promoters described in U.S. Patent Nos. 4,962,028; 5,633,440.

The invention uses tissue-specific or constitutive promoters derived from viruses which can include, e.g., the tobamovirus subgenomic promoter (Kumagai (1995) *Proc. Natl. Acad. Sci. USA* 92:1679-1683; the rice tungro bacilliform virus (RTBV), which replicates only in phloem cells in infected rice plants, with its promoter which drives strong phloem-specific reporter gene expression; the cassava vein mosaic virus (CVMV) promoter, with highest activity in vascular elements, in leaf mesophyll cells, and in root tips (Verdaguer (1996) *Plant Mol. Biol.* 31:1129-1139).

Alternatively, the plant promoter may direct expression of a polypeptide, enzyme, protein, e.g. structural or binding protein-expressing nucleic acid in a specific tissue, organ or cell type (*i.e.* tissue-specific promoters) or may be otherwise under more precise

environmental or developmental control or under the control of an inducible promoter. Examples of environmental conditions that may affect transcription include anaerobic conditions, elevated temperature, the presence of light, or sprayed with chemicals/hormones. For example, the invention incorporates the drought-inducible promoter of maize (Busk (1997) *supra*); the cold, drought, and high salt inducible promoter from potato (Kirch (1997) *Plant Mol. Biol.* 33:897-909).

Tissue-specific promoters can promote transcription only within a certain time frame of developmental stage within that tissue. See, e.g., Blazquez (1998) *Plant Cell* 10:791-800, characterizing the *Arabidopsis* LEAFY gene promoter. See also Cardon (1997) *Plant J* 12:367-77, describing the transcription factor SPL3, which recognizes a conserved sequence motif in the promoter region of the *A. thaliana* floral meristem identity gene AP1; and Mandel (1995) *Plant Molecular Biology*, Vol. 29, pp 995-1004, describing the meristem promoter eIF4. Tissue specific promoters which are active throughout the life cycle of a particular tissue can be used. In one aspect, the nucleic acids of the invention are operably linked to a promoter active primarily only in cotton fiber cells. In one aspect, the nucleic acids of the invention are operably linked to a promoter active primarily during the stages of cotton fiber cell elongation, e.g., as described by Rinehart (1996) *supra*. The nucleic acids can be operably linked to the Fb12A gene promoter to be preferentially expressed in cotton fiber cells (*Ibid*). See also, John (1997) *Proc. Natl. Acad. Sci. USA* 89:5769-5773; John, et al., U.S. Patent Nos. 5,608,148 and 5,602,321, describing cotton fiber-specific promoters and methods for the construction of transgenic cotton plants. Root-specific promoters may also be used to express the nucleic acids of the invention. Examples of root-specific promoters include the promoter from the alcohol dehydrogenase gene (DeLisle (1990) *Int. Rev. Cytol.* 123:39-60). Other promoters that can be used to express the nucleic acids of the invention include, e.g., ovule-specific, embryo-specific, endosperm-specific, integument-specific, seed coat-specific promoters, or some combination thereof; a leaf-specific promoter (see, e.g., Busk (1997) *Plant J.* 11:1285 1295, describing a leaf-specific promoter in maize); the ORF13 promoter from *Agrobacterium rhizogenes* (which exhibits high activity in roots, see, e.g., Hansen (1997) *supra*); a maize pollen specific promoter (see, e.g., Guerrero (1990) *Mol. Gen. Genet.* 224:161 168); a tomato promoter active during fruit ripening, senescence and abscission of leaves and, to a lesser extent, of flowers can be used (see, e.g., Blume (1997) *Plant J.* 12:731 746); a pistil-specific promoter from the potato SK2 gene (see, e.g., Ficker (1997) *Plant Mol. Biol.* 35:425

431); the *Blec4* gene from pea, which is active in epidermal tissue of vegetative and floral shoot apices of transgenic alfalfa making it a useful tool to target the expression of foreign genes to the epidermal layer of actively growing shoots or fibers; the ovule-specific *BEL1* gene (see, e.g., Reiser (1995) *Cell* 83:735-742, GenBank No. U39944); and/or, the promoter in Klee, U.S. Patent No. 5,589,583, describing a plant promoter region is capable of conferring high levels of transcription in meristematic tissue and/or rapidly dividing cells.

Alternatively, plant promoters which are inducible upon exposure to plant hormones, such as auxins, are used to express the nucleic acids of the invention. For example, the invention can use the auxin-response elements E1 promoter fragment (AuxREs) in the soybean (*Glycine max* L.) (Liu (1997) *Plant Physiol.* 115:397-407); the auxin-responsive *Arabidopsis* GST6 promoter (also responsive to salicylic acid and hydrogen peroxide) (Chen (1996) *Plant J.* 10: 955-966); the auxin-inducible *parC* promoter from tobacco (Sakai (1996) 37:906-913); a plant biotin response element (Streit (1997) *Mol. Plant Microbe Interact.* 10:933-937); and, the promoter responsive to the stress hormone abscisic acid (Sheen (1996) *Science* 274:1900-1902).

The nucleic acids of the invention can also be operably linked to plant promoters which are inducible upon exposure to chemicals reagents which can be applied to the plant, such as herbicides or antibiotics. For example, the maize *In2-2* promoter, activated by benzenesulfonamide herbicide safeners, can be used (De Veylder (1997) *Plant Cell Physiol.* 38:568-577); application of different herbicide safeners induces distinct gene expression patterns, including expression in the root, hydathodes, and the shoot apical meristem. Coding sequence can be under the control of, e.g., a tetracycline-inducible promoter, e.g., as described with transgenic tobacco plants containing the *Avena sativa* L. (oat) arginine decarboxylase gene (Masgrau (1997) *Plant J.* 11:465-473); or, a salicylic acid-responsive element (Stange (1997) *Plant J.* 11:1315-1324). Using chemically- (e.g., hormone- or pesticide-) induced promoters, i.e., promoter responsive to a chemical which can be applied to the transgenic plant in the field, expression of a polypeptide of the invention can be induced at a particular stage of development of the plant. Thus, the invention also provides for transgenic plants containing an inducible gene encoding for polypeptides of the invention whose host range is limited to target plant species, such as corn, rice, barley, wheat, potato or other crops, inducible at any stage of development of the crop.

One of skill will recognize that a tissue-specific plant promoter may drive expression of operably linked sequences in tissues other than the target tissue. Thus, a tissue-specific promoter is one that drives expression preferentially in the target tissue or cell type, but may also lead to some expression in other tissues as well.

The nucleic acids of the invention can also be operably linked to plant promoters which are inducible upon exposure to chemicals reagents. These reagents include, e.g., herbicides, synthetic auxins, or antibiotics which can be applied, e.g., sprayed, onto transgenic plants. Inducible expression of the polypeptide, enzyme, protein, e.g. structural or binding protein-producing nucleic acids of the invention will allow the grower to select plants with the optimal polypeptide, enzyme, protein, e.g. structural or binding protein, expression and/or activity. The development of plant parts can thus be controlled. In this way the invention provides the means to facilitate the harvesting of plants and plant parts. For example, in various embodiments, the maize In2-2 promoter, activated by benzenesulfonamide herbicide safeners, is used (De Veylder (1997) *Plant Cell Physiol.* 38:568-577); application of different herbicide safeners induces distinct gene expression patterns, including expression in the root, hydathodes, and the shoot apical meristem. Coding sequences of the invention are also under the control of a tetracycline-inducible promoter, e.g., as described with transgenic tobacco plants containing the *Avena sativa* L. (oat) arginine decarboxylase gene (Masgrau (1997) *Plant J.* 11:465-473); or, a salicylic acid-responsive element (Stange (1997) *Plant J.* 11:1315-1324).

In some aspects, proper polypeptide expression may require polyadenylation region at the 3'-end of the coding region. The polyadenylation region can be derived from the natural gene, from a variety of other plant (or animal or other) genes, or from genes in the *Agrobacterium* T-DNA.

Expression vectors and cloning vehicles

The invention provides expression vectors and cloning vehicles comprising nucleic acids of the invention, e.g., sequences encoding the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention. Expression vectors and cloning vehicles of the invention can comprise viral particles, baculovirus, phage, plasmids, phagemids, cosmids, fosmids, bacterial artificial chromosomes, viral DNA (e.g., vaccinia, adenovirus, fowl pox virus, pseudorabies and derivatives of SV40), P1-based artificial chromosomes, yeast plasmids, yeast artificial chromosomes, and any other vectors specific for specific hosts of interest (such as bacillus, *Aspergillus* and yeast).

Vectors of the invention can include chromosomal, non-chromosomal and synthetic DNA sequences. Large numbers of suitable vectors are known to those of skill in the art, and are commercially available. Exemplary vectors are include: bacterial: pQE vectors (Qiagen), pBLUESCRIPT plasmids, pNH vectors, (lambda-ZAP vectors (Stratagene); ptrc99a, pKK223-3, pDR540, pRIT2T (Pharmacia); Eukaryotic: pXT1, pSG5 (Stratagene), pSVK3, pBPV, pMSG, pSVLSV40 (Pharmacia). However, any other plasmid or other vector may be used so long as they are replicable and viable in the host. Low copy number or high copy number vectors may be employed with the present invention.

The expression vector can comprise a promoter, a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. Mammalian expression vectors can comprise an origin of replication, any necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences, and 5' flanking non-transcribed sequences. In some aspects, DNA sequences derived from the SV40 splice and polyadenylation sites may be used to provide the required non-transcribed genetic elements.

In one aspect, the expression vectors contain one or more selectable marker genes to permit selection of host cells containing the vector. Such selectable markers include genes encoding dihydrofolate reductase or genes conferring neomycin resistance for eukaryotic cell culture, genes conferring tetracycline or ampicillin resistance in *E. coli*, and the *S. cerevisiae* TRP1 gene. Promoter regions can be selected from any desired gene using chloramphenicol transferase (CAT) vectors or other vectors with selectable markers.

Vectors for expressing the polypeptide or fragment thereof in eukaryotic cells can also contain enhancers to increase expression levels. Enhancers are cis-acting elements of DNA that can be from about 10 to about 300 bp in length. They can act on a promoter to increase its transcription. Exemplary enhancers include the SV40 enhancer on the late side of the replication origin bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and the adenovirus enhancers.

A nucleic acid sequence can be inserted into a vector by a variety of procedures. In general, the sequence is ligated to the desired position in the vector following digestion of the insert and the vector with appropriate restriction

endonucleases. Alternatively, blunt ends in both the insert and the vector may be ligated. A variety of cloning techniques are known in the art, e.g., as described in Ausubel and Sambrook. Such procedures and others are deemed to be within the scope of those skilled in the art.

The vector can be in the form of a plasmid, a viral particle, or a phage. Other vectors include chromosomal, non-chromosomal and synthetic DNA sequences, derivatives of SV40; bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus, and pseudorabies. A variety of cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by, e.g., Sambrook.

Particular bacterial vectors which can be used include the commercially available plasmids comprising genetic elements of the well known cloning vector pBR322 (ATCC 37017), pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden), GEM1 (Promega Biotec, Madison, WI, USA) pQE70, pQE60, pQE-9 (Qiagen), pD10, psiX174 pBLUESCRIPT II KS, pNH8A, pNH16a, pNH18A, pNH46A (Stratagene), ptrc99a, pKK223-3, pKK233-3, DR540, pRIT5 (Pharmacia), pKK232-8 and pCM7. Particular eukaryotic vectors include pSV2CAT, pOG44, pXT1, pSG (Stratagene) pSVK3, pBPV, pMSG, and pSVL (Pharmacia). However, any other vector may be used as long as it is replicable and viable in the host cell.

The nucleic acids of the invention can be expressed in expression cassettes, vectors or viruses and transiently or stably expressed in plant cells and seeds. One exemplary transient expression system uses episomal expression systems, e.g., cauliflower mosaic virus (CaMV) viral RNA generated in the nucleus by transcription of an episomal mini-chromosome containing supercoiled DNA, see, e.g., Covey (1990) Proc. Natl. Acad. Sci. USA 87:1633-1637. Alternatively, coding sequences, i.e., all or sub-fragments of sequences of the invention can be inserted into a plant host cell genome becoming an integral part of the host chromosomal DNA. Sense or antisense transcripts can be expressed in this manner. A vector comprising the sequences (e.g., promoters or coding regions) from nucleic acids of the invention can comprise a marker gene that confers a selectable phenotype on a plant cell or a seed. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

Expression vectors capable of expressing nucleic acids and proteins in plants are well known in the art, and can include, *e.g.*, vectors from *Agrobacterium* spp., potato virus X (see, *e.g.*, Angell (1997) EMBO J. 16:3675-3684), tobacco mosaic virus (see, *e.g.*, Casper (1996) Gene 173:69-73), tomato bushy stunt virus (see, *e.g.*, Hillman (1989) Virology 169:42-50), tobacco etch virus (see, *e.g.*, Dolja (1997) Virology 234:243-252), bean golden mosaic virus (see, *e.g.*, Morinaga (1993) Microbiol Immunol. 37:471-476), cauliflower mosaic virus (see, *e.g.*, Cecchini (1997) Mol. Plant Microbe Interact. 10:1094-1101), maize Ac/Ds transposable element (see, *e.g.*, Rubin (1997) Mol. Cell. Biol. 17:6294-6302; Kunze (1996) Curr. Top. Microbiol. Immunol. 204:161-194), and the maize suppressor-mutator (Spm) transposable element (see, *e.g.*, Schlappi (1996) Plant Mol. Biol. 32:717-725); and derivatives thereof.

In one aspect, the expression vector can have two replication systems to allow it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector can contain at least one sequence homologous to the host cell genome. It can contain two homologous sequences which flank the expression construct. The integrating vector can be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art.

Expression vectors of the invention may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed, *e.g.*, genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers can also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways.

The DNA sequence in the expression vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct RNA synthesis. Particular named bacterial promoters include *lacI*, *lacZ*, *T3*, *T7*, *gpt*, *lambda P_R*, *P_L* and *trp*. Eukaryotic promoters include CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus and mouse metallothionein-I. Selection of the appropriate vector and promoter is well within the level of ordinary skill in the art. The expression vector also contains a ribosome binding site for translation initiation and a transcription terminator. The vector may also include appropriate sequences for amplifying expression. Promoter regions can be selected from any desired gene using

chloramphenicol transferase (CAT) vectors or other vectors with selectable markers. In addition, the expression vectors in one aspect contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

Mammalian expression vectors may also comprise an origin of replication, any necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences and 5' flanking nontranscribed sequences. In some aspects, DNA sequences derived from the SV40 splice and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

Vectors for expressing the polypeptide or fragment thereof in eukaryotic cells may also contain enhancers to increase expression levels. Enhancers are cis-acting elements of DNA, usually from about 10 to about 300 bp in length that act on a promoter to increase its transcription. Examples include the SV40 enhancer on the late side of the replication origin bp 100 to 270, the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin and the adenovirus enhancers.

In addition, the expression vectors typically contain one or more selectable marker genes to permit selection of host cells containing the vector. Such selectable markers include genes encoding dihydrofolate reductase or genes conferring neomycin resistance for eukaryotic cell culture, genes conferring tetracycline or ampicillin resistance in *E. coli* and the *S. cerevisiae* *TRP1* gene.

In some aspects, the nucleic acid encoding one of the polypeptides of the invention, or fragments comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof is assembled in appropriate phase with a leader sequence capable of directing secretion of the translated polypeptide or fragment thereof. Optionally, the nucleic acid can encode a fusion polypeptide in which one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof is fused to heterologous peptides or polypeptides, such as N-terminal identification peptides which impart desired characteristics, such as increased stability or simplified purification.

The appropriate DNA sequence may be inserted into the vector by a variety of procedures. In general, the DNA sequence is ligated to the desired position in the vector following digestion of the insert and the vector with appropriate restriction endonucleases. Alternatively, blunt ends in both the insert and the vector may be ligated.

A variety of cloning techniques are disclosed in Ausubel *et al.* Current Protocols in Molecular Biology, John Wiley 503 Sons, Inc. 1997 and Sambrook *et al.*, Molecular Cloning: A Laboratory Manual 2nd Ed., Cold Spring Harbor Laboratory Press (1989). Such procedures and others are deemed to be within the scope of those skilled in the art.

The vector may be, for example, in the form of a plasmid, a viral particle, or a phage. Other vectors include chromosomal, nonchromosomal and synthetic DNA sequences, derivatives of SV40; bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, fowl pox virus and pseudorabies. A variety of cloning and expression vectors for use with prokaryotic and eukaryotic hosts are described by Sambrook, *et al.*, Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, N.Y., (1989).

Host cells and transformed cells

The invention also provides a transformed cell comprising a nucleic acid sequence of the invention, e.g., a sequence encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention, or a vector of the invention. The host cell may be any of the host cells familiar to those skilled in the art, including prokaryotic cells, eukaryotic cells, such as bacterial cells, fungal cells, yeast cells, mammalian cells, insect cells, or plant cells. Exemplary bacterial cells include *E. coli*, *Streptomyces*, *Bacillus subtilis*, *Bacillus cereus*, *Salmonella typhimurium* and various species within the genera *Streptomyces* and *Staphylococcus*. Exemplary insect cells include *Drosophila S2* and *Spodoptera Sf9*. Exemplary animal cells include CHO, COS or Bowes melanoma or any mouse or human cell line. The selection of an appropriate host is within the abilities of those skilled in the art. Techniques for transforming a wide variety of higher plant species are well known and described in the technical and scientific literature. See, e.g., Weising (1988) Ann. Rev. Genet. 22:421-477; U.S. Patent No. 5,750,870.

The vector can be introduced into the host cells using any of a variety of techniques, including transformation, transfection, transduction, viral infection, gene guns, or Ti-mediated gene transfer. Particular methods include calcium phosphate transfection, DEAE-Dextran mediated transfection, lipofection, or electroporation (Davis, L., Dibner, M., Battey, I., Basic Methods in Molecular Biology, (1986)).

In one aspect, the nucleic acids or vectors of the invention are introduced into the cells for screening, thus, the nucleic acids enter the cells in a manner suitable for subsequent expression of the nucleic acid. The method of introduction is largely dictated

by the targeted cell type. Exemplary methods include CaPO_4 precipitation, liposome fusion, lipofection (e.g., LIPOFECTIN™), electroporation, viral infection, etc. The candidate nucleic acids may stably integrate into the genome of the host cell (for example, with retroviral introduction) or may exist either transiently or stably in the cytoplasm (i.e. through the use of traditional plasmids, utilizing standard regulatory sequences, selection markers, etc.). As many pharmaceutically important screens require human or model mammalian cell targets, retroviral vectors capable of transfecting such targets can be used.

Where appropriate, the engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (e.g., temperature shift or chemical induction) and the cells may be cultured for an additional period to allow them to produce the desired polypeptide or fragment thereof.

Cells can be harvested by centrifugation, disrupted by physical or chemical means, and the resulting crude extract is retained for further purification. Microbial cells employed for expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such methods are well known to those skilled in the art. The expressed polypeptide or fragment thereof can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. If desired, high performance liquid chromatography (HPLC) can be employed for final purification steps.

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Depending upon the host employed in a recombinant production procedure, the polypeptides produced by host cells containing the vector may be glycosylated or may be non-glycosylated. Polypeptides of the invention may or may not also include an initial methionine amino acid residue.

Cell-free translation systems can also be employed to produce a polypeptide of the invention. Cell-free translation systems can use mRNAs transcribed from a DNA construct comprising a promoter operably linked to a nucleic acid encoding the polypeptide or fragment thereof. In some aspects, the DNA construct may be linearized prior to conducting an *in vitro* transcription reaction. The transcribed mRNA is then incubated with an appropriate cell-free translation extract, such as a rabbit reticulocyte extract, to produce the desired polypeptide or fragment thereof.

The expression vectors can contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydrofolate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

Host cells containing the polynucleotides of interest, e.g., nucleic acids of the invention, can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying genes. The culture conditions, such as temperature, pH and the like, are those previously used with the host cell selected for expression and will be apparent to the ordinarily skilled artisan. The clones which are identified as having the specified enzyme activity may then be sequenced to identify the polynucleotide sequence encoding an enzyme having the enhanced activity.

The invention provides a method for overexpressing a recombinant polypeptide, enzyme, protein, e.g. structural or binding protein, in a cell comprising expressing a vector comprising a nucleic acid of the invention, e.g., a nucleic acid comprising a nucleic acid sequence with at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to an exemplary sequence of the invention over a region of at least about 100 residues, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection, or, a nucleic acid that hybridizes under stringent conditions to a nucleic acid sequence of the invention. The overexpression can be effected by any means, e.g., use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

The nucleic acids of the invention can be expressed, or overexpressed, in any *in vitro* or *in vivo* expression system. Any cell culture systems can be employed to

express, or over-express, recombinant protein, including bacterial, insect, yeast, fungal or mammalian cultures. Over-expression can be effected by appropriate choice of promoters, enhancers, vectors (e.g., use of replicon vectors, dicistronic vectors (see, e.g., Gurtu (1996) *Biochem. Biophys. Res. Commun.* 229:295-8), media, culture systems and the like. In one aspect, gene amplification using selection markers, e.g., glutamine synthetase (see, e.g., Sanders (1987) *Dev. Biol. Stand.* 66:55-63), in cell systems are used to overexpress the polypeptides of the invention.

The host cell may be any of the host cells familiar to those skilled in the art, including prokaryotic cells, eukaryotic cells, mammalian cells, insect cells, or plant cells. As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Streptomyces*, *Bacillus subtilis*, *Bacillus cereus*, *Salmonella typhimurium* and various species within the genera *Streptomyces* and *Staphylococcus*, fungal cells, such as yeast, insect cells such as *Drosophila S2* and *Spodoptera Sf9*, animal cells such as CHO, COS or Bowes melanoma and adenoviruses. The selection of an appropriate host is within the abilities of those skilled in the art.

The vector may be introduced into the host cells using any of a variety of techniques, including transformation, transfection, transduction, viral infection, gene guns, or Ti-mediated gene transfer. Particular methods include calcium phosphate transfection, DEAE-Dextran mediated transfection, lipofection, or electroporation (Davis, L., Dibner, M., Battey, I., *Basic Methods in Molecular Biology*, (1986)).

Where appropriate, the engineered host cells can be cultured in conventional nutrient media modified as appropriate for activating promoters, selecting transformants or amplifying the genes of the invention. Following transformation of a suitable host strain and growth of the host strain to an appropriate cell density, the selected promoter may be induced by appropriate means (e.g., temperature shift or chemical induction) and the cells may be cultured for an additional period to allow them to produce the desired polypeptide or fragment thereof.

Cells are typically harvested by centrifugation, disrupted by physical or chemical means and the resulting crude extract is retained for further purification. Microbial cells employed for expression of proteins can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents. Such methods are well known to those skilled in the art. The expressed polypeptide or fragment thereof can be recovered and purified from recombinant cell cultures by methods including ammonium sulfate or ethanol precipitation, acid extraction,

anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Protein refolding steps can be used, as necessary, in completing configuration of the polypeptide. If desired, high performance liquid chromatography (HPLC) can be employed for final purification steps.

Various mammalian cell culture systems can also be employed to express recombinant protein. Examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts (described by Gluzman, *Cell*, 23:175, 1981) and other cell lines capable of expressing proteins from a compatible vector, such as the C127, 3T3, CHO, HeLa and BHK cell lines.

The constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Depending upon the host employed in a recombinant production procedure, the polypeptides produced by host cells containing the vector may be glycosylated or may be non-glycosylated. Polypeptides of the invention may or may not also include an initial methionine amino acid residue.

Alternatively, the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids thereof can be synthetically produced by conventional peptide synthesizers. In other aspects, fragments or portions of the polypeptides may be employed for producing the corresponding full-length polypeptide by peptide synthesis; therefore, the fragments may be employed as intermediates for producing the full-length polypeptides.

Cell-free translation systems can also be employed to produce one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids thereof using mRNAs transcribed from a DNA construct comprising a promoter operably linked to a nucleic acid encoding the polypeptide or fragment thereof. In some aspects, the DNA construct may be linearized prior to conducting an *in vitro* transcription reaction. The transcribed mRNA is then incubated with an appropriate cell-free translation extract, such as a rabbit reticulocyte extract, to produce the desired polypeptide or fragment thereof.

Amplification of Nucleic Acids

In practicing the invention, nucleic acids encoding the polypeptides of the invention, or modified nucleic acids, can be reproduced by, e.g., amplification. The invention provides amplification primer sequence pairs for amplifying nucleic acids encoding polypeptides (e.g., enzymes) of the invention. In one aspect, the primer pairs

are capable of amplifying nucleic acid sequences of the invention, e.g., including the exemplary SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, etc., including all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, or a subsequence thereof, etc. One of skill in the art can design amplification primer sequence pairs for any part of or the full length of these sequences.

In one aspect, the invention provides a nucleic acid amplified by a primer pair of the invention, e.g., a primer pair as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more residues of a nucleic acid of the invention, and about the first (the 5') 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more residues of the complementary strand.

The invention provides an amplification primer sequence pair for amplifying a nucleic acid encoding a polypeptide having an enzyme, structural or binding activity, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence of the invention, or fragments or subsequences thereof. One or each member of the amplification primer sequence pair can comprise an oligonucleotide comprising at least about 10 to 50 or more consecutive bases of the sequence, or about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more consecutive bases of the sequence. The invention provides amplification primer pairs, wherein the primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more residues of a nucleic acid of the invention, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 or more residues of the complementary strand of the first member. The invention provides a polypeptide, enzyme, protein, e.g. structural or binding protein, generated by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. The invention provides methods of making a polypeptide, enzyme, protein, e.g. structural or binding protein, by amplification, e.g., polymerase chain reaction (PCR), using an amplification primer pair of the invention. In one aspect, the amplification primer pair amplifies a nucleic acid from a library, e.g., a gene library, such as an environmental library.

Amplification reactions can also be used to quantify the amount of nucleic acid in a sample (such as the amount of message in a cell sample), label the nucleic acid (e.g., to apply it to an array or a blot), detect the nucleic acid, or quantify the amount of a

specific nucleic acid in a sample. In one aspect of the invention, message isolated from a cell or a cDNA library are amplified.

The skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (see, e.g., PCR PROTOCOLS, A GUIDE TO METHODS AND APPLICATIONS, ed. Innis, Academic Press, N.Y. (1990) and PCR STRATEGIES (1995), ed. Innis, Academic Press, Inc., N.Y., ligase chain reaction (LCR) (see, e.g., Wu (1989) Genomics 4:560; Landegren (1988) Science 241:1077; Barringer (1990) Gene 89:117); transcription amplification (see, e.g., Kwok (1989) Proc. Natl. Acad. Sci. USA 86:1173); and, self-sustained sequence replication (see, e.g., Guatelli (1990) Proc. Natl. Acad. Sci. USA 87:1874); Q Beta replicase amplification (see, e.g., Smith (1997) J. Clin. Microbiol. 35:1477-1491), automated Q-beta replicase amplification assay (see, e.g., Burg (1996) Mol. Cell. Probes 10:257-271) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger (1987) Methods Enzymol. 152:307-316; Sambrook; Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Söcknanan (1995) Biotechnology 13:563-564.

Determining the degree of sequence identity

The invention provides nucleic acids comprising sequences having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary nucleic acid of the invention (e.g., SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, etc., including all nucleic acids disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, and nucleic acids encoding SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc., and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898) over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550 or more, residues. The invention provides polypeptides comprising sequences having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%,

79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity to an exemplary polypeptide of the invention. The extent of sequence identity (homology) may be determined using any computer program and associated parameters, including those described herein, such as BLAST 2.2.2. or FASTA version 3.0t78, with the default parameters.

As used herein, the terms "computer," "computer program" and "processor" are used in their broadest general contexts and incorporate all such devices, as described in detail, below.

Nucleic acid sequences of the invention can comprise at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 or more consecutive nucleotides of an exemplary sequence of the invention and sequences substantially identical thereto. Homologous sequences and fragments of nucleic acid sequences of the invention can refer to a sequence having at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity (homology) to these sequences. Homology (sequence identity) may be determined using any of the computer programs and parameters described herein, including FASTA version 3.0t78 with the default parameters. Homologous sequences also include RNA sequences in which uridines replace the thymines in the nucleic acid sequences of the invention. The homologous sequences may be obtained using any of the procedures described herein or may result from the correction of a sequencing error. It will be appreciated that the nucleic acid sequences of the invention can be represented in the traditional single character format (See the inside back cover of Stryer, Lubert. Biochemistry, 3rd Ed., W. H Freeman & Co., New York.) or in any other format which records the identity of the nucleotides in a sequence.

Various sequence comparison programs identified elsewhere in this patent specification are particularly contemplated for use in this aspect of the invention. Protein and/or nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA and CLUSTALW (see, e.g., Pearson and Lipman, Proc. Natl. Acad. Sci. USA 85(8):2444-2448, 1988; Altschul *et al.*, J. Mol. Biol. 215(3):403-410, 1990; Thompson

Nucleic Acids Res. 22(2):4673-4680, 1994; Higgins *et al.*, Methods Enzymol. 266:383-402, 1996; Altschul *et al.*, J. Mol. Biol. 215(3):403-410, 1990; Altschul *et al.*, Nature Genetics 3:266-272, 1993).

Homology or identity is often measured using sequence analysis software (*e.g.*, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705). Such software matches similar sequences by assigning degrees of homology to various deletions, substitutions and other modifications. The terms "homology" and "identity" in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same when compared and aligned for maximum correspondence over a comparison window or designated region as measured using any number of sequence comparison algorithms or by manual alignment and visual inspection.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequence for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482, 1981, by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443, 1970, by the search for similarity method of person & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444, 1988, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection. Other algorithms for determining homology or identity include, for example, in addition to a BLAST program (Basic Local Alignment Search Tool at the National Center

for Biological Information), ALIGN, AMAS (Analysis of Multiply Aligned Sequences), AMPS (Protein Multiple Sequence Alignment), ASSET (Aligned Segment Statistical Evaluation Tool), BANDS, BESTSCOR, BIOSCAN (Biological Sequence Comparative Analysis Node), BLIMPS (BLOCKS IMPROVED Searcher), FASTA, Intervals & Points, BMB, CLUSTAL V, CLUSTAL W, CONSENSUS, LCONSENSUS, WCONSENSUS, Smith-Waterman algorithm, DARWIN, Las Vegas algorithm, FNAT (Forced Nucleotide Alignment Tool), Framealign, Framesearch, DYNAMIC, FILTER, FSAP (Fristensky Sequence Analysis Package), GAP (Global Alignment Program), GENAL, GIBBS, GenQuest, ISSC (Sensitive Sequence Comparison), LALIGN (Local Sequence Alignment), LCP (Local Content Program), MACAW (Multiple Alignment Construction & Analysis Workbench), MAP (Multiple Alignment Program), MBLKP, MBLKN, PIMA (Pattern-Induced Multi-sequence Alignment), SAGA (Sequence Alignment by Genetic Algorithm) and WHAT-IF. Such alignment programs can also be used to screen genome databases to identify polynucleotide sequences having substantially identical sequences. A number of genome databases are available, for example, a substantial portion of the human genome is available as part of the Human Genome Sequencing Project (Gibbs, 1995). At least twenty-one other genomes have already been sequenced, including, for example, *M. genitalium* (Fraser *et al.*, 1995), *M. jannaschii* (Bult *et al.*, 1996), *H. influenzae* (Fleischmann *et al.*, 1995), *E. coli* (Blattner *et al.*, 1997) and yeast (*S. cerevisiae*) (Mewes *et al.*, 1997) and *D. melanogaster* (Adams *et al.*, 2000). Significant progress has also been made in sequencing the genomes of model organism, such as mouse, *C. elegans* and *Arabidopsis sp.* Several databases containing genomic information annotated with some functional information are maintained by different organizations and may be accessible via internet.

One example of a useful algorithm is BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, Nuc. Acids Res. 25:3389-3402, 1997 and Altschul *et al.*, J. Mol. Biol. 215:403-410, 1990, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along

each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3 and expectations (E) of 10 and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915, 1989) alignments (B) of 50, expectation (E) of 10, M=5, N= -4 and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, *e.g.*, Karlin & Altschul, Proc. Natl. Acad. Sci. USA 90:5873, 1993). One measure of similarity provided by BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a references sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more in one aspect less than about 0.01 and most in one aspect less than about 0.001.

In one aspect, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") In particular, five specific BLAST programs are used to perform the following task:

- (1) BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;
- (2) BLASTN compares a nucleotide query sequence against a nucleotide sequence database;
- (3) BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;

(4) TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and

(5) TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is in one aspect obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are in one aspect identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. In one aspect, the scoring matrix used is the BLOSUM62 matrix (Gonnet (1992) *Science* 256:1443-1445; Henikoff and Henikoff (1993) *Proteins* 17:49-61). Less in one aspect, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation). BLAST programs are accessible through the U.S. National Library of Medicine.

The parameters used with the above algorithms may be adapted depending on the sequence length and degree of homology studied. In some aspects, the parameters may be the default parameters used by the algorithms in the absence of instructions from the user.

Computer systems and computer program products

To determine and identify sequence identities, structural homologies, motifs and the like *in silico*, a nucleic acid or polypeptide sequence of the invention can be stored, recorded, and manipulated on any medium which can be read and accessed by a computer.

Accordingly, the invention provides computers, computer systems, computer readable mediums, computer programs products and the like recorded or stored thereon the nucleic acid and polypeptide sequences of the invention. As used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. A skilled artisan can readily adopt any known methods for recording information on a computer readable medium to generate manufactures comprising one or more of the nucleic acid and/or polypeptide sequences of the invention.

The polypeptides of the invention include the polypeptide sequences of the invention, e.g., the exemplary sequences of the invention, and sequences substantially identical thereto, and fragments of any of the preceding sequences. Substantially identical, or homologous, polypeptide sequences refer to a polypeptide sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity (homology) to an exemplary sequence of the invention.

Homology (sequence identity) may be determined using any of the computer programs and parameters described herein. A nucleic acid or polypeptide sequence of the invention can be stored, recorded and manipulated on any medium which can be read and accessed by a computer. As used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. A skilled artisan can readily adopt any of the presently known methods for recording information on a computer readable medium to generate manufactures comprising one or more of the nucleic acid sequences of the invention, one or more of the polypeptide sequences of the invention. Another aspect of the invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, or 20 or more nucleic acid or polypeptide sequences of the invention.

Another aspect of the invention is a computer readable medium having recorded thereon one or more of the nucleic acid sequences of the invention. Another aspect of the invention is a computer readable medium having recorded thereon one or more of the polypeptide sequences of the invention. Another aspect of the invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, or 20 or more of the nucleic acid or polypeptide sequences as set forth above.

Computer readable media include magnetically readable media, optically readable media, electronically readable media and magnetic/optical media. For example, the computer readable media may be a hard disk, a floppy disk, a magnetic tape, CD-ROM, Digital Versatile Disk (DVD), Random Access Memory (RAM), or Read Only Memory (ROM) as well as other types of other media known to those skilled in the art.

Aspects of the invention include systems (e.g., internet based systems), particularly computer systems which store and manipulate the sequence information described herein. One example of a computer system 100 is illustrated in block diagram form in Figure 1. As used herein, "a computer system" refers to the hardware components,

software components and data storage components used to analyze a nucleotide sequence of a nucleic acid sequence of the invention, or a polypeptide sequence of the invention. The computer system 100 typically includes a processor for processing, accessing and manipulating the sequence data. The processor 105 can be any well-known type of central processing unit, such as, for example, the Pentium III from Intel Corporation, or similar processor from Sun, Motorola, Compaq, AMD or International Business Machines.

Typically the computer system 100 is a general purpose system that comprises the processor 105 and one or more internal data storage components 110 for storing data and one or more data retrieving devices for retrieving the data stored on the data storage components. A skilled artisan can readily appreciate that any one of the currently available computer systems are suitable.

In one particular aspect, the computer system 100 includes a processor 105 connected to a bus which is connected to a main memory 115 (in one aspect implemented as RAM) and one or more internal data storage devices 110, such as a hard drive and/or other computer readable media having data recorded thereon. In some aspects, the computer system 100 further includes one or more data retrieving device 118 for reading the data stored on the internal data storage devices 110.

The data retrieving device 118 may represent, for example, a floppy disk drive, a compact disk drive, a magnetic tape drive, or a modem capable of connection to a remote data storage system (e.g., via internet) etc. In some aspects, the internal data storage device 110 is a removable computer readable medium such as a floppy disk, a compact disk, a magnetic tape, etc. containing control logic and/or data recorded thereon. The computer system 100 may advantageously include or be programmed by appropriate software for reading the control logic and/or the data from the data storage component once inserted in the data retrieving device.

The computer system 100 includes a display 120 which is used to display output to a computer user. It should also be noted that the computer system 100 can be linked to other computer systems 125a-c in a network or wide area network to provide centralized access to the computer system 100.

Software for accessing and processing the nucleotide sequences of a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, (such as search tools, compare tools and modeling tools etc.) may reside in main memory 115 during execution.

In some aspects, the computer system 100 may further comprise a sequence comparison algorithm for comparing a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, stored on a computer readable medium to a reference nucleotide or polypeptide sequence(s) stored on a computer readable medium. A "sequence comparison algorithm" refers to one or more programs which are implemented (locally or remotely) on the computer system 100 to compare a nucleotide sequence with other nucleotide sequences and/or compounds stored within a data storage means. For example, the sequence comparison algorithm may compare the nucleotide sequences of a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, stored on a computer readable medium to reference sequences stored on a computer readable medium to identify homologies or structural motifs.

Figure 2 is a flow diagram illustrating one aspect of a process 200 for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database. The database of sequences can be a private database stored within the computer system 100, or a public database such as GENBANK that is available through the Internet.

The process 200 begins at a start state 201 and then moves to a state 202 wherein the new sequence to be compared is stored to a memory in a computer system 100. As discussed above, the memory could be any type of memory, including RAM or an internal storage device.

The process 200 then moves to a state 204 wherein a database of sequences is opened for analysis and comparison. The process 200 then moves to a state 206 wherein the first sequence stored in the database is read into a memory on the computer. A comparison is then performed at a state 210 to determine if the first sequence is the same as the second sequence. It is important to note that this step is not limited to performing an exact comparison between the new sequence and the first sequence in the database. Well-known methods are known to those of skill in the art for comparing two nucleotide or protein sequences, even if they are not identical. For example, gaps can be introduced into one sequence in order to raise the homology level between the two tested sequences. The parameters that control whether gaps or other features are introduced into a sequence during comparison are normally entered by the user of the computer system.

Once a comparison of the two sequences has been performed at the state 210, a determination is made at a decision state 210 whether the two sequences are the same. Of course, the term "same" is not limited to sequences that are absolutely identical. Sequences

that are within the homology parameters entered by the user will be marked as "same" in the process 200.

If a determination is made that the two sequences are the same, the process 200 moves to a state 214 wherein the name of the sequence from the database is displayed to the user. This state notifies the user that the sequence with the displayed name fulfills the homology constraints that were entered. Once the name of the stored sequence is displayed to the user, the process 200 moves to a decision state 218 wherein a determination is made whether more sequences exist in the database. If no more sequences exist in the database, then the process 200 terminates at an end state 220. However, if more sequences do exist in the database, then the process 200 moves to a state 224 wherein a pointer is moved to the next sequence in the database so that it can be compared to the new sequence. In this manner, the new sequence is aligned and compared with every sequence in the database.

It should be noted that if a determination had been made at the decision state 212 that the sequences were not homologous, then the process 200 would move immediately to the decision state 218 in order to determine if any other sequences were available in the database for comparison.

Accordingly, one aspect of the invention is a computer system comprising a processor, a data storage device having stored thereon a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, a data storage device having retrievably stored thereon reference nucleotide sequences or polypeptide sequences to be compared to a nucleic acid sequence of the invention, or a polypeptide sequence of the invention and a sequence comparer for conducting the comparison. The sequence comparer may indicate a homology level between the sequences compared or identify structural motifs in the above described nucleic acid code a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, or it may identify structural motifs in sequences which are compared to these nucleic acid codes and polypeptide codes. In some aspects, the data storage device may have stored thereon the sequences of at least 2, 5, 10, 15, 20, 25, 30 or 40 or more of the nucleic acid sequences of the invention, or the polypeptide sequences of the invention.

Another aspect of the invention is a method for determining the level of homology between a nucleic acid sequence of the invention, or a polypeptide sequence of the invention and a reference nucleotide sequence. The method including reading the nucleic acid code or the polypeptide code and the reference nucleotide or polypeptide sequence through the use of a computer program which determines homology levels and

determining homology between the nucleic acid code or polypeptide code and the reference nucleotide or polypeptide sequence with the computer program. The computer program may be any of a number of computer programs for determining homology levels, including those specifically enumerated herein, (e.g., BLAST2N with the default parameters or with any modified parameters). The method may be implemented using the computer systems described above. The method may also be performed by reading at least 2, 5, 10, 15, 20, 25, 30 or 40 or more of the above described nucleic acid sequences of the invention, or the polypeptide sequences of the invention through use of the computer program and determining homology between the nucleic acid codes or polypeptide codes and reference nucleotide sequences or polypeptide sequences.

Figure 3 is a flow diagram illustrating one aspect of a process 250 in a computer for determining whether two sequences are homologous. The process 250 begins at a start state 252 and then moves to a state 254 wherein a first sequence to be compared is stored to a memory. The second sequence to be compared is then stored to a memory at a state 256. The process 250 then moves to a state 260 wherein the first character in the first sequence is read and then to a state 262 wherein the first character of the second sequence is read. It should be understood that if the sequence is a nucleotide sequence, then the character would normally be either A, T, C, G or U. If the sequence is a protein sequence, then it is in one aspect in the single letter amino acid code so that the first and sequence sequences can be easily compared.

A determination is then made at a decision state 264 whether the two characters are the same. If they are the same, then the process 250 moves to a state 268 wherein the next characters in the first and second sequences are read. A determination is then made whether the next characters are the same. If they are, then the process 250 continues this loop until two characters are not the same. If a determination is made that the next two characters are not the same, the process 250 moves to a decision state 274 to determine whether there are any more characters either sequence to read.

If there are not any more characters to read, then the process 250 moves to a state 276 wherein the level of homology between the first and second sequences is displayed to the user. The level of homology is determined by calculating the proportion of characters between the sequences that were the same out of the total number of sequences in the first sequence. Thus, if every character in a first 100 nucleotide sequence aligned with a every character in a second sequence, the homology level would be 100%.

Alternatively, the computer program may be a computer program which compares the nucleotide sequences of a nucleic acid sequence as set forth in the invention, to one or more reference nucleotide sequences in order to determine whether the nucleic acid code of the invention, differs from a reference nucleic acid sequence at one or more positions. Optionally such a program records the length and identity of inserted, deleted or substituted nucleotides with respect to the sequence of either the reference polynucleotide or a nucleic acid sequence of the invention. In one aspect, the computer program may be a program which determines whether a nucleic acid sequence of the invention, contains a single nucleotide polymorphism (SNP) with respect to a reference nucleotide sequence.

Accordingly, another aspect of the invention is a method for determining whether a nucleic acid sequence of the invention, differs at one or more nucleotides from a reference nucleotide sequence comprising the steps of reading the nucleic acid code and the reference nucleotide sequence through use of a computer program which identifies differences between nucleic acid sequences and identifying differences between the nucleic acid code and the reference nucleotide sequence with the computer program. In some aspects, the computer program is a program which identifies single nucleotide polymorphisms. The method may be implemented by the computer systems described above and the method illustrated in Figure 3. The method may also be performed by reading at least 2, 5, 10, 15, 20, 25, 30, or 40 or more of the nucleic acid sequences of the invention and the reference nucleotide sequences through the use of the computer program and identifying differences between the nucleic acid codes and the reference nucleotide sequences with the computer program.

In other aspects the computer based system may further comprise an identifier for identifying features within a nucleic acid sequence of the invention or a polypeptide sequence of the invention.

An "identifier" refers to one or more programs which identifies certain features within a nucleic acid sequence of the invention, or a polypeptide sequence of the invention. In one aspect, the identifier may comprise a program which identifies an open reading frame in a nucleic acid sequence of the invention.

Figure 4 is a flow diagram illustrating one aspect of an identifier process 300 for detecting the presence of a feature in a sequence. The process 300 begins at a start state 302 and then moves to a state 304 wherein a first sequence that is to be checked for features is stored to a memory 115 in the computer system 100. The process 300 then moves to a state 306 wherein a database of sequence features is opened. Such a database

would include a list of each feature's attributes along with the name of the feature. For example, a feature name could be "Initiation Codon" and the attribute would be "ATG". Another example would be the feature name "TAATAA Box" and the feature attribute would be "TAATAA". An example of such a database is produced by the University of Wisconsin Genetics Computer Group. Alternatively, the features may be structural polypeptide motifs such as alpha helices, beta sheets, or functional polypeptide motifs such as enzymatic active sites, helix-turn-helix motifs or other motifs known to those skilled in the art.

Once the database of features is opened at the state 306, the process 300 moves to a state 308 wherein the first feature is read from the database. A comparison of the attribute of the first feature with the first sequence is then made at a state 310. A determination is then made at a decision state 316 whether the attribute of the feature was found in the first sequence. If the attribute was found, then the process 300 moves to a state 318 wherein the name of the found feature is displayed to the user.

The process 300 then moves to a decision state 320 wherein a determination is made whether more features exist in the database. If no more features do exist, then the process 300 terminates at an end state 324. However, if more features do exist in the database, then the process 300 reads the next sequence feature at a state 326 and loops back to the state 310 wherein the attribute of the next feature is compared against the first sequence. It should be noted, that if the feature attribute is not found in the first sequence at the decision state 316, the process 300 moves directly to the decision state 320 in order to determine if any more features exist in the database.

Accordingly, another aspect of the invention is a method of identifying a feature within a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, comprising reading the nucleic acid code(s) or polypeptide code(s) through the use of a computer program which identifies features therein and identifying features within the nucleic acid code(s) with the computer program. In one aspect, computer program comprises a computer program which identifies open reading frames. The method may be performed by reading a single sequence or at least 2, 5, 10, 15, 20, 25, 30, or 40 of the nucleic acid sequences of the invention, or the polypeptide sequences of the invention, through the use of the computer program and identifying features within the nucleic acid codes or polypeptide codes with the computer program.

A nucleic acid sequence of the invention, or a polypeptide sequence of the invention, may be stored and manipulated in a variety of data processor programs in a

variety of formats. For example, a nucleic acid sequence of the invention, or a polypeptide sequence of the invention, may be stored as text in a word processing file, such as Microsoft WORD™ or WORDPERFECT™ or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2™, SYBASE™, or ORACLE™. In addition, many computer programs and databases may be used as sequence comparison algorithms, identifiers, or sources of reference nucleotide sequences or polypeptide sequences to be compared to a nucleic acid sequence of the invention, or a polypeptide sequence of the invention. The following list is intended not to limit the invention but to provide guidance to programs and databases which are useful with the nucleic acid sequences of the invention, or the polypeptide sequences of the invention.

The programs and databases which may be used include, but are not limited to: MacPattern (EMBL), DiscoveryBase (Molecular Applications Group), GeneMine (Molecular Applications Group), Look (Molecular Applications Group), MacLook (Molecular Applications Group), BLAST and BLAST2 (NCBI), BLASTN and BLASTX (Altschul et al, J. Mol. Biol. 215: 403, 1990), FASTA (Pearson and Lipman, Proc. Natl. Acad. Sci. USA, 85: 2444, 1988), FASTDB (Brutlag *et al.* Comp. App. Biosci. 6:237-245, 1990), Catalyst (Molecular Simulations Inc.), Catalyst/SHAPE (Molecular Simulations Inc.), Cerius².DBAccess (Molecular Simulations Inc.), HypoGen (Molecular Simulations Inc.), Insight II, (Molecular Simulations Inc.), Discover (Molecular Simulations Inc.), CHARMm (Molecular Simulations Inc.), Felix (Molecular Simulations Inc.), DelPhi, (Molecular Simulations Inc.), QuanteMM, (Molecular Simulations Inc.), Homology (Molecular Simulations Inc.), Modeler (Molecular Simulations Inc.), ISIS (Molecular Simulations Inc.), Quanta/Protein Design (Molecular Simulations Inc.), WebLab (Molecular Simulations Inc.), WebLab Diversity Explorer (Molecular Simulations Inc.), Gene Explorer (Molecular Simulations Inc.), SeqFold (Molecular Simulations Inc.), the MDL Available Chemicals Directory database, the MDL Drug Data Report data base, the Comprehensive Medicinal Chemistry database, Derwents's World Drug Index database, the BioByteMasterFile database, the Genbank database and the Genseqn database. Many other programs and data bases would be apparent to one of skill in the art given the present disclosure.

Motifs which may be detected using the above programs include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites, ubiquitination sites, alpha helices and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in

transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites and enzymatic cleavage sites.

Hybridization of nucleic acids

The invention provides isolated or recombinant nucleic acids that hybridize under stringent conditions to an exemplary sequence of the invention (e.g., SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9). The stringent conditions can be highly stringent conditions, medium stringent conditions and/or low stringent conditions, including the high and reduced stringency conditions described herein. In one aspect, it is the stringency of the wash conditions that set forth the conditions which determine whether a nucleic acid is within the scope of the invention, as discussed below.

"Hybridization" refers to the process by which a nucleic acid strand joins with a complementary strand through base pairing. Hybridization reactions can be sensitive and selective so that a particular sequence of interest can be identified even in samples in which it is present at low concentrations. Suitably stringent conditions can be defined by, for example, the concentrations of salt or formamide in the prehybridization and hybridization solutions, or by the hybridization temperature and are well known in the art. In particular, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature. In alternative aspects, nucleic acids of the invention are defined by their ability to hybridize under various stringency conditions (e.g., high, medium, and low), as set forth herein.

For example, hybridization under high stringency conditions could occur in about 50% formamide at about 37°C to 42°C. Hybridization could occur under reduced stringency conditions in about 35% to 25% formamide at about 30°C to 35°C. In one aspect, hybridization occurs under high stringency conditions, e.g., at 42°C in 50% formamide, 5X SSPE, 0.3% SDS and 200 n/ml sheared and denatured salmon sperm DNA. Hybridization could occur under these reduced stringency conditions, but in 35% formamide at a reduced temperature of 35°C. The temperature range corresponding to a particular level of stringency can be further narrowed by calculating the purine to pyrimidine ratio of the nucleic acid of interest and adjusting the temperature accordingly. Variations on the above ranges and conditions are well known in the art.

In alternative aspects, nucleic acids of the invention as defined by their ability to hybridize under stringent conditions can be between about five residues and the full length of nucleic acid of the invention; e.g., they can be at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 55, 60, 65, 70, 75, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600,

650, 700, 750, 800, 850, 900, 950, 1000, or more, residues in length. Nucleic acids shorter than full length are also included. These nucleic acids can be useful as, e.g., hybridization probes, labeling probes, PCR oligonucleotide probes, iRNA (single or double stranded), antisense or sequences encoding antibody binding peptides (epitopes), motifs, active sites and the like.

In one aspect, nucleic acids of the invention are defined by their ability to hybridize under high stringency comprising conditions of about 50% formamide at about 37°C to 42°C. In one aspect, nucleic acids of the invention are defined by their ability to hybridize under reduced stringency comprising conditions in about 35% to 25% formamide at about 30°C to 35°C.

Alternatively, nucleic acids of the invention are defined by their ability to hybridize under high stringency comprising conditions at 42°C in 50% formamide, 5X SSPE, 0.3% SDS, and a repetitive sequence blocking nucleic acid, such as cot-1 or salmon sperm DNA (e.g., 200 n/ml sheared and denatured salmon sperm DNA). In one aspect, nucleic acids of the invention are defined by their ability to hybridize under reduced stringency conditions comprising 35% formamide at a reduced temperature of 35°C.

In nucleic acid hybridization reactions, the conditions used to achieve a particular level of stringency will vary, depending on the nature of the nucleic acids being hybridized. For example, the length, degree of complementarity, nucleotide sequence composition (e.g., GC v. AT content) and nucleic acid type (e.g., RNA v. DNA) of the hybridizing regions of the nucleic acids can be considered in selecting hybridization conditions. An additional consideration is whether one of the nucleic acids is immobilized, for example, on a filter.

Hybridization may be carried out under conditions of low stringency, moderate stringency or high stringency. As an example of nucleic acid hybridization, a polymer membrane containing immobilized denatured nucleic acids is first prehybridized for 30 minutes at 45°C in a solution consisting of 0.9 M NaCl, 50 mM NaH₂PO₄, pH 7.0, 5.0 mM Na₂EDTA, 0.5% SDS, 10X Denhardt's and 0.5 mg/ml polyriboadenylic acid. Approximately 2×10^7 cpm (specific activity $4-9 \times 10^8$ cpm/ug) of ³²P end-labeled oligonucleotide probe are then added to the solution. After 12-16 hours of incubation, the membrane is washed for 30 minutes at room temperature in 1X SET (150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na₂EDTA) containing 0.5% SDS, followed by a 30 minute wash in fresh 1X SET at T_m-10°C for the oligonucleotide probe. The

membrane is then exposed to auto-radiographic film for detection of hybridization signals.

All of the foregoing hybridizations would be considered to be under conditions of high stringency.

Following hybridization, a filter can be washed to remove any non-specifically bound detectable probe. The stringency used to wash the filters can also be varied depending on the nature of the nucleic acids being hybridized, the length of the nucleic acids being hybridized, the degree of complementarity, the nucleotide sequence composition (*e.g.*, GC v. AT content) and the nucleic acid type (*e.g.*, RNA v. DNA). Examples of progressively higher stringency condition washes are as follows: 2X SSC, 0.1% SDS at room temperature for 15 minutes (low stringency); 0.1X SSC, 0.5% SDS at room temperature for 30 minutes to 1 hour (moderate stringency); 0.1X SSC, 0.5% SDS for 15 to 30 minutes at between the hybridization temperature and 68°C (high stringency); and 0.15M NaCl for 15 minutes at 72°C (very high stringency). A final low stringency wash can be conducted in 0.1X SSC at room temperature. The examples above are merely illustrative of one set of conditions that can be used to wash filters. One of skill in the art would know that there are numerous recipes for different stringency washes. Some other examples are given below.

In one aspect, hybridization conditions comprise a wash step comprising a wash for 30 minutes at room temperature in a solution comprising 1X 150 mM NaCl, 20 mM Tris hydrochloride, pH 7.8, 1 mM Na₂EDTA, 0.5% SDS, followed by a 30 minute wash in fresh solution.

Nucleic acids which have hybridized to the probe are identified by autoradiography or other conventional techniques.

The above procedure may be modified to identify nucleic acids having decreasing levels of homology to the probe sequence. For example, to obtain nucleic acids of decreasing homology to the detectable probe, less stringent conditions may be used. For example, the hybridization temperature may be decreased in increments of 5°C from 68°C to 42°C in a hybridization buffer having a Na⁺ concentration of approximately 1M. Following hybridization, the filter may be washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be "moderate" conditions above 50°C and "low" conditions below 50°C. A specific example of "moderate" hybridization conditions is when the above hybridization is conducted at 55°C. A specific example of "low stringency" hybridization conditions is when the above hybridization is conducted at 45°C.

Alternatively, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50°C. These conditions are considered to be "moderate" conditions above 25% formamide and "low" conditions below 25% formamide. A specific example of "moderate" hybridization conditions is when the above hybridization is conducted at 30% formamide. A specific example of "low stringency" hybridization conditions is when the above hybridization is conducted at 10% formamide.

However, the selection of a hybridization format is not critical - it is the stringency of the wash conditions that set forth the conditions which determine whether a nucleic acid is within the scope of the invention. Wash conditions used to identify nucleic acids within the scope of the invention include, e.g.: a salt concentration of about 0.02 molar at pH 7 and a temperature of at least about 50°C or about 55°C to about 60°C; or, a salt concentration of about 0.15 M NaCl at 72°C for about 15 minutes; or, a salt concentration of about 0.2X SSC at a temperature of at least about 50°C or about 55°C to about 60°C for about 15 to about 20 minutes; or, the hybridization complex is washed twice with a solution with a salt concentration of about 2X SSC containing 0.1% SDS at room temperature for 15 minutes and then washed twice by 0.1X SSC containing 0.1% SDS at 68°C for 15 minutes; or, equivalent conditions. See Sambrook, Tijssen and Ausubel for a description of SSC buffer and equivalent conditions.

These methods may be used to isolate nucleic acids of the invention. For example, the preceding methods may be used to isolate nucleic acids having a sequence with at least about 97%, at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, or at least 50% sequence identity (homology) to a nucleic acid sequence selected from the group consisting of one of the sequences of the invention, or fragments comprising at least about 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases thereof and the sequences complementary thereto. Sequence identity (homology) may be measured using the alignment algorithm. For example, the homologous polynucleotides may have a coding sequence which is a naturally occurring allelic variant of one of the coding sequences described herein. Such allelic variants may have a substitution, deletion or addition of one or more nucleotides when compared to the nucleic acids of the invention. Additionally, the above procedures may be used to isolate nucleic acids which encode

polypeptides having at least about 99%, 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, or at least 50% sequence identity (homology) to a polypeptide of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined using a sequence alignment algorithm (e.g., such as the FASTA version 3.0t78 algorithm with the default parameters).

Oligonucleotides probes and methods for using them

The invention also provides nucleic acid probes that can be used, e.g., for identifying nucleic acids encoding a polypeptide with an enzyme, structural or binding activity or fragments thereof or for identifying polypeptide, enzyme, protein, e.g. structural or binding protein, genes. In one aspect, the probe comprises at least 10 consecutive bases of a nucleic acid of the invention. Alternatively, a probe of the invention can be at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 110, 120, 130, 150 or about 10 to 50, about 20 to 60 about 30 to 70, consecutive bases of a sequence as set forth in a nucleic acid of the invention. The probes identify a nucleic acid by binding and/or hybridization. The probes can be used in arrays of the invention, see discussion below, including, e.g., capillary arrays. The probes of the invention can also be used to isolate other nucleic acids or polypeptides.

The isolated nucleic acids of the invention, the sequences complementary thereto, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of the invention, or the sequences complementary thereto may also be used as probes to determine whether a biological sample, such as a soil sample, contains an organism having a nucleic acid sequence of the invention or an organism from which the nucleic acid was obtained. In such procedures, a biological sample potentially harboring the organism from which the nucleic acid was isolated is obtained and nucleic acids are obtained from the sample. The nucleic acids are contacted with the probe under conditions which permit the probe to specifically hybridize to any complementary sequences from which are present therein.

Where necessary, conditions which permit the probe to specifically hybridize to complementary sequences may be determined by placing the probe in contact with complementary sequences from samples known to contain the complementary sequence as well as control sequences which do not contain the complementary sequence. Hybridization conditions, such as the salt concentration of the hybridization buffer, the

formamide concentration of the hybridization buffer, or the hybridization temperature, may be varied to identify conditions which allow the probe to hybridize specifically to complementary nucleic acids.

If the sample contains the organism from which the nucleic acid was isolated, specific hybridization of the probe is then detected. Hybridization may be detected by labeling the probe with a detectable agent such as a radioactive isotope, a fluorescent dye or an enzyme capable of catalyzing the formation of a detectable product.

Many methods for using the labeled probes to detect the presence of complementary nucleic acids in a sample are familiar to those skilled in the art. These include Southern Blots, Northern Blots, colony hybridization procedures and dot blots. Protocols for each of these procedures are provided in Ausubel *et al.* *Current Protocols in Molecular Biology*, John Wiley 503 Sons, Inc. (1997) and Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual* 2nd Ed., Cold Spring Harbor Laboratory Press (1989).

Alternatively, more than one probe (at least one of which is capable of specifically hybridizing to any complementary sequences which are present in the nucleic acid sample), may be used in an amplification reaction to determine whether the sample contains an organism containing a nucleic acid sequence of the invention (e.g., an organism from which the nucleic acid was isolated). Typically, the probes comprise oligonucleotides. In one aspect, the amplification reaction may comprise a PCR reaction. PCR protocols are described in Ausubel and Sambrook, *supra*. Alternatively, the amplification may comprise a ligase chain reaction, 3SR, or strand displacement reaction. (See Barany, F., "The Ligase Chain Reaction in a PCR World", *PCR Methods and Applications* 1:5-16, 1991; E. Fahy *et al.*, "Self-sustained Sequence Replication (3SR): An Isothermal Transcription-based Amplification System Alternative to PCR", *PCR Methods and Applications* 1:25-33, 1991; and Walker G.T. *et al.*, "Strand Displacement Amplification-an Isothermal *in vitro* DNA Amplification Technique", *Nucleic Acid Research* 20:1691-1696, 1992). In such procedures, the nucleic acids in the sample are contacted with the probes, the amplification reaction is performed and any resulting amplification product is detected. The amplification product may be detected by performing gel electrophoresis on the reaction products and staining the gel with an intercalator such as ethidium bromide. Alternatively, one or more of the probes may be labeled with a radioactive isotope and the presence of a radioactive amplification product may be detected by autoradiography after gel electrophoresis.

Probes derived from sequences near the ends of the sequences of the invention, may also be used in chromosome walking procedures to identify clones containing genomic sequences located adjacent to the sequences of the invention. Such methods allow the isolation of genes which encode additional proteins from the host organism.

The isolated nucleic acids of the invention, the sequences complementary thereto, or a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive bases of one of the sequences of the invention, or the sequences complementary thereto may be used as probes to identify and isolate related nucleic acids. In some aspects, the related nucleic acids may be cDNAs or genomic DNAs from organisms other than the one from which the nucleic acid was isolated. For example, the other organisms may be related organisms. In such procedures, a nucleic acid sample is contacted with the probe under conditions which permit the probe to specifically hybridize to related sequences. Hybridization of the probe to nucleic acids from the related organism is then detected using any of the methods described above.

By varying the stringency of the hybridization conditions used to identify nucleic acids, such as cDNAs or genomic DNAs, which hybridize to the detectable probe, nucleic acids having different levels of homology to the probe can be identified and isolated. Stringency may be varied by conducting the hybridization at varying temperatures below the melting temperatures of the probes. The melting temperature, T_m , is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly complementary probe. Very stringent conditions are selected to be equal to or about 5°C lower than the T_m for a particular probe. The melting temperature of the probe may be calculated using the following formulas:

For probes between 14 and 70 nucleotides in length the melting temperature (T_m) is calculated using the formula: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (600/N)$ where N is the length of the probe.

If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation: $T_m = 81.5 + 16.6(\log [Na^+]) + 0.41(\text{fraction G+C}) - (0.63\% \text{ formamide}) - (600/N)$ where N is the length of the probe.

Prehybridization may be carried out in 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100µg denatured fragmented salmon sperm DNA or 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100µg denatured fragmented salmon sperm DNA, 50% formamide. The formulas for SSC and Denhardt's solutions are listed in Sambrook *et al.*, *supra*.

Hybridization is conducted by adding the detectable probe to the prehybridization solutions listed above. Where the probe comprises double stranded DNA, it is denatured before addition to the hybridization solution. The filter is contacted with the hybridization solution for a sufficient period of time to allow the probe to hybridize to cDNAs or genomic DNAs containing sequences complementary thereto or homologous thereto. For probes over 200 nucleotides in length, the hybridization may be carried out at 15-25°C below the T_m . For shorter probes, such as oligonucleotide probes, the hybridization may be conducted at 5-10°C below the T_m . In one aspect, for hybridizations in 6X SSC, the hybridization is conducted at approximately 68°C. Usually, for hybridizations in 50% formamide containing solutions, the hybridization is conducted at approximately 42°C.

Inhibiting Expression of Polypeptides, Enzymes, Proteins

The invention provides nucleic acids complementary to (e.g., antisense sequences to) the nucleic acids of the invention, e.g., nucleic acids comprising antisense, iRNA, ribozymes. Nucleic acids of the invention comprising antisense sequences can be capable of inhibiting the transport, splicing or transcription of polypeptide, enzyme, protein, e.g. structural or binding protein genes. The inhibition can be effected through the targeting of genomic DNA or messenger RNA. The transcription or function of targeted nucleic acid can be inhibited, for example, by hybridization and/or cleavage. In one aspect, inhibitors of the invention include oligonucleotides which are able to either bind a polypeptide, enzyme, protein, e.g. structural or binding protein, gene or message, in either case preventing or inhibiting the production or function of a polypeptide, enzyme, protein, e.g. structural or binding protein. The association can be through sequence specific hybridization. Another useful class of inhibitors includes oligonucleotides which cause inactivation or cleavage of a polypeptide, enzyme, protein, e.g. structural or binding protein, message. The oligonucleotide can have enzyme activity which causes such cleavage, such as ribozymes. The oligonucleotide can be chemically modified or conjugated to an enzyme or composition capable of cleaving the complementary nucleic acid. A pool of many different such oligonucleotides can be screened for those with the desired activity. Thus, the invention provides various compositions for the inhibition of a polypeptide, enzyme, protein, e.g. structural or binding protein, expression on a nucleic acid and/or protein level, e.g., antisense, iRNA and ribozymes comprising a polypeptide, enzyme, protein, e.g. structural or binding protein, sequences of the invention and the

anti-polypeptide, anti-enzyme, anti-protein, e.g. anti-structural or anti-binding protein antibodies of the invention.

Inhibition of a polypeptide, enzyme, protein, e.g. structural or binding protein, expression can have a variety of industrial applications. For example, inhibition of a polypeptide, enzyme, protein, e.g. structural or binding protein, expression can slow or prevent spoilage. In one aspect, use of compositions of the invention that inhibit the expression and/or activity of a polypeptide, enzyme, protein, e.g. structural or binding protein, e.g., antibodies, antisense oligonucleotides, ribozymes and RNAi, are used to slow or prevent spoilage. Thus, in one aspect, the invention provides methods and compositions comprising application onto a plant or plant product (e.g., a cereal, a grain, a fruit, seed, root, leaf, etc.) antibodies, antisense oligonucleotides, ribozymes and RNAi of the invention to slow or prevent spoilage. These compositions also can be expressed by the plant (e.g., a transgenic plant) or another organism (e.g., a bacterium or other microorganism transformed with a polypeptide, enzyme, protein, e.g. structural or binding protein, gene of the invention).

The compositions of the invention for the inhibition of a polypeptide, enzyme, protein, e.g. structural or binding protein, expression, e.g., antisense, iRNA (e.g., siRNA, miRNA), ribozymes, antibodies, can be used as pharmaceutical compositions, e.g., as anti-pathogen agents or in other therapies, e.g., as anti-microbials for, e.g., *Salmonella*, or to neutralize a biological warfare agent, e.g., anthrax.

Antisense Oligonucleotides

The invention provides antisense oligonucleotides capable of binding a polypeptide, enzyme, protein, e.g. structural or binding protein, message which, in one aspect, can inhibit a polypeptide, enzyme, protein, e.g. structural or binding protein, activity by targeting mRNA. Strategies for designing antisense oligonucleotides are well described in the scientific and patent literature, and the skilled artisan can design such a polypeptide, enzyme, protein, e.g. structural or binding protein, oligonucleotides using the novel reagents of the invention. For example, gene walking/ RNA mapping protocols to screen for effective antisense oligonucleotides are well known in the art, see, e.g., Ho (2000) *Methods Enzymol.* 314:168-183, describing an RNA mapping assay, which is based on standard molecular techniques to provide an easy and reliable method for potent antisense sequence selection. See also Smith (2000) *Eur. J. Pharm. Sci.* 11:191-198.

Naturally occurring nucleic acids are used as antisense oligonucleotides. The antisense oligonucleotides can be of any length; for example, in alternative aspects,

the antisense oligonucleotides are between about 5 to 100, about 10 to 80, about 15 to 60, about 18 to 40. The optimal length can be determined by routine screening. The antisense oligonucleotides can be present at any concentration. The optimal concentration can be determined by routine screening. A wide variety of synthetic, non-naturally occurring nucleotide and nucleic acid analogues are known which can address this potential problem. For example, peptide nucleic acids (PNAs) containing non-ionic backbones, such as N-(2-aminoethyl) glycine units can be used. Antisense oligonucleotides having phosphorothioate linkages can also be used, as described in WO 97/03211; WO 96/39154; Mata (1997) *Toxicol Appl Pharmacol* 144:189-197; *Antisense Therapeutics*, ed. Agrawal (Humana Press, Totowa, N.J., 1996). Antisense oligonucleotides having synthetic DNA backbone analogues provided by the invention can also include phosphoro-dithioate, methylphosphonate, phosphoramidate, alkyl phosphotriester, sulfamate, 3'-thioacetal, methylene(methylimino), 3'-N-carbamate, and morpholino carbamate nucleic acids, as described above.

Combinatorial chemistry methodology can be used to create vast numbers of oligonucleotides that can be rapidly screened for specific oligonucleotides that have appropriate binding affinities and specificities toward any target, such as the sense and antisense a polypeptide, enzyme, protein, e.g. structural or binding protein, sequences of the invention (see, e.g., Gold (1995) *J. of Biol. Chem.* 270:13581-13584).

Inhibitory Ribozymes

The invention provides ribozymes capable of binding a polypeptide, enzyme, protein, e.g. structural or binding protein, message. These ribozymes can inhibit a polypeptide, enzyme, protein, e.g. structural or binding protein, activity by, e.g., targeting mRNA. Strategies for designing ribozymes and selecting the polypeptide, enzyme, protein, e.g. structural or binding protein-specific antisense sequence for targeting are well described in the scientific and patent literature, and the skilled artisan can design such ribozymes using the novel reagents of the invention. Ribozymes act by binding to a target RNA through the target RNA binding portion of a ribozyme which is held in close proximity to an enzymatic portion of the RNA that cleaves the target RNA. Thus, the ribozyme recognizes and binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cleave and inactivate the target RNA. Cleavage of a target RNA in such a manner will destroy its ability to direct synthesis of an encoded protein if the cleavage occurs in the coding sequence. After a

ribozyme has bound and cleaved its RNA target, it can be released from that RNA to bind and cleave new targets repeatedly.

In some circumstances, the enzymatic nature of a ribozyme can be advantageous over other technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its transcription, translation or association with another molecule) as the effective concentration of ribozyme necessary to effect a therapeutic treatment can be lower than that of an antisense oligonucleotide. This potential advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, a ribozyme is typically a highly specific inhibitor, with the specificity of inhibition depending not only on the base pairing mechanism of binding, but also on the mechanism by which the molecule inhibits the expression of the RNA to which it binds. That is, the inhibition is caused by cleavage of the RNA target and so specificity is defined as the ratio of the rate of cleavage of the targeted RNA over the rate of cleavage of non-targeted RNA. This cleavage mechanism is dependent upon factors additional to those involved in base pairing. Thus, the specificity of action of a ribozyme can be greater than that of antisense oligonucleotide binding the same RNA site.

The ribozyme of the invention, e.g., an enzymatic ribozyme RNA molecule, can be formed in a hammerhead motif, a hairpin motif, as a hepatitis delta virus motif, a group I intron motif and/or an RNaseP-like RNA in association with an RNA guide sequence. Examples of hammerhead motifs are described by, e.g., Rossi (1992) *Aids Research and Human Retroviruses* 8:183; hairpin motifs by Hampel (1989) *Biochemistry* 28:4929, and Hampel (1990) *Nuc. Acids Res.* 18:299; the hepatitis delta virus motif by Perrotta (1992) *Biochemistry* 31:16; the RNaseP motif by Guerrier-Takada (1983) *Cell* 35:849; and the group I intron by Cech U.S. Pat. No. 4,987,071. The recitation of these specific motifs is not intended to be limiting. Those skilled in the art will recognize that a ribozyme of the invention, e.g., an enzymatic RNA molecule of this invention, can have a specific substrate binding site complementary to one or more of the target gene RNA regions. A ribozyme of the invention can have a nucleotide sequence within or surrounding that substrate binding site which imparts an RNA cleaving activity to the molecule.

RNA interference (RNAi)

In one aspect, the invention provides an RNA inhibitory molecule, a so-called "RNAi" molecule, comprising a polypeptide, enzyme, protein, e.g. structural or

binding protein, sequence of the invention. The RNAi molecule comprises a double-stranded RNA (dsRNA) molecule. The RNAi can inhibit expression of a polypeptide, enzyme, protein, e.g. structural or binding protein, gene. In one aspect, the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length. While the invention is not limited by any particular mechanism of action, the RNAi can enter a cell and cause the degradation of a single-stranded RNA (ssRNA) of similar or identical sequences, including endogenous mRNAs. When a cell is exposed to double-stranded RNA (dsRNA), mRNA from the homologous gene is selectively degraded by a process called RNA interference (RNAi). A possible basic mechanism behind RNAi, e.g., siRNA for inhibiting transcription and/or miRNA to inhibit translation, is the breaking of a double-stranded RNA (dsRNA) matching a specific gene sequence into short pieces called short interfering RNA, which trigger the degradation of mRNA that matches its sequence. In one aspect, the RNAi's of the invention are used in gene-silencing therapeutics, see, e.g., Shuey (2002) Drug Discov. Today 7:1040-1046. In one aspect, the invention provides methods to selectively degrade RNA using the RNAi's of the invention. The process may be practiced *in vitro*, *ex vivo* or *in vivo*. In one aspect, the RNAi molecules of the invention can be used to generate a loss-of-function mutation in a cell, an organ or an animal. Methods for making and using RNAi molecules for selectively degrade RNA are well known in the art, see, e.g., U.S. Patent No. 6,506,559; 6,511,824; 6,515,109; 6,489,127.

Modification of Nucleic Acids

The invention provides methods of generating variants of the nucleic acids of the invention, e.g., those encoding a polypeptide, enzyme, protein, e.g. structural or binding protein. These methods can be repeated or used in various combinations to generate a polypeptide, enzyme, protein, e.g. structural or binding protein, having an altered or different activity or an altered or different stability from that of a polypeptide, enzyme, protein, e.g. structural or binding protein, encoded by the template nucleic acid. These methods also can be repeated or used in various combinations, e.g., to generate variations in gene/ message expression, message translation or message stability. In another aspect, the genetic composition of a cell is altered by, e.g., modification of a homologous gene *ex vivo*, followed by its reinsertion into the cell.

A nucleic acid of the invention can be altered by any means. For example, random or stochastic methods, or, non-stochastic, or "directed evolution," methods, see, e.g., U.S. Patent No. 6,361,974. Methods for random mutation of genes are well known

in the art, see, e.g., U.S. Patent No. 5,830,696. For example, mutagens can be used to randomly mutate a gene. Mutagens include, e.g., ultraviolet light or gamma irradiation, or a chemical mutagen, e.g., mitomycin, nitrous acid, photoactivated psoralens, alone or in combination, to induce DNA breaks amenable to repair by recombination. Other chemical mutagens include, for example, sodium bisulfite, nitrous acid, hydroxylamine, hydrazine or formic acid. Other mutagens are analogues of nucleotide precursors, e.g., nitrosoguanidine, 5-bromouracil, 2-aminopurine, or acridine. These agents can be added to a PCR reaction in place of the nucleotide precursor thereby mutating the sequence. Intercalating agents such as proflavine, acriflavine, quinacrine and the like can also be used.

Any technique in molecular biology can be used, e.g., random PCR mutagenesis, see, e.g., Rice (1992) *Proc. Natl. Acad. Sci. USA* 89:5467-5471; or, combinatorial multiple cassette mutagenesis, see, e.g., Cramer (1995) *Biotechniques* 18:194-196. Alternatively, nucleic acids, e.g., genes, can be reassembled after random, or "stochastic," fragmentation, see, e.g., U.S. Patent Nos. 6,291,242; 6,287,862; 6,287,861; 5,955,358; 5,830,721; 5,824,514; 5,811,238; 5,605,793. In alternative aspects, modifications, additions or deletions are introduced by error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR), recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation, and/or a combination of these and other methods.

The following publications describe a variety of recursive recombination procedures and/or methods which can be incorporated into the methods of the invention: Stemmer (1999) "Molecular breeding of viruses for targeting and other clinical properties" *Tumor Targeting* 4:1-4; Ness (1999) *Nature Biotechnology* 17:893-896; Chang (1999) "Evolution of a cytokine using DNA family shuffling" *Nature Biotechnology* 17:793-797; Minshull (1999) "Protein evolution by molecular breeding" *Current Opinion in Chemical Biology* 3:284-290; Christians (1999) "Directed evolution

of thymidine kinase for AZT phosphorylation using DNA family shuffling" *Nature Biotechnology* 17:259-264; Cramer (1998) "DNA shuffling of a family of genes from diverse species accelerates directed evolution" *Nature* 391:288-291; Cramer (1997) "Molecular evolution of an arsenate detoxification pathway by DNA shuffling," *Nature Biotechnology* 15:436-438; Zhang (1997) "Directed evolution of an effective fucosidase from a galactosidase by DNA shuffling and screening" *Proc. Natl. Acad. Sci. USA* 94:4504-4509; Patten et al. (1997) "Applications of DNA Shuffling to Pharmaceuticals and Vaccines" *Current Opinion in Biotechnology* 8:724-733; Cramer et al. (1996) "Construction and evolution of antibody-phage libraries by DNA shuffling" *Nature Medicine* 2:100-103; Gates et al. (1996) "Affinity selective isolation of ligands from peptide libraries through display on a lac repressor 'headpiece dimer'" *Journal of Molecular Biology* 255:373-386; Stemmer (1996) "Sexual PCR and Assembly PCR" In: *The Encyclopedia of Molecular Biology*. VCH Publishers, New York. pp.447-457; Cramer and Stemmer (1995) "Combinatorial multiple cassette mutagenesis creates all the permutations of mutant and wildtype cassettes" *BioTechniques* 18:194-195; Stemmer et al. (1995) "Single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides" *Gene*, 164:49-53; Stemmer (1995) "The Evolution of Molecular Computation" *Science* 270: 1510; Stemmer (1995) "Searching Sequence Space" *Bio/Technology* 13:549-553; Stemmer (1994) "Rapid evolution of a protein in vitro by DNA shuffling" *Nature* 370:389-391; and Stemmer (1994) "DNA shuffling by random fragmentation and reassembly: In vitro recombination for molecular evolution." *Proc. Natl. Acad. Sci. USA* 91:10747-10751.

Mutational methods of generating diversity include, for example, site-directed mutagenesis (Ling et al. (1997) "Approaches to DNA mutagenesis: an overview" *Anal Biochem.* 254(2): 157-178; Dale et al. (1996) "Oligonucleotide-directed random mutagenesis using the phosphorothioate method" *Methods Mol. Biol.* 57:369-374; Smith (1985) "In vitro mutagenesis" *Ann. Rev. Genet.* 19:423-462; Botstein & Shortle (1985) "Strategies and applications of in vitro mutagenesis" *Science* 229:1193-1201; Carter (1986) "Site-directed mutagenesis" *Biochem. J.* 237:1-7; and Kunkel (1987) "The efficiency of oligonucleotide directed mutagenesis" in *Nucleic Acids & Molecular Biology* (Eckstein, F. and Lilley, D. M. J. eds., Springer Verlag, Berlin)); mutagenesis using uracil containing templates (Kunkel (1985) "Rapid and efficient site-specific mutagenesis without phenotypic selection" *Proc. Natl. Acad. Sci. USA* 82:488-492; Kunkel et al. (1987) "Rapid and efficient site-specific mutagenesis without phenotypic

selection" Methods in Enzymol. 154, 367-382; and Bass et al. (1988) "Mutant Trp repressors with new DNA-binding specificities" Science 242:240-245); oligonucleotide-directed mutagenesis (Methods in Enzymol. 100: 468-500 (1983); Methods in Enzymol. 154: 329-350 (1987); Zoller (1982) "Oligonucleotide-directed mutagenesis using M13-derived vectors: an efficient and general procedure for the production of point mutations in any DNA fragment" Nucleic Acids Res. 10:6487-6500; Zoller & Smith (1983) "Oligonucleotide-directed mutagenesis of DNA fragments cloned into M13 vectors" Methods in Enzymol. 100:468-500; and Zoller (1987) Oligonucleotide-directed mutagenesis: a simple method using two oligonucleotide primers and a single-stranded DNA template" Methods in Enzymol. 154:329-350); phosphorothioate-modified DNA mutagenesis (Taylor (1985) "The use of phosphorothioate-modified DNA in restriction enzyme reactions to prepare nicked DNA" Nucl. Acids Res. 13: 8749-8764; Taylor (1985) "The rapid generation of oligonucleotide-directed mutations at high frequency using phosphorothioate-modified DNA" Nucl. Acids Res. 13: 8765-8787 (1985); Nakamaye (1986) "Inhibition of restriction endonuclease Nci I cleavage by phosphorothioate groups and its application to oligonucleotide-directed mutagenesis" Nucl. Acids Res. 14: 9679-9698; Sayers (1988) "Y-T Exonucleases in phosphorothioate-based oligonucleotide-directed mutagenesis" Nucl. Acids Res. 16:791-802; and Sayers et al. (1988) "Strand specific cleavage of phosphorothioate-containing DNA by reaction with restriction endonucleases in the presence of ethidium bromide" Nucl. Acids Res. 16: 803-814); mutagenesis using gapped duplex DNA (Kramer et al. (1984) "The gapped duplex DNA approach to oligonucleotide-directed mutation construction" Nucl. Acids Res. 12: 9441-9456; Kramer & Fritz (1987) Methods in Enzymol. "Oligonucleotide-directed construction of mutations via gapped duplex DNA" 154:350-367; Kramer (1988) "Improved enzymatic *in vitro* reactions in the gapped duplex DNA approach to oligonucleotide-directed construction of mutations" Nucl. Acids Res. 16: 7207; and Fritz (1988) "Oligonucleotide-directed construction of mutations: a gapped duplex DNA procedure without enzymatic reactions *in vitro*" Nucl. Acids Res. 16: 6987-6999).

Additional protocols that can be used to practice the invention include point mismatch repair (Kramer (1984) "Point Mismatch Repair" Cell 38:879-887), mutagenesis using repair-deficient host strains (Carter et al. (1985) "Improved oligonucleotide site-directed mutagenesis using M13 vectors" Nucl. Acids Res. 13: 4431-4443; and Carter (1987) "Improved oligonucleotide-directed mutagenesis using M13 vectors" Methods in Enzymol. 154: 382-403), deletion mutagenesis (Eghtedarzadeh

(1986) "Use of oligonucleotides to generate large deletions" Nucl. Acids Res. 14: 5115), restriction-selection and restriction-selection and restriction-purification (Wells et al. (1986) "Importance of hydrogen-bond formation in stabilizing the transition state of subtilisin" Phil. Trans. R. Soc. Lond. A 317: 415-423), mutagenesis by total gene synthesis (Nambiar et al. (1984) "Total synthesis and cloning of a gene coding for the ribonuclease S protein" Science 223: 1299-1301; Sakamar and Khorana (1988) "Total synthesis and expression of a gene for the α -subunit of bovine rod outer segment guanine nucleotide-binding protein (transducin)" Nucl. Acids Res. 14: 6361-6372; Wells et al. (1985) "Cassette mutagenesis: an efficient method for generation of multiple mutations at defined sites" Gene 34:315-323; and Grundstrom et al. (1985) "Oligonucleotide-directed mutagenesis by microscale 'shot-gun' gene synthesis" Nucl. Acids Res. 13: 3305-3316), double-strand break repair (Mandecki (1986); Arnold (1993) "Protein engineering for unusual environments" Current Opinion in Biotechnology 4:450-455. "Oligonucleotide-directed double-strand break repair in plasmids of Escherichia coli: a method for site-specific mutagenesis" Proc. Natl. Acad. Sci. USA, 83:7177-7181). Additional details on many of the above methods can be found in Methods in Enzymology Volume 154, which also describes useful controls for trouble-shooting problems with various mutagenesis methods.

Protocols that can be used to practice the invention are described, e.g., in U.S. Patent Nos. 5,605,793 to Stemmer (Feb. 25, 1997), "Methods for In Vitro Recombination;" U.S. Pat. No. 5,811,238 to Stemmer et al. (Sep. 22, 1998) "Methods for Generating Polynucleotides having Desired Characteristics by Iterative Selection and Recombination;" U.S. Pat. No. 5,830,721 to Stemmer et al. (Nov. 3, 1998), "DNA Mutagenesis by Random Fragmentation and Reassembly;" U.S. Pat. No. 5,834,252 to Stemmer, et al. (Nov. 10, 1998) "End-Complementary Polymerase Reaction;" U.S. Pat. No. 5,837,458 to Minshull, et al. (Nov. 17, 1998), "Methods and Compositions for Cellular and Metabolic Engineering;" WO 95/22625, Stemmer and Cramer, "Mutagenesis by Random Fragmentation and Reassembly;" WO 96/33207 by Stemmer and Lipschutz "End Complementary Polymerase Chain Reaction;" WO 97/20078 by Stemmer and Cramer "Methods for Generating Polynucleotides having Desired Characteristics by Iterative Selection and Recombination;" WO 97/35966 by Minshull and Stemmer, "Methods and Compositions for Cellular and Metabolic Engineering;" WO 99/41402 by Punnonen et al. "Targeting of Genetic Vaccine Vectors;" WO 99/41383 by Punnonen et al. "Antigen Library Immunization;" WO 99/41369 by Punnonen et al.

"Genetic Vaccine Vector Engineering;" WO 99/41368 by Punnonen et al. "Optimization of Immunomodulatory Properties of Genetic Vaccines;" EP 752008 by Stemmer and Crameri, "DNA Mutagenesis by Random Fragmentation and Reassembly;" EP 0932670 by Stemmer "Evolving Cellular DNA Uptake by Recursive Sequence Recombination;" WO 99/23107 by Stemmer et al., "Modification of Virus Tropism and Host Range by Viral Genome Shuffling;" WO 99/21979 by Apt et al., "Human Papillomavirus Vectors;" WO 98/31837 by del Cardayre et al. "Evolution of Whole Cells and Organisms by Recursive Sequence Recombination;" WO 98/27230 by Patten and Stemmer, "Methods and Compositions for Polypeptide Engineering;" WO 98/27230 by Stemmer et al., "Methods for Optimization of Gene Therapy by Recursive Sequence Shuffling and Selection," WO 00/00632, "Methods for Generating Highly Diverse Libraries," WO 00/09679, "Methods for Obtaining in Vitro Recombined Polynucleotide Sequence Banks and Resulting Sequences," WO 98/42832 by Arnold et al., "Recombination of Polynucleotide Sequences Using Random or Defined Primers," WO 99/29902 by Arnold et al., "Method for Creating Polynucleotide and Polypeptide Sequences," WO 98/41653 by Vind, "An in Vitro Method for Construction of a DNA Library," WO 98/41622 by Borchert et al., "Method for Constructing a Library Using DNA Shuffling," and WO 98/42727 by Pati and Zarling, "Sequence Alterations using Homologous Recombination."

Protocols that can be used to practice the invention (providing details regarding various diversity generating methods) are described, e.g., in U.S. Patent application serial no. (USSN) 09/407,800, "SHUFFLING OF CODON ALTERED GENES" by Patten et al. filed Sep. 28, 1999; "EVOLUTION OF WHOLE CELLS AND ORGANISMS BY RECURSIVE SEQUENCE RECOMBINATION" by del Cardayre et al., United States Patent No. 6,379,964; "OLIGONUCLEOTIDE MEDIATED NUCLEIC ACID RECOMBINATION" by Crameri et al., United States Patent Nos. 6,319,714; 6,368,861; 6,376,246; 6,423,542; 6,426,224 and PCT/US00/01203; "USE OF CODON-VARIED OLIGONUCLEOTIDE SYNTHESIS FOR SYNTHETIC SHUFFLING" by Welch et al., United States Patent No. 6,436,675; "METHODS FOR MAKING CHARACTER STRINGS, POLYNUCLEOTIDES & POLYPEPTIDES HAVING DESIRED CHARACTERISTICS" by Selifonov et al., filed Jan. 18, 2000, (PCT/US00/01202) and, e.g. "METHODS FOR MAKING CHARACTER STRINGS, POLYNUCLEOTIDES & POLYPEPTIDES HAVING DESIRED CHARACTERISTICS" by Selifonov et al., filed Jul. 18, 2000 (U.S. Ser. No. 09/618,579); "METHODS OF POPULATING DATA STRUCTURES FOR USE IN

EVOLUTIONARY SIMULATIONS" by Selifonov and Stemmer, filed Jan. 18, 2000 (PCT/US00/01138); and "SINGLE-STRANDED NUCLEIC ACID TEMPLATE-MEDIATED RECOMBINATION AND NUCLEIC ACID FRAGMENT ISOLATION" by Affholter, filed Sep. 6, 2000 (U.S. Ser. No. 09/656,549); and United States Patent Nos. 6,177,263; 6,153,410.

Non-stochastic, or "directed evolution," methods include, e.g., saturation mutagenesis, such as Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR), or a combination thereof are used to modify the nucleic acids of the invention to generate a polypeptide, enzyme, protein, e.g. structural or binding protein, with new or altered properties (e.g., activity under highly acidic or alkaline conditions, high or low temperatures, and the like). Polypeptides encoded by the modified nucleic acids can be screened for an activity before testing for glucan hydrolysis or other activity. Any testing modality or protocol can be used, e.g., using a capillary array platform. See, e.g., U.S. Patent Nos. 6,361,974; 6,280,926; 5,939,250.

Gene Site Saturation mutagenesis, or, GSSM

The invention also provides methods for making enzyme using Gene Site Saturation mutagenesis, or, GSSM, as described herein, and also in U.S. Patent Nos. 6,171,820 and 6,579,258.

In one aspect, codon primers containing a degenerate N,N,G/T sequence are used to introduce point mutations into a polynucleotide, e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, or an antibody of the invention, so as to generate a set of progeny polypeptides in which a full range of single amino acid substitutions is represented at each amino acid position, e.g., an amino acid residue in an enzyme active site or ligand binding site targeted to be modified. These oligonucleotides can comprise a contiguous first homologous sequence, a degenerate N,N,G/T sequence, and, optionally, a second homologous sequence. The downstream progeny translational products from the use of such oligonucleotides include all possible amino acid changes at each amino acid site along the polypeptide, because the degeneracy of the N,N,G/T sequence includes codons for all 20 amino acids. In one aspect, one such degenerate oligonucleotide (comprised of, e.g., one degenerate N,N,G/T cassette) is used for subjecting each original codon in a parental polynucleotide template to a full range of codon substitutions. In another aspect, at least two degenerate cassettes are used – either in the same oligonucleotide or not, for subjecting at least two original codons in a parental polynucleotide template to a full range of codon substitutions. For example, more than

one N,N,G/T sequence can be contained in one oligonucleotide to introduce amino acid mutations at more than one site. This plurality of N,N,G/T sequences can be directly contiguous, or separated by one or more additional nucleotide sequence(s). In another aspect, oligonucleotides serviceable for introducing additions and deletions can be used either alone or in combination with the codons containing an N,N,G/T sequence, to introduce any combination or permutation of amino acid additions, deletions, and/or substitutions.

In one aspect, simultaneous mutagenesis of two or more contiguous amino acid positions is done using an oligonucleotide that contains contiguous N,N,G/T triplets, i.e. a degenerate (N,N,G/T)_n sequence. In another aspect, degenerate cassettes having less degeneracy than the N,N,G/T sequence are used. For example, it may be desirable in some instances to use (e.g. in an oligonucleotide) a degenerate triplet sequence comprised of only one N, where said N can be in the first second or third position of the triplet. Any other bases including any combinations and permutations thereof can be used in the remaining two positions of the triplet. Alternatively, it may be desirable in some instances to use (e.g. in an oligo) a degenerate N,N,N triplet sequence.

In one aspect, use of degenerate triplets (e.g., N,N,G/T triplets) allows for systematic and easy generation of a full range of possible natural amino acids (for a total of 20 amino acids) into each and every amino acid position in a polypeptide (in alternative aspects, the methods also include generation of less than all possible substitutions per amino acid residue, or codon, position). For example, for a 100 amino acid polypeptide, 2000 distinct species (i.e. 20 possible amino acids per position X 100 amino acid positions) can be generated. Through the use of an oligonucleotide or set of oligonucleotides containing a degenerate N,N,G/T triplet, 32 individual sequences can code for all 20 possible natural amino acids. Thus, in a reaction vessel in which a parental polynucleotide sequence is subjected to saturation mutagenesis using at least one such oligonucleotide, there are generated 32 distinct progeny polynucleotides encoding 20 distinct polypeptides. In contrast, the use of a non-degenerate oligonucleotide in site-directed mutagenesis leads to only one progeny polypeptide product per reaction vessel. Nondegenerate oligonucleotides can optionally be used in combination with degenerate primers disclosed; for example, nondegenerate oligonucleotides can be used to generate specific point mutations in a working polynucleotide. This provides one means to generate specific silent point mutations, point mutations leading to corresponding amino

acid changes, and point mutations that cause the generation of stop codons and the corresponding expression of polypeptide fragments.

In one aspect, each saturation mutagenesis reaction vessel contains polynucleotides encoding at least 20 progeny polypeptide (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein,) molecules such that all 20 natural amino acids are represented at the one specific amino acid position corresponding to the codon position mutagenized in the parental polynucleotide (other aspects use less than all 20 natural combinations). The 32-fold degenerate progeny polypeptides generated from each saturation mutagenesis reaction vessel can be subjected to clonal amplification (e.g. cloned into a suitable host, e.g., *E. coli* host, using, e.g., an expression vector) and subjected to expression screening. When an individual progeny polypeptide is identified by screening to display a favorable change in property (when compared to the parental polypeptide, such as increased glucan hydrolysis activity under alkaline or acidic conditions), it can be sequenced to identify the correspondingly favorable amino acid substitution contained therein.

In one aspect, upon mutagenizing each and every amino acid position in a parental polypeptide using saturation mutagenesis as disclosed herein, favorable amino acid changes may be identified at more than one amino acid position. One or more new progeny molecules can be generated that contain a combination of all or part of these favorable amino acid substitutions. For example, if 2 specific favorable amino acid changes are identified in each of 3 amino acid positions in a polypeptide, the permutations include 3 possibilities at each position (no change from the original amino acid, and each of two favorable changes) and 3 positions. Thus, there are $3 \times 3 \times 3$ or 27 total possibilities, including 7 that were previously examined - 6 single point mutations (i.e. 2 at each of three positions) and no change at any position.

In yet another aspect, site-saturation mutagenesis can be used together with shuffling, chimerization, recombination and other mutagenizing processes, along with screening. This invention provides for the use of any mutagenizing process(es), including saturation mutagenesis, in an iterative manner. In one exemplification, the iterative use of any mutagenizing process(es) is used in combination with screening.

The invention also provides for the use of proprietary codon primers (containing a degenerate N,N,N sequence) to introduce point mutations into a polynucleotide, so as to generate a set of progeny polypeptides in which a full range of single amino acid substitutions is represented at each amino acid position; e.g., with Gene

Site Saturation Mutagenesis (GSSM). The oligos used are comprised contiguously of a first homologous sequence, a degenerate N,N,N sequence and in one aspect but not necessarily a second homologous sequence. The downstream progeny translational products from the use of such oligos include all possible amino acid changes at each amino acid site along the polypeptide, because the degeneracy of the N,N,N sequence includes codons for all 20 amino acids.

In one aspect, one such degenerate oligo (comprised of one degenerate N,N,N cassette) is used for subjecting each original codon in a parental polynucleotide template to a full range of codon substitutions. In another aspect, at least two degenerate N,N,N cassettes are used – either in the same oligo or not, for subjecting at least two original codons in a parental polynucleotide template to a full range of codon substitutions. Thus, more than one N,N,N sequence can be contained in one oligo to introduce amino acid mutations at more than one site. This plurality of N,N,N sequences can be directly contiguous, or separated by one or more additional nucleotide sequence(s). In another aspect, oligos serviceable for introducing additions and deletions can be used either alone or in combination with the codons containing an N,N,N sequence, to introduce any combination or permutation of amino acid additions, deletions and/or substitutions.

In a particular exemplification, it is possible to simultaneously mutagenize two or more contiguous amino acid positions using an oligo that contains contiguous N,N,N triplets, *i.e.* a degenerate (N,N,N)_n sequence.

In another aspect, the present invention provides for the use of degenerate cassettes having less degeneracy than the N,N,N sequence. For example, it may be desirable in some instances to use (*e.g.* in an oligo) a degenerate triplet sequence comprised of only one N, where the N can be in the first second or third position of the triplet. Any other bases including any combinations and permutations thereof can be used in the remaining two positions of the triplet. Alternatively, it may be desirable in some instances to use (*e.g.*, in an oligo) a degenerate N,N,N triplet sequence, N,N,G/T, or an N,N, G/C triplet sequence.

It is appreciated, however, that the use of a degenerate triplet (such as N,N,G/T or an N,N, G/C triplet sequence) as disclosed in the instant invention is advantageous for several reasons. In one aspect, this invention provides a means to systematically and fairly easily generate the substitution of the full range of possible amino acids (for a total of 20 amino acids) into each and every amino acid position in a

polypeptide. Thus, for a 100 amino acid polypeptide, the invention provides a way to systematically and fairly easily generate 2000 distinct species (*i.e.*, 20 possible amino acids per position times 100 amino acid positions). It is appreciated that there is provided, through the use of an oligo containing a degenerate N,N,G/T or an N,N, G/C triplet sequence, 32 individual sequences that code for 20 possible amino acids. Thus, in a reaction vessel in which a parental polynucleotide sequence is subjected to saturation mutagenesis using one such oligo, there are generated 32 distinct progeny polynucleotides encoding 20 distinct polypeptides. In contrast, the use of a non-degenerate oligo in site-directed mutagenesis leads to only one progeny polypeptide product per reaction vessel.

This invention also provides for the use of nondegenerate oligos, which can optionally be used in combination with degenerate primers disclosed. It is appreciated that in some situations, it is advantageous to use nondegenerate oligos to generate specific point mutations in a working polynucleotide. This provides a means to generate specific silent point mutations, point mutations leading to corresponding amino acid changes and point mutations that cause the generation of stop codons and the corresponding expression of polypeptide fragments.

Thus, in one aspect of this invention, each saturation mutagenesis reaction vessel contains polynucleotides encoding at least 20 progeny polypeptide molecules such that all 20 amino acids are represented at the one specific amino acid position corresponding to the codon position mutagenized in the parental polynucleotide. The 32-fold degenerate progeny polypeptides generated from each saturation mutagenesis reaction vessel can be subjected to clonal amplification (*e.g.*, cloned into a suitable *E. coli* host using an expression vector) and subjected to expression screening. When an individual progeny polypeptide is identified by screening to display a favorable change in property (when compared to the parental polypeptide), it can be sequenced to identify the correspondingly favorable amino acid substitution contained therein.

It is appreciated that upon mutagenizing each and every amino acid position in a parental polypeptide using saturation mutagenesis as disclosed herein, favorable amino acid changes may be identified at more than one amino acid position. One or more new progeny molecules can be generated that contain a combination of all or part of these favorable amino acid substitutions. For example, if 2 specific favorable amino acid changes are identified in each of 3 amino acid positions in a polypeptide, the permutations include 3 possibilities at each position (no change from the original amino acid and each of two favorable changes) and 3 positions. Thus, there are $3 \times 3 \times 3$ or 27

total possibilities, including 7 that were previously examined - 6 single point mutations (*i.e.*, 2 at each of three positions) and no change at any position.

Thus, in a non-limiting exemplification, this invention provides for the use of saturation mutagenesis in combination with additional mutagenization processes, such as process where two or more related polynucleotides are introduced into a suitable host cell such that a hybrid polynucleotide is generated by recombination and reductive reassortment.

In addition to performing mutagenesis along the entire sequence of a gene, the instant invention provides that mutagenesis can be used to replace each of any number of bases in a polynucleotide sequence, wherein the number of bases to be mutagenized is in one aspect every integer from 15 to 100,000. Thus, instead of mutagenizing every position along a molecule, one can subject every or a discrete number of bases (in one aspect a subset totaling from 15 to 100,000) to mutagenesis. In one aspect, a separate nucleotide is used for mutagenizing each position or group of positions along a polynucleotide sequence. A group of 3 positions to be mutagenized may be a codon. The mutations can be introduced using a mutagenic primer, containing a heterologous cassette, also referred to as a mutagenic cassette. Exemplary cassettes can have from 1 to 500 bases. Each nucleotide position in such heterologous cassettes be N, A, C, G, T, A/C, A/G, A/T, C/G, C/T, G/T, C/G/T, A/G/T, A/C/T, A/C/G, or E, where E is any base that is not A, C, G, or T (E can be referred to as a designer oligo).

In a general sense, saturation mutagenesis is comprised of mutagenizing a complete set of mutagenic cassettes (wherein each cassette is in one aspect about 1-500 bases in length) in defined polynucleotide sequence to be mutagenized (wherein the sequence to be mutagenized is in one aspect from about 15 to 100,000 bases in length). Thus, a group of mutations (ranging from 1 to 100 mutations) is introduced into each cassette to be mutagenized. A grouping of mutations to be introduced into one cassette can be different or the same from a second grouping of mutations to be introduced into a second cassette during the application of one round of saturation mutagenesis. Such groupings are exemplified by deletions, additions, groupings of particular codons and groupings of particular nucleotide cassettes.

Defined sequences to be mutagenized include a whole gene, pathway, cDNA, an entire open reading frame (ORF) and entire promoter, enhancer, repressor/transactivator, origin of replication, intron, operator, or any polynucleotide functional group. Generally, a "defined sequences" for this purpose may be any

polynucleotide that a 15 base-polynucleotide sequence and polynucleotide sequences of lengths between 15 bases and 15,000 bases (this invention specifically names every integer in between). Considerations in choosing groupings of codons include types of amino acids encoded by a degenerate mutagenic cassette.

In one exemplification a grouping of mutations that can be introduced into a mutagenic cassette, this invention specifically provides for degenerate codon substitutions (using degenerate oligos) that code for 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 and 20 amino acids at each position and a library of polypeptides encoded thereby.

Synthetic Ligation Reassembly (SLR)

The invention provides a non-stochastic gene modification system termed "synthetic ligation reassembly," or simply "SLR," a "directed evolution process," to generate polypeptides, e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, or antibodies of the invention, with new or altered properties. SLR is a method of ligating oligonucleotide fragments together non-stochastically. This method differs from stochastic oligonucleotide shuffling in that the nucleic acid building blocks are not shuffled, concatenated or chimerized randomly, but rather are assembled non-stochastically. See, e.g., U.S. Patent Nos. 6,773,900; 6,740,506; 6,713,282; 6,635,449; 6,605,449; 6,537,776.

In one aspect, SLR comprises the following steps: (a) providing a template polynucleotide, wherein the template polynucleotide comprises sequence encoding a homologous gene; (b) providing a plurality of building block polynucleotides, wherein the building block polynucleotides are designed to cross-over reassemble with the template polynucleotide at a predetermined sequence, and a building block polynucleotide comprises a sequence that is a variant of the homologous gene and a sequence homologous to the template polynucleotide flanking the variant sequence; (c) combining a building block polynucleotide with a template polynucleotide such that the building block polynucleotide cross-over reassembles with the template polynucleotide to generate polynucleotides comprising homologous gene sequence variations.

SLR does not depend on the presence of high levels of homology between polynucleotides to be rearranged. Thus, this method can be used to non-stochastically generate libraries (or sets) of progeny molecules comprised of over 10^{100} different chimeras. SLR can be used to generate libraries comprised of over 10^{1000} different progeny chimeras. Thus, aspects of the present invention include non-stochastic methods

of producing a set of finalized chimeric nucleic acid molecule having an overall assembly order that is chosen by design. This method includes the steps of generating by design a plurality of specific nucleic acid building blocks having serviceable mutually compatible ligatable ends, and assembling these nucleic acid building blocks, such that a designed overall assembly order is achieved.

The mutually compatible ligatable ends of the nucleic acid building blocks to be assembled are considered to be "serviceable" for this type of ordered assembly if they enable the building blocks to be coupled in predetermined orders. Thus, the overall assembly order in which the nucleic acid building blocks can be coupled is specified by the design of the ligatable ends. If more than one assembly step is to be used, then the overall assembly order in which the nucleic acid building blocks can be coupled is also specified by the sequential order of the assembly step(s). In one aspect, the annealed building pieces are treated with an enzyme, such as a ligase (e.g. T4 DNA ligase), to achieve covalent bonding of the building pieces.

In one aspect, the design of the oligonucleotide building blocks is obtained by analyzing a set of progenitor nucleic acid sequence templates that serve as a basis for producing a progeny set of finalized chimeric polynucleotides. These parental oligonucleotide templates thus serve as a source of sequence information that aids in the design of the nucleic acid building blocks that are to be mutagenized, e.g., chimerized or shuffled. In one aspect of this method, the sequences of a plurality of parental nucleic acid templates are aligned in order to select one or more demarcation points. The demarcation points can be located at an area of homology, and are comprised of one or more nucleotides. These demarcation points are in one aspect shared by at least two of the progenitor templates. The demarcation points can thereby be used to delineate the boundaries of oligonucleotide building blocks to be generated in order to rearrange the parental polynucleotides. The demarcation points identified and selected in the progenitor molecules serve as potential chimerization points in the assembly of the final chimeric progeny molecules. A demarcation point can be an area of homology (comprised of at least one homologous nucleotide base) shared by at least two parental polynucleotide sequences. Alternatively, a demarcation point can be an area of homology that is shared by at least half of the parental polynucleotide sequences, or, it can be an area of homology that is shared by at least two thirds of the parental polynucleotide sequences. Even more in one aspect a serviceable demarcation points is an area of homology that is shared by at least three fourths of the parental polynucleotide sequences,

or, it can be shared by at almost all of the parental polynucleotide sequences. In one aspect, a demarcation point is an area of homology that is shared by all of the parental polynucleotide sequences.

In one aspect, a ligation reassembly process is performed exhaustively in order to generate an exhaustive library of progeny chimeric polynucleotides. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same time, in another aspect, the assembly order (i.e. the order of assembly of each building block in the 5' to 3' sequence of each finalized chimeric nucleic acid) in each combination is by design (or non-stochastic) as described above. Because of the non-stochastic nature of this invention, the possibility of unwanted side products is greatly reduced.

In another aspect, the ligation reassembly method is performed systematically. For example, the method is performed in order to generate a systematically compartmentalized library of progeny molecules, with compartments that can be screened systematically, e.g. one by one. In other words this invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, a design can be achieved where specific sets of progeny products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, these methods allow a potentially very large number of progeny molecules to be examined systematically in smaller groups. Because of its ability to perform chimerizations in a manner that is highly flexible yet exhaustive and systematic as well, particularly when there is a low level of homology among the progenitor molecules, these methods provide for the generation of a library (or set) comprised of a large number of progeny molecules. Because of the non-stochastic nature of the instant ligation reassembly invention, the progeny molecules generated in one aspect comprise a library of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design. The saturation mutagenesis and optimized directed evolution methods also can be used to generate different progeny molecular species. It is appreciated that the invention provides freedom of choice and control regarding the selection of demarcation points, the size and number of the nucleic acid building blocks, and the size and design of the couplings. It is appreciated, furthermore, that the requirement for intermolecular homology is highly relaxed for the operability of this invention. In fact, demarcation points can even be chosen in areas of little or no

intermolecular homology. For example, because of codon wobble, i.e. the degeneracy of codons, nucleotide substitutions can be introduced into nucleic acid building blocks without altering the amino acid originally encoded in the corresponding progenitor template. Alternatively, a codon can be altered such that the coding for an originally amino acid is altered. This invention provides that such substitutions can be introduced into the nucleic acid building block in order to increase the incidence of intermolecular homologous demarcation points and thus to allow an increased number of couplings to be achieved among the building blocks, which in turn allows a greater number of progeny chimeric molecules to be generated.

In one aspect, the present invention provides a non-stochastic method termed synthetic gene reassembly, that is somewhat related to stochastic shuffling, save that the nucleic acid building blocks are not shuffled or concatenated or chimerized randomly, but rather are assembled non-stochastically.

The synthetic gene reassembly method does not depend on the presence of a high level of homology between polynucleotides to be shuffled. The invention can be used to non-stochastically generate libraries (or sets) of progeny molecules comprised of over 10^{100} different chimeras. Conceivably, synthetic gene reassembly can even be used to generate libraries comprised of over 10^{1000} different progeny chimeras.

Thus, in one aspect, the invention provides a non-stochastic method of producing a set of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design, which method is comprised of the steps of generating by design a plurality of specific nucleic acid building blocks having serviceable mutually compatible ligatable ends and assembling these nucleic acid building blocks, such that a designed overall assembly order is achieved.

The mutually compatible ligatable ends of the nucleic acid building blocks to be assembled are considered to be "serviceable" for this type of ordered assembly if they enable the building blocks to be coupled in predetermined orders. Thus, in one aspect, the overall assembly order in which the nucleic acid building blocks can be coupled is specified by the design of the ligatable ends and, if more than one assembly step is to be used, then the overall assembly order in which the nucleic acid building blocks can be coupled is also specified by the sequential order of the assembly step(s). In one aspect of the invention, the annealed building pieces are treated with an enzyme, such as a ligase (e.g., T4 DNA ligase) to achieve covalent bonding of the building pieces.

In another aspect, the design of nucleic acid building blocks is obtained upon analysis of the sequences of a set of progenitor nucleic acid templates that serve as a basis for producing a progeny set of finalized chimeric nucleic acid molecules. These progenitor nucleic acid templates thus serve as a source of sequence information that aids in the design of the nucleic acid building blocks that are to be mutagenized, *i.e.* chimerized or shuffled.

In one exemplification, the invention provides for the chimerization of a family of related genes and their encoded family of related products. In a particular exemplification, the encoded products are enzymes. The polypeptide, enzyme, protein, *e.g.* structural or binding proteins of the present invention can be mutagenized in accordance with the methods described herein.

Thus according to one aspect of the invention, the sequences of a plurality of progenitor nucleic acid templates (*e.g.*, polynucleotides of the invention) are aligned in order to select one or more demarcation points, which demarcation points can be located at an area of homology. The demarcation points can be used to delineate the boundaries of nucleic acid building blocks to be generated. Thus, the demarcation points identified and selected in the progenitor molecules serve as potential chimerization points in the assembly of the progeny molecules.

Typically a serviceable demarcation point is an area of homology (comprised of at least one homologous nucleotide base) shared by at least two progenitor templates, but the demarcation point can be an area of homology that is shared by at least half of the progenitor templates, at least two thirds of the progenitor templates, at least three fourths of the progenitor templates and in one aspect at almost all of the progenitor templates. Even more in one aspect still a serviceable demarcation point is an area of homology that is shared by all of the progenitor templates.

In one aspect, the gene reassembly process is performed exhaustively in order to generate an exhaustive library. In other words, all possible ordered combinations of the nucleic acid building blocks are represented in the set of finalized chimeric nucleic acid molecules. At the same time, the assembly order (*i.e.* the order of assembly of each building block in the 5' to 3' sequence of each finalized chimeric nucleic acid) in each combination is by design (or non-stochastic). Because of the non-stochastic nature of the method, the possibility of unwanted side products is greatly reduced.

In another aspect, the method provides that the gene reassembly process is performed systematically, for example to generate a systematically compartmentalized

library, with compartments that can be screened systematically, *e.g.*, one by one. In other words the invention provides that, through the selective and judicious use of specific nucleic acid building blocks, coupled with the selective and judicious use of sequentially stepped assembly reactions, an experimental design can be achieved where specific sets of progeny products are made in each of several reaction vessels. This allows a systematic examination and screening procedure to be performed. Thus, it allows a potentially very large number of progeny molecules to be examined systematically in smaller groups.

Because of its ability to perform chimerizations in a manner that is highly flexible yet exhaustive and systematic as well, particularly when there is a low level of homology among the progenitor molecules, the instant invention provides for the generation of a library (or set) comprised of a large number of progeny molecules. Because of the non-stochastic nature of the instant gene reassembly invention, the progeny molecules generated in one aspect comprise a library of finalized chimeric nucleic acid molecules having an overall assembly order that is chosen by design. In a particularly aspect, such a generated library is comprised of greater than 10^3 to greater than 10^{1000} different progeny molecular species.

In one aspect, a set of finalized chimeric nucleic acid molecules, produced as described is comprised of a polynucleotide encoding a polypeptide. According to one aspect, this polynucleotide is a gene, which may be a man-made gene. According to another aspect, this polynucleotide is a gene pathway, which may be a man-made gene pathway. The invention provides that one or more man-made genes generated by the invention may be incorporated into a man-made gene pathway, such as pathway operable in a eukaryotic organism (including a plant).

In another exemplification, the synthetic nature of the step in which the building blocks are generated allows the design and introduction of nucleotides (*e.g.*, one or more nucleotides, which may be, for example, codons or introns or regulatory sequences) that can later be optionally removed in an *in vitro* process (*e.g.*, by mutagenesis) or in an *in vivo* process (*e.g.*, by utilizing the gene splicing ability of a host organism). It is appreciated that in many instances the introduction of these nucleotides may also be desirable for many other reasons in addition to the potential benefit of creating a serviceable demarcation point.

Thus, according to another aspect, the invention provides that a nucleic acid building block can be used to introduce an intron. Thus, the invention provides that

functional introns may be introduced into a man-made gene of the invention. The invention also provides that functional introns may be introduced into a man-made gene pathway of the invention. Accordingly, the invention provides for the generation of a chimeric polynucleotide that is a man-made gene containing one (or more) artificially introduced intron(s).

Accordingly, the invention also provides for the generation of a chimeric polynucleotide that is a man-made gene pathway containing one (or more) artificially introduced intron(s). In one aspect, the artificially introduced intron(s) are functional in one or more host cells for gene splicing much in the way that naturally-occurring introns serve functionally in gene splicing. The invention provides a process of producing man-made intron-containing polynucleotides to be introduced into host organisms for recombination and/or splicing.

A man-made gene produced using the invention can also serve as a substrate for recombination with another nucleic acid. Likewise, a man-made gene pathway produced using the invention can also serve as a substrate for recombination with another nucleic acid. In one aspect, the recombination is facilitated by, or occurs at, areas of homology between the man-made, intron-containing gene and a nucleic acid, which serves as a recombination partner. In one aspect, the recombination partner may also be a nucleic acid generated by the invention, including a man-made gene or a man-made gene pathway. Recombination may be facilitated by or may occur at areas of homology that exist at the one (or more) artificially introduced intron(s) in the man-made gene.

The synthetic gene reassembly method of the invention utilizes a plurality of nucleic acid building blocks, each of which in one aspect has two ligatable ends. The two ligatable ends on each nucleic acid building block may be two blunt ends (*i.e.* each having an overhang of zero nucleotides), or in one aspect one blunt end and one overhang, or more in one aspect still two overhangs.

A useful overhang for this purpose may be a 3' overhang or a 5' overhang. Thus, a nucleic acid building block may have a 3' overhang or alternatively a 5' overhang or alternatively two 3' overhangs or alternatively two 5' overhangs. The overall order in which the nucleic acid building blocks are assembled to form a finalized chimeric nucleic acid molecule is determined by purposeful experimental design and is not random.

In one aspect, a nucleic acid building block is generated by chemical synthesis of two single-stranded nucleic acids (also referred to as single-stranded oligos)

and contacting them so as to allow them to anneal to form a double-stranded nucleic acid building block.

A double-stranded nucleic acid building block can be of variable size. The sizes of these building blocks can be small or large. Exemplary sizes for building block range from 1 base pair (not including any overhangs) to 100,000 base pairs (not including any overhangs). Other exemplary size ranges are also provided, which have lower limits of from 1 bp to 10,000 bp (including every integer value in between) and upper limits of from 2 bp to 100, 000 bp (including every integer value in between).

Many methods exist by which a double-stranded nucleic acid building block can be generated that is serviceable for the invention; and these are known in the art and can be readily performed by the skilled artisan.

According to one aspect, a double-stranded nucleic acid building block is generated by first generating two single stranded nucleic acids and allowing them to anneal to form a double-stranded nucleic acid building block. The two strands of a double-stranded nucleic acid building block may be complementary at every nucleotide apart from any that form an overhang; thus containing no mismatches, apart from any overhang(s). According to another aspect, the two strands of a double-stranded nucleic acid building block are complementary at fewer than every nucleotide apart from any that form an overhang. Thus, according to this aspect, a double-stranded nucleic acid building block can be used to introduce codon degeneracy. In one aspect the codon degeneracy is introduced using the site-saturation mutagenesis described herein, using one or more N,N,G/T cassettes or alternatively using one or more N,N,N cassettes.

The *in vivo* recombination method of the invention can be performed blindly on a pool of unknown hybrids or alleles of a specific polynucleotide or sequence. However, it is not necessary to know the actual DNA or RNA sequence of the specific polynucleotide.

The approach of using recombination within a mixed population of genes can be useful for the generation of any useful proteins, for example, interleukin I, antibodies, tPA and growth hormone. This approach may be used to generate proteins having altered specificity or activity. The approach may also be useful for the generation of hybrid nucleic acid sequences, for example, promoter regions, introns, exons, enhancer sequences, 3' untranslated regions or 5' untranslated regions of genes. Thus this approach may be used to generate genes having increased rates of expression. This

approach may also be useful in the study of repetitive DNA sequences. Finally, this approach may be useful to mutate ribozymes or aptamers.

In one aspect the invention described herein is directed to the use of repeated cycles of reductive reassortment, recombination and selection which allow for the directed molecular evolution of highly complex linear sequences, such as DNA, RNA or proteins thorough recombination.

Optimized Directed Evolution System

The invention provides a non-stochastic gene modification system termed "optimized directed evolution system" to generate polypeptides, e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, or antibodies of the invention, with new or altered properties. Optimized directed evolution is directed to the use of repeated cycles of reductive reassortment, recombination and selection that allow for the directed molecular evolution of nucleic acids through recombination. Optimized directed evolution allows generation of a large population of evolved chimeric sequences, wherein the generated population is significantly enriched for sequences that have a predetermined number of crossover events.

A crossover event is a point in a chimeric sequence where a shift in sequence occurs from one parental variant to another parental variant. Such a point is normally at the juncture of where oligonucleotides from two parents are ligated together to form a single sequence. This method allows calculation of the correct concentrations of oligonucleotide sequences so that the final chimeric population of sequences is enriched for the chosen number of crossover events. This provides more control over choosing chimeric variants having a predetermined number of crossover events.

In addition, this method provides a convenient means for exploring a tremendous amount of the possible protein variant space in comparison to other systems. Previously, if one generated, for example, 10^{13} chimeric molecules during a reaction, it would be extremely difficult to test such a high number of chimeric variants for a particular activity. Moreover, a significant portion of the progeny population would have a very high number of crossover events which resulted in proteins that were less likely to have increased levels of a particular activity. By using these methods, the population of chimerics molecules can be enriched for those variants that have a particular number of crossover events. Thus, although one can still generate 10^{13} chimeric molecules during a reaction, each of the molecules chosen for further analysis most likely has, for example, only three crossover events. Because the resulting progeny population can be skewed to

have a predetermined number of crossover events, the boundaries on the functional variety between the chimeric molecules is reduced. This provides a more manageable number of variables when calculating which oligonucleotide from the original parental polynucleotides might be responsible for affecting a particular trait.

One method for creating a chimeric progeny polynucleotide sequence is to create oligonucleotides corresponding to fragments or portions of each parental sequence. Each oligonucleotide in one aspect includes a unique region of overlap so that mixing the oligonucleotides together results in a new variant that has each oligonucleotide fragment assembled in the correct order. Alternatively protocols for practicing these methods of the invention can be found in U.S. Patent Nos. 6,773,900; 6,740,506; 6,713,282; 6,635,449; 6,605,449; 6,537,776; 6,361,974.

The number of oligonucleotides generated for each parental variant bears a relationship to the total number of resulting crossovers in the chimeric molecule that is ultimately created. For example, three parental nucleotide sequence variants might be provided to undergo a ligation reaction in order to find a chimeric variant having, for example, greater activity at high temperature. As one example, a set of 50 oligonucleotide sequences can be generated corresponding to each portions of each parental variant. Accordingly, during the ligation reassembly process there could be up to 50 crossover events within each of the chimeric sequences. The probability that each of the generated chimeric polynucleotides will contain oligonucleotides from each parental variant in alternating order is very low. If each oligonucleotide fragment is present in the ligation reaction in the same molar quantity it is likely that in some positions oligonucleotides from the same parental polynucleotide will ligate next to one another and thus not result in a crossover event. If the concentration of each oligonucleotide from each parent is kept constant during any ligation step in this example, there is a 1/3 chance (assuming 3 parents) that an oligonucleotide from the same parental variant will ligate within the chimeric sequence and produce no crossover.

Accordingly, a probability density function (PDF) can be determined to predict the population of crossover events that are likely to occur during each step in a ligation reaction given a set number of parental variants, a number of oligonucleotides corresponding to each variant, and the concentrations of each variant during each step in the ligation reaction. The statistics and mathematics behind determining the PDF is described below. By utilizing these methods, one can calculate such a probability density function, and thus enrich the chimeric progeny population for a predetermined number of

crossover events resulting from a particular ligation reaction. Moreover, a target number of crossover events can be predetermined, and the system then programmed to calculate the starting quantities of each parental oligonucleotide during each step in the ligation reaction to result in a probability density function that centers on the predetermined number of crossover events. These methods are directed to the use of repeated cycles of reductive reassortment, recombination and selection that allow for the directed molecular evolution of a nucleic acid encoding a polypeptide through recombination. This system allows generation of a large population of evolved chimeric sequences, wherein the generated population is significantly enriched for sequences that have a predetermined number of crossover events. A crossover event is a point in a chimeric sequence where a shift in sequence occurs from one parental variant to another parental variant. Such a point is normally at the juncture of where oligonucleotides from two parents are ligated together to form a single sequence. The method allows calculation of the correct concentrations of oligonucleotide sequences so that the final chimeric population of sequences is enriched for the chosen number of crossover events. This provides more control over choosing chimeric variants having a predetermined number of crossover events.

In addition, these methods provide a convenient means for exploring a tremendous amount of the possible protein variant space in comparison to other systems. By using the methods described herein, the population of chimeric molecules can be enriched for those variants that have a particular number of crossover events. Thus, although one can still generate 10^{13} chimeric molecules during a reaction, each of the molecules chosen for further analysis most likely has, for example, only three crossover events. Because the resulting progeny population can be skewed to have a predetermined number of crossover events, the boundaries on the functional variety between the chimeric molecules is reduced. This provides a more manageable number of variables when calculating which oligonucleotide from the original parental polynucleotides might be responsible for affecting a particular trait.

In one aspect, the method creates a chimeric progeny polynucleotide sequence by creating oligonucleotides corresponding to fragments or portions of each parental sequence. Each oligonucleotide in one aspect includes a unique region of overlap so that mixing the oligonucleotides together results in a new variant that has each oligonucleotide fragment assembled in the correct order. See also USSN 09/332,835.

Determining Crossover Events

Aspects of the invention include a system and software that receive a desired crossover probability density function (PDF), the number of parent genes to be reassembled, and the number of fragments in the reassembly as inputs. The output of this program is a "fragment PDF" that can be used to determine a recipe for producing reassembled genes, and the estimated crossover PDF of those genes. The processing described herein is in one aspect performed in MATLAB™ (The Mathworks, Natick, Massachusetts) a programming language and development environment for technical computing.

Iterative Processes

In practicing the invention, these processes can be iteratively repeated. For example, a nucleic acid (or, the nucleic acid) responsible for an altered or new a polypeptide, enzyme, protein, e.g. structural or binding protein, phenotype is identified, re-isolated, again modified, re-tested for activity. This process can be iteratively repeated until a desired phenotype is engineered. For example, an entire biochemical anabolic or catabolic pathway can be engineered into a cell, including, e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, activity.

Similarly, if it is determined that a particular oligonucleotide has no affect at all on the desired trait (e.g., a new a polypeptide, enzyme, protein, e.g. structural or binding protein, phenotype), it can be removed as a variable by synthesizing larger parental oligonucleotides that include the sequence to be removed. Since incorporating the sequence within a larger sequence prevents any crossover events, there will no longer be any variation of this sequence in the progeny polynucleotides. This iterative practice of determining which oligonucleotides are most related to the desired trait, and which are unrelated, allows more efficient exploration all of the possible protein variants that might be provide a particular trait or activity.

In vivo shuffling

In vivo shuffling of molecules is use in methods of the invention that provide variants of polypeptides of the invention, e.g., antibodies, a polypeptide, enzyme, protein, e.g. structural or binding protein, and the like. *In vivo* shuffling can be performed utilizing the natural property of cells to recombine multimers. While recombination *in vivo* has provided the major natural route to molecular diversity, genetic recombination remains a relatively complex process that involves 1) the recognition of homologies; 2)

strand cleavage, strand invasion, and metabolic steps leading to the production of recombinant chiasma; and finally 3) the resolution of chiasma into discrete recombined molecules. The formation of the chiasma requires the recognition of homologous sequences.

In another aspect, the invention includes a method for producing a hybrid polynucleotide from at least a first polynucleotide and a second polynucleotide. The invention can be used to produce a hybrid polynucleotide by introducing at least a first polynucleotide and a second polynucleotide (e.g., one, or both, being an exemplary polypeptide-, enzyme-, protein-, e.g. structural or binding protein-encoding sequence of the invention) which share at least one region of partial sequence homology into a suitable host cell. The regions of partial sequence homology promote processes which result in sequence reorganization producing a hybrid polynucleotide. The term "hybrid polynucleotide", as used herein, is any nucleotide sequence which results from the method of the present invention and contains sequence from at least two original polynucleotide sequences. Such hybrid polynucleotides can result from intermolecular recombination events which promote sequence integration between DNA molecules. In addition, such hybrid polynucleotides can result from intramolecular reductive reassortment processes which utilize repeated sequences to alter a nucleotide sequence within a DNA molecule.

In vivo reassortment is focused on "inter-molecular" processes collectively referred to as "recombination" which in bacteria, is generally viewed as a "RecA-dependent" phenomenon. The invention can rely on recombination processes of a host cell to recombine and re-assort sequences, or the cells' ability to mediate reductive processes to decrease the complexity of quasi-repeated sequences in the cell by deletion. This process of "reductive reassortment" occurs by an "intra-molecular", RecA-independent process.

Therefore, in another aspect of the invention, novel polynucleotides can be generated by the process of reductive reassortment. The method involves the generation of constructs containing consecutive sequences (original encoding sequences), their insertion into an appropriate vector and their subsequent introduction into an appropriate host cell. The reassortment of the individual molecular identities occurs by combinatorial processes between the consecutive sequences in the construct possessing regions of homology, or between quasi-repeated units. The reassortment process recombines and/or reduces the complexity and extent of the repeated sequences and results in the production

of novel molecular species. Various treatments may be applied to enhance the rate of reassortment. These could include treatment with ultra-violet light, or DNA damaging chemicals and/or the use of host cell lines displaying enhanced levels of "genetic instability". Thus the reassortment process may involve homologous recombination or the natural property of quasi-repeated sequences to direct their own evolution.

Repeated or "quasi-repeated" sequences play a role in genetic instability. In the present invention, "quasi-repeats" are repeats that are not restricted to their original unit structure. Quasi-repeated units can be presented as an array of sequences in a construct; consecutive units of similar sequences. Once ligated, the junctions between the consecutive sequences become essentially invisible and the quasi-repetitive nature of the resulting construct is now continuous at the molecular level. The deletion process the cell performs to reduce the complexity of the resulting construct operates between the quasi-repeated sequences. The quasi-repeated units provide a practically limitless repertoire of templates upon which slippage events can occur. The constructs containing the quasi-repeats thus effectively provide sufficient molecular elasticity that deletion (and potentially insertion) events can occur virtually anywhere within the quasi-repetitive units.

When the quasi-repeated sequences are all ligated in the same orientation, for instance head to tail or vice versa, the cell cannot distinguish individual units. Consequently, the reductive process can occur throughout the sequences. In contrast, when for example, the units are presented head to head, rather than head to tail, the inversion delineates the endpoints of the adjacent unit so that deletion formation will favor the loss of discrete units. Thus, it is preferable with the present method that the sequences are in the same orientation. Random orientation of quasi-repeated sequences will result in the loss of reassortment efficiency, while consistent orientation of the sequences will offer the highest efficiency. However, while having fewer of the contiguous sequences in the same orientation decreases the efficiency, it may still provide sufficient elasticity for the effective recovery of novel molecules. Constructs can be made with the quasi-repeated sequences in the same orientation to allow higher efficiency.

Sequences can be assembled in a head to tail orientation using any of a variety of methods, including the following:

- a) Primers that include a poly-A head and poly-T tail which when made single-stranded would provide orientation can be utilized. This is accomplished by

having the first few bases of the primers made from RNA and hence easily removed RNaseH.

- b) Primers that include unique restriction cleavage sites can be utilized. Multiple sites, a battery of unique sequences and repeated synthesis and ligation steps would be required.
- c) The inner few bases of the primer could be thiolated and an exonuclease used to produce properly tailed molecules.

The recovery of the re-assorted sequences relies on the identification of cloning vectors with a reduced repetitive index (RI). The re-assorted encoding sequences can then be recovered by amplification. The products are re-cloned and expressed. The recovery of cloning vectors with reduced RI can be affected by:

- 1) The use of vectors only stably maintained when the construct is reduced in complexity.
- 2) The physical recovery of shortened vectors by physical procedures. In this case, the cloning vector would be recovered using standard plasmid isolation procedures and size fractionated on either an agarose gel, or column with a low molecular weight cut off utilizing standard procedures.
- 3) The recovery of vectors containing interrupted genes which can be selected when insert size decreases.
- 4) The use of direct selection techniques with an expression vector and the appropriate selection.

Encoding sequences (for example, genes) from related organisms may demonstrate a high degree of homology and encode quite diverse protein products. These types of sequences are particularly useful in the present invention as quasi-repeats. However, while the examples illustrated below demonstrate the reassortment of nearly identical original encoding sequences (quasi-repeats), this process is not limited to such nearly identical repeats.

The following example demonstrates a method of the invention. Encoding nucleic acid sequences (quasi-repeats) derived from three (3) unique species are described. Each sequence encodes a protein with a distinct set of properties. Each of the sequences differs by a single or a few base pairs at a unique position in the sequence. The quasi-repeated sequences are separately or collectively amplified and ligated into random assemblies such that all possible permutations and combinations are available in the population of ligated molecules. The number of quasi-repeat units can be controlled by

the assembly conditions. The average number of quasi-repeated units in a construct is defined as the repetitive index (RI).

Once formed, the constructs may, or may not be size fractionated on an agarose gel according to published protocols, inserted into a cloning vector and transfected into an appropriate host cell. The cells are then propagated and "reductive reassortment" is effected. The rate of the reductive reassortment process may be stimulated by the introduction of DNA damage if desired. Whether the reduction in RI is mediated by deletion formation between repeated sequences by an "intra-molecular" mechanism, or mediated by recombination-like events through "inter-molecular" mechanisms is immaterial. The end result is a reassortment of the molecules into all possible combinations.

Optionally, the method comprises the additional step of screening the library members of the shuffled pool to identify individual shuffled library members having the ability to bind or otherwise interact, or catalyze a particular reaction (*e.g.*, such as catalytic domain of an enzyme) with a predetermined macromolecule, such as for example a proteinaceous receptor, an oligosaccharide, virion, or other predetermined compound or structure.

The polypeptides that are identified from such libraries can be used for therapeutic, diagnostic, research and related purposes (*e.g.*, catalysts, solutes for increasing osmolarity of an aqueous solution and the like) and/or can be subjected to one or more additional cycles of shuffling and/or selection.

In another aspect, it is envisioned that prior to or during recombination or reassortment, polynucleotides generated by the method of the invention can be subjected to agents or processes which promote the introduction of mutations into the original polynucleotides. The introduction of such mutations would increase the diversity of resulting hybrid polynucleotides and polypeptides encoded therefrom. The agents or processes which promote mutagenesis can include, but are not limited to: (+)-CC-1065, or a synthetic analog such as (+)-CC-1065-(N3-Adenine (*See* Sun and Hurley, (1992); an N-acetylated or deacetylated 4'-fluoro-4-aminobiphenyl adduct capable of inhibiting DNA synthesis (*See*, for example, van de Poll *et al.* (1992))); or a N-acetylated or deacetylated 4-aminobiphenyl adduct capable of inhibiting DNA synthesis (*See* also, van de Poll *et al.* (1992), pp. 751-758); trivalent chromium, a trivalent chromium salt, a polycyclic aromatic hydrocarbon (PAH) DNA adduct capable of inhibiting DNA replication, such as 7-bromomethyl-benz[*a*]anthracene ("BMA"), tris(2,3-dibromopropyl)phosphate ("Tris-

BP”), 1,2-dibromo-3-chloropropane (“DBCP”), 2-bromoacrolein (2BA), benzo[*a*]pyrene-7,8-dihydrodiol-9-10-epoxide (“BPDE”), a platinum(II) halogen salt, N-hydroxy-2-amino-3-methylimidazo[4,5-*f*]-quinoline (“N-hydroxy-IQ”) and N-hydroxy-2-amino-1-methyl-6-phenylimidazo[4,5-*f*]-pyridine (“N-hydroxy-PhIP”). Exemplary means for slowing or halting PCR amplification consist of UV light (+)-CC-1065 and (+)-CC-1065-(N3-Adenine). Particularly encompassed means are DNA adducts or polynucleotides comprising the DNA adducts from the polynucleotides or polynucleotides pool, which can be released or removed by a process including heating the solution comprising the polynucleotides prior to further processing.

In another aspect the invention is directed to a method of producing recombinant proteins having biological activity by treating a sample comprising double-stranded template polynucleotides encoding a wild-type protein under conditions according to the invention which provide for the production of hybrid or re-assorted polynucleotides.

Producing sequence variants

The invention also provides additional methods for making sequence variants of the nucleic acid (e.g., polypeptide, enzyme, protein, e.g. structural or binding protein) sequences of the invention. The invention also provides additional methods for isolating a polypeptide, enzyme, protein, e.g. structural or binding protein, using the nucleic acids and polypeptides of the invention. In one aspect, the invention provides for variants of a polypeptide, enzyme, protein, e.g. structural or binding protein, coding sequence (e.g., a gene, cDNA or message) of the invention, which can be altered by any means, including, e.g., random or stochastic methods, or, non-stochastic, or “directed evolution,” methods, as described above.

The isolated variants may be naturally occurring. Variant can also be created *in vitro*. Variants may be created using genetic engineering techniques such as site directed mutagenesis, random chemical mutagenesis, Exonuclease III deletion procedures, and standard cloning techniques. Alternatively, such variants, fragments, analogs, or derivatives may be created using chemical synthesis or modification procedures. Other methods of making variants are also familiar to those skilled in the art. These include procedures in which nucleic acid sequences obtained from natural isolates are modified to generate nucleic acids which encode polypeptides having characteristics which enhance their value in industrial or laboratory applications. In such procedures, a large number of variant sequences having one or more nucleotide differences with respect

to the sequence obtained from the natural isolate are generated and characterized. These nucleotide differences can result in amino acid changes with respect to the polypeptides encoded by the nucleic acids from the natural isolates.

For example, variants may be created using error prone PCR. In error prone PCR, PCR is performed under conditions where the copying fidelity of the DNA polymerase is low, such that a high rate of point mutations is obtained along the entire length of the PCR product. Error prone PCR is described, e.g., in Leung (1989) Technique 1:11-15) and Caldwell (1992) PCR Methods Applic. 2:28-33. Briefly, in such procedures, nucleic acids to be mutagenized are mixed with PCR primers, reaction buffer, MgCl₂, MnCl₂, Taq polymerase and an appropriate concentration of dNTPs for achieving a high rate of point mutation along the entire length of the PCR product. For example, the reaction may be performed using 20 fmoles of nucleic acid to be mutagenized, 30 pmole of each PCR primer, a reaction buffer comprising 50mM KCl, 10mM Tris HCl (pH 8.3) and 0.01% gelatin, 7mM MgCl₂, 0.5mM MnCl₂, 5 units of Taq polymerase, 0.2mM dGTP, 0.2mM dATP, 1mM dCTP, and 1mM dTTP. PCR may be performed for 30 cycles of 94°C for 1 min, 45°C for 1 min, and 72°C for 1 min. However, it will be appreciated that these parameters may be varied as appropriate. The mutagenized nucleic acids are cloned into an appropriate vector and the activities of the polypeptides encoded by the mutagenized nucleic acids are evaluated.

Variants may also be created using oligonucleotide directed mutagenesis to generate site-specific mutations in any cloned DNA of interest. Oligonucleotide mutagenesis is described, e.g., in Reidhaar-Olson (1988) Science 241:53-57. Briefly, in such procedures a plurality of double stranded oligonucleotides bearing one or more mutations to be introduced into the cloned DNA are synthesized and inserted into the cloned DNA to be mutagenized. Clones containing the mutagenized DNA are recovered and the activities of the polypeptides they encode are assessed.

Another method for generating variants is assembly PCR. Assembly PCR involves the assembly of a PCR product from a mixture of small DNA fragments. A large number of different PCR reactions occur in parallel in the same vial, with the products of one reaction priming the products of another reaction. Assembly PCR is described in, e.g., U.S. Patent No. 5,965,408.

Still another method of generating variants is sexual PCR mutagenesis. In sexual PCR mutagenesis, forced homologous recombination occurs between DNA molecules of different but highly related DNA sequence *in vitro*, as a result of random

fragmentation of the DNA molecule based on sequence homology, followed by fixation of the crossover by primer extension in a PCR reaction. Sexual PCR mutagenesis is described, e.g., in Stemmer (1994) Proc. Natl. Acad. Sci. USA 91:10747-10751. Briefly, in such procedures a plurality of nucleic acids to be recombined are digested with DNase to generate fragments having an average size of 50-200 nucleotides. Fragments of the desired average size are purified and resuspended in a PCR mixture. PCR is conducted under conditions which facilitate recombination between the nucleic acid fragments. For example, PCR may be performed by resuspending the purified fragments at a concentration of 10-30ng/ μ l in a solution of 0.2mM of each dNTP, 2.2mM $MgCl_2$, 50mM KCL, 10mM Tris HCl, pH 9.0, and 0.1% Triton X-100. 2.5 units of Taq polymerase per 100:1 of reaction mixture is added and PCR is performed using the following regime: 94°C for 60 seconds, 94°C for 30 seconds, 50-55°C for 30 seconds, 72°C for 30 seconds (30-45 times) and 72°C for 5 minutes. However, it will be appreciated that these parameters may be varied as appropriate. In some aspects, oligonucleotides may be included in the PCR reactions. In other aspects, the Klenow fragment of DNA polymerase I may be used in a first set of PCR reactions and Taq polymerase may be used in a subsequent set of PCR reactions. Recombinant sequences are isolated and the activities of the polypeptides they encode are assessed.

Variants may also be created by *in vivo* mutagenesis. In some aspects, random mutations in a sequence of interest are generated by propagating the sequence of interest in a bacterial strain, such as an E. coli strain, which carries mutations in one or more of the DNA repair pathways. Such "mutator" strains have a higher random mutation rate than that of a wild-type parent. Propagating the DNA in one of these strains will eventually generate random mutations within the DNA. Mutator strains suitable for use for *in vivo* mutagenesis are described in PCT Publication No. WO 91/16427, published October 31, 1991, entitled "Methods for Phenotype Creation from Multiple Gene Populations".

Variants may also be generated using cassette mutagenesis. In cassette mutagenesis a small region of a double stranded DNA molecule is replaced with a synthetic oligonucleotide "cassette" that differs from the native sequence. The oligonucleotide often contains completely and/or partially randomized native sequence.

Recursive ensemble mutagenesis may also be used to generate variants. Recursive ensemble mutagenesis is an algorithm for protein engineering (protein mutagenesis) developed to produce diverse populations of phenotypically related mutants

whose members differ in amino acid sequence. This method uses a feedback mechanism to control successive rounds of combinatorial cassette mutagenesis. Recursive ensemble mutagenesis is described, e.g., in Arkin (1992) *Proc. Natl. Acad. Sci. USA* 89:7811-7815.

In some aspects, variants are created using exponential ensemble mutagenesis. Exponential ensemble mutagenesis is a process for generating combinatorial libraries with a high percentage of unique and functional mutants, wherein small groups of residues are randomized in parallel to identify, at each altered position, amino acids which lead to functional proteins. Exponential ensemble mutagenesis is described, e.g., in Delegrave (1993) *Biotechnology Res.* 11:1548-1552. Random and site-directed mutagenesis are described, e.g., in Arnold (1993) *Current Opinion in Biotechnology* 4:450-455.

In some aspects, the variants are created using shuffling procedures wherein portions of a plurality of nucleic acids which encode distinct polypeptides are fused together to create chimeric nucleic acid sequences which encode chimeric polypeptides as described in U.S. Patent No. 5,965,408, filed July 9, 1996, entitled, "Method of DNA Reassembly by Interrupting Synthesis" and U.S. Patent No. 5,939,250, filed May 22, 1996, entitled, "Production of Enzymes Having Desired Activities by Mutagenesis.

The variants of the polypeptides of the invention may be variants in which one or more of the amino acid residues of the polypeptides of the sequences of the invention are substituted with a conserved or non-conserved amino acid residue (in one aspect a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code.

Conservative substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the following replacements: replacements of an aliphatic amino acid such as Alanine, Valine, Leucine and Isoleucine with another aliphatic amino acid; replacement of a Serine with a Threonine or vice versa; replacement of an acidic residue such as Aspartic acid and Glutamic acid with another acidic residue; replacement of a residue bearing an amide group, such as Asparagine and Glutamine, with another residue bearing an amide group; exchange of a basic residue such as Lysine and Arginine with another basic residue; and replacement of an aromatic residue such as Phenylalanine, Tyrosine with another aromatic residue.

Other variants are those in which one or more of the amino acid residues of a polypeptide of the invention includes a substituent group.

Still other variants are those in which the polypeptide is associated with another compound, such as a compound to increase the half-life of the polypeptide (for example, polyethylene glycol).

Additional variants are those in which additional amino acids are fused to the polypeptide, such as a leader sequence, a secretory sequence, a proprotein sequence or a sequence which facilitates purification, enrichment, or stabilization of the polypeptide.

In some aspects, the fragments, derivatives and analogs retain the same biological function or activity as the polypeptides of the invention. In other aspects, the fragment, derivative, or analog includes a proprotein, such that the fragment, derivative, or analog can be activated by cleavage of the proprotein portion to produce an active polypeptide.

Optimizing codons to achieve high levels of protein expression in host cells

The invention provides methods for modifying polypeptide-, enzyme-, protein-, e.g. structural or binding protein-encoding nucleic acids to modify codon usage. In one aspect, the invention provides methods for modifying codons in a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, to increase or decrease its expression in a host cell. The invention also provides nucleic acids encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, modified to increase its expression in a host cell, a polypeptide, enzyme, protein, e.g. structural or binding protein, so modified, and methods of making the modified a polypeptide, enzyme, protein, e.g. structural or binding protein. The method comprises identifying a "non-preferred" or a "less preferred" codon in a polypeptide-, enzyme-, protein-, e.g. structural or binding protein-encoding nucleic acid and replacing one or more of these non-preferred or less preferred codons with a "preferred codon" encoding the same amino acid as the replaced codon and at least one non-preferred or less preferred codon in the nucleic acid has been replaced by a preferred codon encoding the same amino acid. A preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell.

Host cells for expressing the nucleic acids, expression cassettes and vectors of the invention include bacteria, yeast, fungi, plant cells, insect cells and mammalian cells. Thus, the invention provides methods for optimizing codon usage in

all of these cells, codon-altered nucleic acids and polypeptides made by the codon-altered nucleic acids. Exemplary host cells include gram negative bacteria, such as *Escherichia coli*; gram positive bacteria, such as *Streptomyces* sp., *Lactobacillus gasseri*, *Lactococcus lactis*, *Lactococcus cremoris*, *Bacillus subtilis*, *Bacillus cereus*. Exemplary host cells also include eukaryotic organisms, e.g., various yeast, such as *Saccharomyces* sp., including *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Pichia pastoris*, and *Kluyveromyces lactis*, *Hansenula polymorpha*, *Aspergillus niger*, and mammalian cells and cell lines and insect cells and cell lines. Thus, the invention also includes nucleic acids and polypeptides optimized for expression in these organisms and species.

For example, the codons of a nucleic acid encoding a polypeptide, enzyme, protein, e.g. structural or binding protein, isolated from a bacterial cell are modified such that the nucleic acid is optimally expressed in a bacterial cell different from the bacteria from which the polypeptide, enzyme, protein, e.g. structural or binding protein was derived, a yeast, a fungi, a plant cell, an insect cell or a mammalian cell. Methods for optimizing codons are well known in the art, see, e.g., U.S. Patent No. 5,795,737; Baca (2000) Int. J. Parasitol. 30:113-118; Hale (1998) Protein Expr. Purif. 12:185-188; Narum (2001) Infect. Immun. 69:7250-7253. See also Narum (2001) Infect. Immun. 69:7250-7253, describing optimizing codons in mouse systems; Outchkourov (2002) Protein Expr. Purif. 24:18-24, describing optimizing codons in yeast; Feng (2000) Biochemistry 39:15399-15409, describing optimizing codons in *E. coli*; Humphreys (2000) Protein Expr. Purif. 20:252-264, describing optimizing codon usage that affects secretion in *E. coli*.

Transgenic non-human animals

The invention provides transgenic non-human animals comprising a nucleic acid, a polypeptide (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein), an expression cassette or vector or a transfected or transformed cell of the invention. The invention also provides methods of making and using these transgenic non-human animals.

The transgenic non-human animals can be, e.g., goats, rabbits, sheep, pigs (including all swine, hogs and related animals), cows, rats and mice, comprising the nucleic acids of the invention. These animals can be used, e.g., as *in vivo* models to study a polypeptide, enzyme, protein, e.g. structural or binding protein, activity, or, as models to screen for agents that change the polypeptide, enzyme, protein, e.g. structural or binding protein activity *in vivo*. The coding sequences for the polypeptides to be

expressed in the transgenic non-human animals can be designed to be constitutive, or, under the control of tissue-specific, developmental-specific or inducible transcriptional regulatory factors. Transgenic non-human animals can be designed and generated using any method known in the art; see, e.g., U.S. Patent Nos. 6,211,428; 6,187,992; 6,156,952; 6,118,044; 6,111,166; 6,107,541; 5,959,171; 5,922,854; 5,892,070; 5,880,327; 5,891,698; 5,639,940; 5,573,933; 5,387,742; 5,087,571, describing making and using transformed cells and eggs and transgenic mice, rats, rabbits, sheep, pigs and cows. See also, e.g., Pollock (1999) *J. Immunol. Methods* 231:147-157, describing the production of recombinant proteins in the milk of transgenic dairy animals; Baguisi (1999) *Nat. Biotechnol.* 17:456-461, demonstrating the production of transgenic goats. U.S. Patent No. 6,211,428, describes making and using transgenic non-human mammals which express in their brains a nucleic acid construct comprising a DNA sequence. U.S. Patent No. 5,387,742, describes injecting cloned recombinant or synthetic DNA sequences into fertilized mouse eggs, implanting the injected eggs in pseudo-pregnant females, and growing to term transgenic mice. U.S. Patent No. 6,187,992, describes making and using a transgenic mouse.

"Knockout animals" can also be used to practice the methods of the invention. For example, in one aspect, the transgenic or modified animals of the invention comprise a "knockout animal," e.g., a "knockout mouse," engineered not to express an endogenous gene, which is replaced with a gene expressing a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention, or, a fusion protein comprising a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention.

Transgenic Plants and Seeds

The invention provides transgenic plants and seeds comprising a nucleic acid, a polypeptide (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein,), an expression cassette or vector or a transfected or transformed cell of the invention. The invention also provides plant products, e.g., oils, seeds, leaves, extracts and the like, comprising a nucleic acid and/or a polypeptide (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein,) of the invention. The transgenic plant can be dicotyledonous (a dicot) or monocotyledonous (a monocot). The invention also provides methods of making and using these transgenic plants and seeds. The transgenic plant or plant cell expressing a polypeptide of the present invention may be constructed in

accordance with any method known in the art. See, for example, U.S. Patent No. 6,309,872.

Nucleic acids and expression constructs of the invention can be introduced into a plant cell by any means. For example, nucleic acids or expression constructs can be introduced into the genome of a desired plant host, or, the nucleic acids or expression constructs can be episomes. Introduction into the genome of a desired plant can be such that the host's a polypeptide, enzyme, protein, e.g. structural or binding protein, production is regulated by endogenous transcriptional or translational control elements. The invention also provides "knockout plants" where insertion of gene sequence by, e.g., homologous recombination, has disrupted the expression of the endogenous gene. Means to generate "knockout" plants are well-known in the art, see, e.g., Strepp (1998) *Proc Natl. Acad. Sci. USA* 95:4368-4373; Miao (1995) *Plant J* 7:359-365. See discussion on transgenic plants, below.

The nucleic acids of the invention can be used to confer desired traits on essentially any plant, e.g., on starch-producing plants, such as potato, wheat, rice, barley, and the like. Nucleic acids of the invention can be used to manipulate metabolic pathways of a plant in order to optimize or alter host's expression of polypeptide, enzyme, protein, e.g. structural or binding protein. The can change a polypeptide, enzyme, protein, e.g. structural or binding protein, activity in a plant. Alternatively, a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention can be used in production of a transgenic plant to produce a compound not naturally produced by that plant. This can lower production costs or create a novel product.

In one aspect, the first step in production of a transgenic plant involves making an expression construct for expression in a plant cell. These techniques are well known in the art. They can include selecting and cloning a promoter, a coding sequence for facilitating efficient binding of ribosomes to mRNA and selecting the appropriate gene terminator sequences. One exemplary constitutive promoter is CaMV35S, from the cauliflower mosaic virus, which generally results in a high degree of expression in plants. Other promoters are more specific and respond to cues in the plant's internal or external environment. An exemplary light-inducible promoter is the promoter from the *cab* gene, encoding the major chlorophyll *a/b* binding protein.

In one aspect, the nucleic acid is modified to achieve greater expression in a plant cell. For example, a sequence of the invention is likely to have a higher percentage of A-T nucleotide pairs compared to that seen in a plant, some of which prefer

G-C nucleotide pairs. Therefore, A-T nucleotides in the coding sequence can be substituted with G-C nucleotides without significantly changing the amino acid sequence to enhance production of the gene product in plant cells.

Selectable marker gene can be added to the gene construct in order to identify plant cells or tissues that have successfully integrated the transgene. This may be necessary because achieving incorporation and expression of genes in plant cells is a rare event, occurring in just a few percent of the targeted tissues or cells. Selectable marker genes encode proteins that provide resistance to agents that are normally toxic to plants, such as antibiotics or herbicides. Only plant cells that have integrated the selectable marker gene will survive when grown on a medium containing the appropriate antibiotic or herbicide. As for other inserted genes, marker genes also require promoter and termination sequences for proper function.

In one aspect, making transgenic plants or seeds comprises incorporating sequences of the invention and, optionally, marker genes into a target expression construct (e.g., a plasmid), along with positioning of the promoter and the terminator sequences. This can involve transferring the modified gene into the plant through a suitable method. For example, a construct may be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation and microinjection of plant cell protoplasts, or the constructs can be introduced directly to plant tissue using ballistic methods, such as DNA particle bombardment. For example, see, e.g., Christou (1997) *Plant Mol. Biol.* 35:197-203; Pawlowski (1996) *Mol. Biotechnol.* 6:17-30; Klein (1987) *Nature* 327:70-73; Takumi (1997) *Genes Genet. Syst.* 72:63-69, discussing use of particle bombardment to introduce transgenes into wheat; and Adam (1997) *supra*, for use of particle bombardment to introduce YACs into plant cells. For example, Rinehart (1997) *supra*, used particle bombardment to generate transgenic cotton plants. Apparatus for accelerating particles is described U.S. Pat. No. 5,015,580; and, the commercially available BioRad (Biolistics) PDS-2000 particle acceleration instrument; see also, John, U.S. Patent No. 5,608,148; and Ellis, U.S. Patent No. 5,681,730, describing particle-mediated transformation of gymnosperms.

In one aspect, protoplasts can be immobilized and injected with a nucleic acids, e.g., an expression construct. Although plant regeneration from protoplasts is not easy with cereals, plant regeneration is possible in legumes using somatic embryogenesis from protoplast derived callus. Organized tissues can be transformed with naked DNA using gene gun technique, where DNA is coated on tungsten microprojectiles, shot

1/100th the size of cells, which carry the DNA deep into cells and organelles.

Transformed tissue is then induced to regenerate, usually by somatic embryogenesis. This technique has been successful in several cereal species including maize and rice.

Nucleic acids, e.g., expression constructs, can also be introduced in to plant cells using recombinant viruses. Plant cells can be transformed using viral vectors, such as, e.g., tobacco mosaic virus derived vectors (Rouwendal (1997) *Plant Mol. Biol.* 33:989-999), see Porta (1996) "Use of viral replicons for the expression of genes in plants," *Mol. Biotechnol.* 5:209-221.

Alternatively, nucleic acids, e.g., an expression construct, can be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. *Agrobacterium tumefaciens*-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, e.g., Horsch (1984) *Science* 233:496-498; Fraley (1983) *Proc. Natl. Acad. Sci. USA* 80:4803 (1983); *Gene Transfer to Plants*, Potrykus, ed. (Springer-Verlag, Berlin 1995). The DNA in an *A. tumefaciens* cell is contained in the bacterial chromosome as well as in another structure known as a Ti (tumor-inducing) plasmid. The Ti plasmid contains a stretch of DNA termed T-DNA (~20 kb long) that is transferred to the plant cell in the infection process and a series of vir (virulence) genes that direct the infection process. *A. tumefaciens* can only infect a plant through wounds: when a plant root or stem is wounded it gives off certain chemical signals, in response to which, the vir genes of *A. tumefaciens* become activated and direct a series of events necessary for the transfer of the T-DNA from the Ti plasmid to the plant's chromosome. The T-DNA enters the plant cell through the wound. One speculation is that the T-DNA waits until the plant DNA is being replicated or transcribed, then inserts itself into the exposed plant DNA. In order to use *A. tumefaciens* as a transgene vector, the tumor-inducing section of T-DNA have to be removed, while retaining the T-DNA border regions and the vir genes. The transgene is then inserted between the T-DNA border regions, where it is transferred to the plant cell and becomes integrated into the plant's chromosomes.

The invention provides for the transformation of monocotyledonous plants using the nucleic acids of the invention, including important cereals, see Hiei (1997) *Plant Mol. Biol.* 35:205-218. See also, e.g., Horsch, *Science* (1984) 233:496; Fraley (1983)

Proc. Natl. Acad. Sci USA 80:4803; Thykjaer (1997) *supra*; Park (1996) Plant Mol. Biol. 32:1135-1148, discussing T-DNA integration into genomic DNA. See also D'Halluin, U.S. Patent No. 5,712,135, describing a process for the stable integration of a DNA comprising a gene that is functional in a cell of a cereal, or other monocotyledonous plant.

In one aspect, the third step can involve selection and regeneration of whole plants capable of transmitting the incorporated target gene to the next generation. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker that has been introduced together with the desired nucleotide sequences. Plant regeneration from cultured protoplasts is described in Evans et al., *Protoplasts Isolation and Culture, Handbook of Plant Cell Culture*, pp. 124-176, MacMillan Publishing Company, New York, 1983; and Binding, *Regeneration of Plants, Plant Protoplasts*, pp. 21-73, CRC Press, Boca Raton, 1985. Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee (1987) Ann. Rev. of Plant Phys. 38:467-486. To obtain whole plants from transgenic tissues such as immature embryos, they can be grown under controlled environmental conditions in a series of media containing nutrients and hormones, a process known as tissue culture. Once whole plants are generated and produce seed, evaluation of the progeny begins.

After the expression cassette is stably incorporated in transgenic plants, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. Since transgenic expression of the nucleic acids of the invention leads to phenotypic changes, plants comprising the recombinant nucleic acids of the invention can be sexually crossed with a second plant to obtain a final product. Thus, the seed of the invention can be derived from a cross between two transgenic plants of the invention, or a cross between a plant of the invention and another plant. The desired effects (e.g., expression of the polypeptides of the invention to produce a plant in which flowering behavior is altered) can be enhanced when both parental plants express the polypeptides (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein,) of the invention. The desired effects can be passed to future plant generations by standard propagation means.

The nucleic acids and polypeptides of the invention are expressed in or inserted in any plant or seed. Transgenic plants of the invention can be dicotyledonous or

monocotyledonous. Examples of monocot transgenic plants of the invention are grasses, such as meadow grass (blue grass, *Poa*), forage grass such as *festuca*, *lolium*, temperate grass, such as *Agrostis*, and cereals, e.g., wheat, oats, rye, barley, rice, sorghum, and maize (corn). Examples of dicot transgenic plants of the invention are tobacco, legumes, such as lupins, potato, sugar beet, pea, bean and soybean, and cruciferous plants (family *Brassicaceae*), such as cauliflower, rape seed, and the closely related model organism *Arabidopsis thaliana*. Thus, the transgenic plants and seeds of the invention include a broad range of plants, including, but not limited to, species from the genera *Anacardium*, *Arachis*, *Asparagus*, *Atropa*, *Avena*, *Brassica*, *Citrus*, *Citrullus*, *Capsicum*, *Carthamus*, *Cocos*, *Coffea*, *Cucumis*, *Cucurbita*, *Daucus*, *Elaeis*, *Fragaria*, *Glycine*, *Gossypium*, *Helianthus*, *Heterocallis*, *Hordeum*, *Hyoscyamus*, *Lactuca*, *Linum*, *Lolium*, *Lupinus*, *Lycopersicon*, *Malus*, *Manihot*, *Majorana*, *Medicago*, *Nicotiana*, *Olea*, *Oryza*, *Panicum*, *Pennisetum*, *Persea*, *Phaseolus*, *Pistachia*, *Pisum*, *Pyrus*, *Prunus*, *Raphanus*, *Ricinus*, *Secale*, *Senecio*, *Sinapis*, *Solanum*, *Sorghum*, *Theobromus*, *Trigonella*, *Triticum*, *Vicia*, *Vitis*, *Vigna*, and *Zea*.

In alternative embodiments, the nucleic acids of the invention are expressed in plants which contain fiber cells, including, e.g., cotton, silk cotton tree (Kapok, *Ceiba pentandra*), desert willow, creosote bush, winterfat, balsa, ramie, kenaf, hemp, roselle, jute, sisal abaca and flax. In alternative embodiments, the transgenic plants of the invention can be members of the genus *Gossypium*, including members of any *Gossypium* species, such as *G. arboreum*, *G. herbaceum*, *G. barbadense*, and *G. hirsutum*.

The invention also provides for transgenic plants to be used for producing large amounts of the polypeptides (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, or antibody) of the invention. For example, see Palmgren (1997) Trends Genet. 13:348; Chong (1997) Transgenic Res. 6:289-296 (producing human milk protein beta-casein in transgenic potato plants using an auxin-inducible, bidirectional mannopine synthase (*mas1',2'*) promoter with *Agrobacterium tumefaciens*-mediated leaf disc transformation methods).

Using known procedures, one of skill can screen for plants of the invention by detecting the increase or decrease of transgene mRNA or protein in transgenic plants. Means for detecting and quantitation of mRNAs or proteins are well known in the art.

Polypeptides and peptides

In one aspect, the invention provides isolated or recombinant polypeptides having a sequence identity (e.g., at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or complete (100%) sequence identity, or homology) to an exemplary sequence of the invention, e.g., proteins having a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, etc., and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898). The percent sequence identity can be over the full length of the polypeptide, or, the identity can be over a region of at least about 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700 or more residues.

“Amino acid” or “amino acid sequence” as used herein refer to an oligopeptide, peptide, polypeptide, or protein sequence, or to a fragment, portion, or subunit of any of these and to naturally occurring or synthetic molecules. “Amino acid” or “amino acid sequence” include an oligopeptide, peptide, polypeptide, or protein sequence, or to a fragment, portion, or subunit of any of these, and to naturally occurring or synthetic molecules. The term “polypeptide” as used herein, refers to amino acids joined to each other by peptide bonds or modified peptide bonds, *i.e.*, peptide isosteres and may contain modified amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as post-translational processing, or by chemical modification techniques which are well known in the art. Modifications can occur anywhere in the polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also a given polypeptide may have many types of modifications. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of a phosphatidylinositol, cross-linking cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation,

pegylation, glucan hydrolase processing, phosphorylation, prenylation, racemization, selenoylation, sulfation and transfer-RNA mediated addition of amino acids to protein such as arginylation. (See Creighton, T.E., *Proteins – Structure and Molecular Properties* 2nd Ed., W.H. Freeman and Company, New York (1993); *Posttranslational Covalent Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York, pp. 1-12 (1983)). The peptides and polypeptides of the invention also include all “mimetic” and “peptidomimetic” forms, as described in further detail, below.

As used herein, the term “isolated” means that the material is removed from its original environment (*e.g.*, the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition and still be isolated in that such vector or composition is not part of its natural environment. As used herein, the term “purified” does not require absolute purity; rather, it is intended as a relative definition. Individual nucleic acids obtained from a library have been conventionally purified to electrophoretic homogeneity. The sequences obtained from these clones could not be obtained directly either from the library or from total human DNA. The purified nucleic acids of the invention have been purified from the remainder of the genomic DNA in the organism by at least 10^4 - 10^6 fold. However, the term “purified” also includes nucleic acids which have been purified from the remainder of the genomic DNA or from other sequences in a library or other environment by at least one order of magnitude, typically two or three orders and more typically four or five orders of magnitude.

“Recombinant” polypeptides or proteins refer to polypeptides or proteins produced by recombinant DNA techniques; *i.e.*, produced from cells transformed by an exogenous DNA construct encoding the desired polypeptide or protein. “Synthetic” polypeptides or protein are those prepared by chemical synthesis. Solid-phase chemical peptide synthesis methods can also be used to synthesize the polypeptide or fragments of the invention. Such method have been known in the art since the early 1960's (Merrifield, R. B., *J. Am. Chem. Soc.*, 85:2149-2154, 1963) (See also Stewart, J. M. and Young, J. D., *Solid Phase Peptide Synthesis*, 2nd Ed., Pierce Chemical Co., Rockford, Ill., pp. 11-12)) and have recently been employed in commercially available laboratory peptide design and synthesis kits (Cambridge Research Biochemicals). Such commercially available laboratory kits have generally utilized the teachings of H. M. Geysen *et al*, *Proc. Natl. Acad. Sci., USA*, 81:3998

(1984) and provide for synthesizing peptides upon the tips of a multitude of "rods" or "pins" all of which are connected to a single plate.

Polypeptides of the invention can also be shorter than the full length of exemplary polypeptides. In alternative aspects, the invention provides polypeptides (peptides, fragments) ranging in size between about 5 and the full length of a polypeptide, e.g., an enzyme, such as a polypeptide, enzyme, protein, e.g. structural or binding protein,; exemplary sizes being of about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 125, 150, 175, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, or more residues, e.g., contiguous residues of an exemplary a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention. Peptides of the invention (e.g., a subsequence of an exemplary polypeptide of the invention) can be useful as, e.g., labeling probes, antigens, toleragens, motifs, a polypeptide, enzyme, protein, e.g. structural or binding protein, active sites (e.g., "catalytic domains"), signal sequences and/or prepro domains.

In alternative aspects, polypeptides of the invention having enzyme, structural or binding activity are members of a genus of polypeptides sharing specific structural elements, e.g., amino acid residues, that correlate with enzyme, structural or binding activity. These shared structural elements can be used for the routine generation of polypeptide, enzyme, protein, e.g. structural or binding protein, variants. These shared structural elements of a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention can be used as guidance for the routine generation of a polypeptide, enzyme, protein, e.g. structural or binding protein, variants within the scope of the genus of polypeptides of the invention.

Polypeptides and peptides of the invention can be isolated from natural sources, be synthetic, or be recombinantly generated polypeptides. Peptides and proteins can be recombinantly expressed *in vitro* or *in vivo*. The peptides and polypeptides of the invention can be made and isolated using any method known in the art. Polypeptide and peptides of the invention can also be synthesized, whole or in part, using chemical methods well known in the art. See e.g., Caruthers (1980) Nucleic Acids Res. Symp. Ser. 215-223; Horn (1980) Nucleic Acids Res. Symp. Ser. 225-232; Banga, A.K., Therapeutic Peptides and Proteins, Formulation, Processing and Delivery Systems (1995) Technomic Publishing Co., Lancaster, PA. For example, peptide synthesis can be performed using various solid-phase techniques (see e.g., Roberge (1995) Science 269:202; Merrifield (1997) Methods Enzymol. 289:3-13) and automated synthesis may be achieved, e.g.,

using the ABI 431A Peptide Synthesizer (Perkin Elmer) in accordance with the instructions provided by the manufacturer.

The peptides and polypeptides of the invention can also be glycosylated. The glycosylation can be added post-translationally either chemically or by cellular biosynthetic mechanisms, wherein the later incorporates the use of known glycosylation motifs, which can be native to the sequence or can be added as a peptide or added in the nucleic acid coding sequence. The glycosylation can be O-linked or N-linked.

The peptides and polypeptides of the invention, as defined above, include all "mimetic" and "peptidomimetic" forms. The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound which has substantially the same structural and/or functional characteristics of the polypeptides of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogues of amino acids, or, is a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity. As with polypeptides of the invention which are conservative variants or members of a genus of polypeptides of the invention (e.g., having about 50% or more sequence identity to an exemplary sequence of the invention), routine experimentation will determine whether a mimetic is within the scope of the invention, i.e., that its structure and/or function is not substantially altered. Thus, in one aspect, a mimetic composition is within the scope of the invention if it has a polypeptide, enzyme, protein, e.g. structural or binding protein's activity.

Polypeptide mimetic compositions of the invention can contain any combination of non-natural structural components. In alternative aspect, mimetic compositions of the invention include one or all of the following three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, i.e., to induce or stabilize a secondary structure, e.g., a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. For example, a polypeptide of the invention can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, e.g., glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-

diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, e.g., ketomethylene (e.g., $-C(=O)-CH_2-$ for $-C(=O)-NH-$), aminomethylene (CH_2-NH), ethylene, olefin ($CH=CH$), ether (CH_2-O), thioether (CH_2-S), tetrazole (CN_4), thiazole, retroamide, thioamide, or ester (see, e.g., Spatola (1983) in *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, Vol. 7, pp 267-357, "Peptide Backbone Modifications," Marcell Dekker, NY).

A polypeptide of the invention can also be characterized as a mimetic by containing all or some non-natural residues in place of naturally occurring amino acid residues. Non-natural residues are well described in the scientific and patent literature; a few exemplary non-natural compositions useful as mimetics of natural amino acid residues and guidelines are described below. Mimetics of aromatic amino acids can be generated by replacing by, e.g., D- or L- naphylalanine; D- or L- phenylglycine; D- or L- 2 thieneylalanine; D- or L-1, -2, 3-, or 4- pyreneylalanine; D- or L-3 thieneylalanine; D- or L-(2-pyridinyl)-alanine; D- or L-(3-pyridinyl)-alanine; D- or L-(2-pyrazinyl)-alanine; D- or L-(4-isopropyl)-phenylglycine; D-(trifluoromethyl)-phenylglycine; D-(trifluoromethyl)-phenylalanine; D-p-fluoro-phenylalanine; D- or L-p-biphenylphenylalanine; D- or L-p-methoxy-biphenylphenylalanine; D- or L-2-indole(alkyl)alanines; and, D- or L-alkylainines, where alkyl can be substituted or unsubstituted methyl, ethyl, propyl, hexyl, butyl, pentyl, isopropyl, iso-butyl, sec-isotyl, iso-pentyl, or a non-acidic amino acids. Aromatic rings of a non-natural amino acid include, e.g., thiazolyl, thiophenyl, pyrazolyl, benzimidazolyl, naphthyl, furanyl, pyrrolyl, and pyridyl aromatic rings.

Mimetics of acidic amino acids can be generated by substitution by, e.g., non-carboxylate amino acids while maintaining a negative charge; (phosphono)alanine; sulfated threonine. Carboxyl side groups (e.g., aspartyl or glutamyl) can also be selectively modified by reaction with carbodiimides ($R'-N-C-N-R'$) such as, e.g., 1-cyclohexyl-3(2-morpholinyl-(4-ethyl) carbodiimide or 1-ethyl-3(4-azonia- 4,4-dimetholpentyl) carbodiimide. Aspartyl or glutamyl can also be converted to asparaginyll and glutaminyl residues by reaction with ammonium ions. Mimetics of basic amino acids can be generated by substitution with, e.g., (in addition to lysine and arginine) the amino acids ornithine, citrulline, or (guanidino)-acetic acid, or (guanidino)alkyl-acetic acid, where alkyl is defined above. Nitrile derivative (e.g., containing the CN-moiety in place of COOH) can be substituted for asparagine or glutamine. Asparaginyll and glutaminyl

residues can be deaminated to the corresponding aspartyl or glutamyl residues. Arginine residue mimetics can be generated by reacting arginyl with, e.g., one or more conventional reagents, including, e.g., phenylglyoxal, 2,3-butanedione, 1,2-cyclohexanedione, or ninhydrin, in one aspect under alkaline conditions. Tyrosine residue mimetics can be generated by reacting tyrosyl with, e.g., aromatic diazonium compounds or tetranitromethane. N-acetylimidizol and tetranitromethane can be used to form O-acetyl tyrosyl species and 3-nitro derivatives, respectively. Cysteine residue mimetics can be generated by reacting cysteinyl residues with, e.g., alpha-haloacetates such as 2-chloroacetic acid or chloroacetamide and corresponding amines; to give carboxymethyl or carboxyamidomethyl derivatives. Cysteine residue mimetics can also be generated by reacting cysteinyl residues with, e.g., bromo-trifluoroacetone, alpha-bromo-beta-(5-imidazolyl) propionic acid; chloroacetyl phosphate, N-alkylmaleimides, 3-nitro-2-pyridyl disulfide; methyl 2-pyridyl disulfide; p-chloromercuribenzoate; 2-chloromercuri-4-nitrophenol; or, chloro-7-nitrobenzo-oxa-1,3-diazole. Lysine mimetics can be generated (and amino terminal residues can be altered) by reacting lysinyl with, e.g., succinic or other carboxylic acid anhydrides. Lysine and other alpha-amino-containing residue mimetics can also be generated by reaction with imidoesters, such as methyl picolinimidate, pyridoxal phosphate, pyridoxal, chloroborohydride, trinitrobenzenesulfonic acid, O-methylisourea, 2,4, pentanedione, and transamidase-catalyzed reactions with glyoxylate. Mimetics of methionine can be generated by reaction with, e.g., methionine sulfoxide. Mimetics of proline include, e.g., pipecolic acid, thiazolidine carboxylic acid, 3- or 4- hydroxy proline, dehydropoline, 3- or 4-methylproline, or 3,3,-dimethylproline. Histidine residue mimetics can be generated by reacting histidyl with, e.g., diethylprocarbonate or para-bromophenacyl bromide. Other mimetics include, e.g., those generated by hydroxylation of proline and lysine; phosphorylation of the hydroxyl groups of seryl or threonyl residues; methylation of the alpha-amino groups of lysine, arginine and histidine; acetylation of the N-terminal amine; methylation of main chain amide residues or substitution with N-methyl amino acids; or amidation of C-terminal carboxyl groups.

A residue, e.g., an amino acid, of a polypeptide of the invention can also be replaced by an amino acid (or peptidomimetic residue) of the opposite chirality. Thus, any amino acid naturally occurring in the L-configuration (which can also be referred to as the R or S, depending upon the structure of the chemical entity) can be replaced with the amino acid of the same chemical structural type or a peptidomimetic, but of the

opposite chirality, referred to as the D- amino acid, but also can be referred to as the R- or S- form.

The invention also provides methods for modifying the polypeptides of the invention by either natural processes, such as post-translational processing (e.g., phosphorylation, acylation, etc), or by chemical modification techniques, and the resulting modified polypeptides. Modifications can occur anywhere in the polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also a given polypeptide may have many types of modifications. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of a phosphatidylinositol, cross-linking cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, and transfer-RNA mediated addition of amino acids to protein such as arginylation. See, e.g., Creighton, T.E., *Proteins – Structure and Molecular Properties* 2nd Ed., W.H. Freeman and Company, New York (1993); *Posttranslational Covalent Modification of Proteins*, B.C. Johnson, Ed., Academic Press, New York, pp. 1-12 (1983).

Solid-phase chemical peptide synthesis methods can also be used to synthesize the polypeptide or fragments of the invention. Such method have been known in the art since the early 1960's (Merrifield, R. B., *J. Am. Chem. Soc.*, 85:2149-2154, 1963) (See also Stewart, J. M. and Young, J. D., *Solid Phase Peptide Synthesis*, 2nd Ed., Pierce Chemical Co., Rockford, Ill., pp. 11-12)) and have recently been employed in commercially available laboratory peptide design and synthesis kits (Cambridge Research Biochemicals). Such commercially available laboratory kits have generally utilized the teachings of H. M. Geysen et al, *Proc. Natl. Acad. Sci., USA*, 81:3998 (1984) and provide for synthesizing peptides upon the tips of a multitude of "rods" or "pins" all of which are connected to a single plate. When such a system is utilized, a plate of rods or pins is inverted and inserted into a second plate of corresponding wells or reservoirs, which contain solutions for attaching or anchoring an appropriate amino acid to the pin's or rod's

tips. By repeating such a process step, i.e., inverting and inserting the rod's and pin's tips into appropriate solutions, amino acids are built into desired peptides. In addition, a number of available Fmoc peptide synthesis systems are available. For example, assembly of a polypeptide or fragment can be carried out on a solid support using an Applied Biosystems, Inc. Model 431A™ automated peptide synthesizer. Such equipment provides ready access to the peptides of the invention, either by direct synthesis or by synthesis of a series of fragments that can be coupled using other known techniques.

The polypeptides of the invention include a polypeptide, enzyme, protein, e.g. structural or binding protein, in an active or inactive form. For example, the polypeptides of the invention include proproteins before "maturation" or processing of prepro sequences, e.g., by a proprotein-processing enzyme, such as a proprotein convertase to generate an "active" mature protein. The polypeptides of the invention include a polypeptide, enzyme, protein, e.g. structural or binding protein, inactive for other reasons, e.g., before "activation" by a post-translational processing event, e.g., an endo- or exo-peptidase or proteinase action, a phosphorylation event, an amidation, a glycosylation or a sulfation, a dimerization event, and the like. The polypeptides of the invention include all active forms, including active subsequences, e.g., catalytic domains or active sites, of the enzyme.

The invention includes immobilized polypeptides, enzymes, proteins, e.g. structural or binding proteins, anti-polypeptides, anti-enzymes, anti-proteins, e.g. anti-structural or anti-binding proteins, antibodies and fragments thereof. The invention provides methods for inhibiting a polypeptide, enzyme, protein, e.g. structural or binding protein, activity, e.g., using dominant negative mutants or anti-polypeptide, anti-enzyme, anti-protein, e.g. anti-structural or anti-binding protein antibodies of the invention. The invention includes heterocomplexes, e.g., fusion proteins, heterodimers, etc., comprising the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention.

Polypeptides of the invention can have an enzyme, structural or binding activity under various conditions, e.g., extremes in pH and/or temperature, oxidizing agents, and the like. The invention provides methods leading to alternative a polypeptide, enzyme, protein, e.g. structural or binding protein, preparations with different catalytic efficiencies and stabilities, e.g., towards temperature, oxidizing agents and changing wash conditions. In one aspect, a polypeptide, enzyme, protein, e.g. structural or binding protein, variants can be produced using techniques of site-directed mutagenesis and/or random mutagenesis. In one aspect, directed evolution can be used to produce a great

variety of a polypeptide, enzyme, protein, e.g. structural or binding protein, variants with alternative specificities and stability.

The proteins of the invention are also useful as research reagents to identify a polypeptide, enzyme, protein, e.g. structural or binding protein, modulators, e.g., activators or inhibitors of a polypeptide, enzyme, protein, e.g. structural or binding protein, activity. Briefly, test samples (compounds, broths, extracts, and the like) are added to a polypeptide, enzyme, protein, e.g. structural or binding protein, assays to determine their ability to inhibit substrate cleavage. Inhibitors identified in this way can be used in industry and research to reduce or prevent undesired proteolysis. As with a polypeptide, enzyme, protein, e.g. structural or binding protein, inhibitors can be combined to increase the spectrum of activity.

The enzymes of the invention are also useful as research reagents to digest proteins or in protein sequencing. For example, the polypeptide, enzyme, protein, e.g. structural or binding proteins may be used to break polypeptides into smaller fragments for sequencing using, e.g. an automated sequencer.

The invention also provides methods of discovering new a polypeptide, enzyme, protein, e.g. structural or binding protein, using the nucleic acids, polypeptides and antibodies of the invention. In one aspect, phagemid libraries are screened for expression-based discovery of a polypeptide, enzyme, protein, e.g. structural or binding protein, . In another aspect, lambda phage libraries are screened for expression-based discovery of a polypeptide, enzyme, protein, e.g. structural or binding protein, . Screening of the phage or phagemid libraries can allow the detection of toxic clones; improved access to substrate; reduced need for engineering a host, by-passing the potential for any bias resulting from mass excision of the library; and, faster growth at low clone densities. Screening of phage or phagemid libraries can be in liquid phase or in solid phase. In one aspect, the invention provides screening in liquid phase. This gives a greater flexibility in assay conditions; additional substrate flexibility; higher sensitivity for weak clones; and ease of automation over solid phase screening.

The invention provides screening methods using the proteins and nucleic acids of the invention and robotic automation to enable the execution of many thousands of biocatalytic reactions and screening assays in a short period of time, e.g., per day, as well as ensuring a high level of accuracy and reproducibility (see discussion of arrays, below). As a result, a library of derivative compounds can be produced in a matter of

weeks. For further teachings on modification of molecules, including small molecules, see PCT/US94/09174.

In one aspect, polypeptides or fragments of the invention may be obtained through biochemical enrichment or purification procedures. The sequence of potentially homologous polypeptides or fragments may be determined by a polypeptide, enzyme, protein, e.g. structural or binding protein, assays, gel electrophoresis and/or microsequencing. The sequence of the prospective polypeptide or fragment of the invention can be compared to an exemplary polypeptide of the invention, or a fragment, e.g., comprising at least about 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 or more consecutive amino acids thereof using any of the programs described above.

Another aspect of the invention is an assay for identifying fragments or variants of the invention, which retain the enzymatic function of the polypeptides of the invention. For example the fragments or variants of said polypeptides, may be used to catalyze biochemical reactions (e.g., production of a nootkatone from a valencene), which indicate that the fragment or variant retains the enzymatic activity of a polypeptide of the invention.

An exemplary assay for determining if fragments of variants retain the enzymatic activity of the polypeptides of the invention includes the steps of: contacting the polypeptide fragment or variant with a substrate molecule under conditions which allow the polypeptide fragment or variant to function and detecting either a decrease in the level of substrate or an increase in the level of the specific reaction product of the reaction between the polypeptide and substrate.

The present invention exploits the unique catalytic properties of enzymes. Whereas the use of biocatalysts (i.e., purified or crude enzymes, non-living or living cells) in chemical transformations normally requires the identification of a particular biocatalyst that reacts with a specific starting compound, the present invention uses selected biocatalysts and reaction conditions that are specific for functional groups that are present in many starting compounds, such as small molecules. Each biocatalyst is specific for one functional group, or several related functional groups and can react with many starting compounds containing this functional group.

The biocatalytic reactions produce a population of derivatives from a single starting compound. These derivatives can be subjected to another round of biocatalytic reactions to produce a second population of derivative compounds. Thousands of

variations of the original small molecule or compound can be produced with each iteration of biocatalytic derivatization.

Enzymes react at specific sites of a starting compound without affecting the rest of the molecule, a process which is very difficult to achieve using traditional chemical methods. This high degree of biocatalytic specificity provides the means to identify a single active compound within the library. The library is characterized by the series of biocatalytic reactions used to produce it, a so-called "biosynthetic history". Screening the library for biological activities and tracing the biosynthetic history identifies the specific reaction sequence producing the active compound. The reaction sequence is repeated and the structure of the synthesized compound determined. This mode of identification, unlike other synthesis and screening approaches, does not require immobilization technologies and compounds can be synthesized and tested free in solution using virtually any type of screening assay. It is important to note, that the high degree of specificity of enzyme reactions on functional groups allows for the "tracking" of specific enzymatic reactions that make up the biocatalytically produced library.

Many of the procedural steps are performed using robotic automation enabling the execution of many thousands of biocatalytic reactions and screening assays per day as well as ensuring a high level of accuracy and reproducibility. As a result, a library of derivative compounds can be produced in a matter of weeks, which would take years to produce using current chemical methods.

In a particular aspect, the invention provides a method for modifying small molecules, comprising contacting a polypeptide encoded by a polynucleotide described herein or enzymatically active fragments thereof with a small molecule to produce a modified small molecule. A library of modified small molecules is tested to determine if a modified small molecule is present within the library, which exhibits a desired activity. A specific biocatalytic reaction which produces the modified small molecule of desired activity is identified by systematically eliminating each of the biocatalytic reactions used to produce a portion of the library and then testing the small molecules produced in the portion of the library for the presence or absence of the modified small molecule with the desired activity. The specific biocatalytic reactions which produce the modified small molecule of desired activity is optionally repeated. The biocatalytic reactions are conducted with a group of biocatalysts that react with distinct structural moieties found within the structure of a small molecule, each biocatalyst is specific for one structural

moiety or a group of related structural moieties; and each biocatalyst reacts with many different small molecules which contain the distinct structural moiety.

A polypeptide, enzyme, protein, e.g. structural or binding protein, signal sequences, prepro and catalytic domains

The invention provides a polypeptide, enzyme, protein, e.g. structural or binding protein, signal sequences (e.g., signal peptides (SPs)), prepro domains and catalytic domains (CDs). The SPs, prepro domains and/or CDs of the invention can be isolated or recombinant peptides or can be part of a fusion protein, e.g., as a heterologous domain in a chimeric protein. The invention provides nucleic acids encoding these catalytic domains (CDs), prepro domains and signal sequences (SPs, e.g., a peptide having a sequence comprising/ consisting of amino terminal residues of a polypeptide of the invention).

The invention provides isolated or recombinant signal sequences (e.g., signal peptides) consisting of or comprising a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1 to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43, 1 to 44, 1 to 45, 1 to 46, or 1 to 47, or more, of a polypeptide of the invention, e.g., SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, and all polypeptides disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:3 through SEQ ID NO:26,898. In one aspect, the invention provides signal sequences comprising the first 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70 or more amino terminal residues of a polypeptide of the invention.

The invention also provides isolated or recombinant signal sequences comprising/ consisting of the signal sequences set forth in Table 4, and polypeptides comprising these signal sequences. The polypeptide can be enzyme or protein of the invention. For example, reading Table 4, the invention provides an isolated or recombinant signal sequence as set forth by residues 1 to 16 of SEQ ID NO:10010. This can be determined by reading the second column for the first row, "Probability: 0.992 AA1: 16 AA2: 17", wherein the cleavage of signal sequence takes place between amino acid 16 (AA16) and amino acid 17 (AA17), with a probability of 0.992 that this is the correct cleavage site. Therefore, the signal sequence is predicted to be from the amino acid in position 1 of SEQ ID NO:10010 up to and including the amino acid in position 16 of SEQ ID NO:10010. This signal sequence, in one aspect, is encoded by a subsequence of SEQ ID NO:10009.

Table 4

SEQ ID NO:	Signalp Cleavage Site	Predicted Signal Sequence
10009, 10010	Probability: 0.992 AA1: 16 AA2: 17	MKSYFLLLLFLLPLFA
10111, 10112	Probability: 0.964 AA1: 17 AA2: 18	MKYIFILVFLTTTLFA
1013, 1014	Probability: 0.584 AA1: 20 AA2: 21	MKRVLLAIIIGIILAIIVVVG
10147, 10148	Probability: 0.999 AA1: 19 AA2: 20	MNKILIFIIISLFSNLISA
10157, 10158	Probability: 0.941 AA1: 19 AA2: 20	MLKRIFILSLAILICSNG
10217, 10218	Probability: 0.999 AA1: 18 AA2: 19	MKKISILIIFILSTLTLS
10309, 10310	Probability: 0.994 AA1: 20 AA2: 21	MRANLKKSYYLIGLLLLFSLA
10327, 10328	Probability: 0.647 AA1: 16 AA2: 17	MRYLFSLFIFTTLIFA
10355, 10356	Probability: 0.592 AA1: 19 AA2: 20	MTKKVIVLSLIILLFINSS
10441, 10442	Probability: 0.683 AA1: 17 AA2: 18	MKRTFLTITAAAFILVG
10447, 10448	Probability: 0.928 AA1: 17 AA2: 18	MKNKLIIILFIFSLFLLA
10525, 10526	Probability: 0.728 AA1: 16 AA2: 17	MRVLFFIFISLTTLFA
10537, 10538	Probability: 0.998 AA1: 17 AA2: 18	MKKIILLSTLLFLALNA
10543, 10544	Probability: 0.991 AA1: 17 AA2: 18	MKRKWFIFILTALVTIA
10591, 10592	Probability: 0.922 AA1: 17 AA2: 18	MFKLLIGIFISVAYS
10659, 10660	Probability: 0.967 AA1: 20 AA2: 21	MKDVIIGAGGAGLSAGLSA
10673, 10674	Probability: 0.711 AA1: 19 AA2: 20	MKIWSTIKLVFISLVALVA
10711, 10712	Probability: 0.876 AA1: 16 AA2: 17	MMKGISPGAALVFLMA
10731, 10732	Probability: 0.997 AA1: 19 AA2: 20	MLKLLMITILLSTSGVANS
1079, 1080	Probability: 0.929 AA1: 17 AA2: 18	MRIIKLFALFFLTACN
10915, 10916	Probability: 0.934 AA1: 17 AA2: 18	MKSRLLLSGFFIFVLMS
11047, 11048	Probability: 0.530 AA1: 16 AA2: 17	MPEAAFSMSLPSKVFA
1109, 1110	Probability: 0.777 AA1: 18 AA2: 19	MKVLLYILILFSGFKSFG
1111, 1112	Probability: 0.765 AA1: 18 AA2: 19	MKVLLYILILFSGFKSFG
1119, 1120	Probability: 0.870 AA1: 18 AA2: 19	MKKLFLILCIFFSVESFS
11209, 11210	Probability: 0.910 AA1: 19 AA2: 20	MKQIILLFSILFIVGKSYS
11253, 11254	Probability: 0.987 AA1: 19 AA2: 20	MKNIFFFSILLFLSFTGKA
11339, 11340	Probability: 0.510 AA1: 19 AA2: 20	MLKSISLFILITIVTGCSV
1137, 1138	Probability: 0.992 AA1: 18 AA2: 19	MKILTIVFLVGFFCFVQA
11401, 11402	Probability: 0.992 AA1: 19 AA2: 20	MTISKKNKLLIASLLSVAFT
11495, 11496	Probability: 0.647 AA1: 16 AA2: 17	MRYLFSLFIFTTLIFA

11719, 11720	Probability: 0.998 AA1: 17 AA2: 18	MKIILLIFFLLLSFSFA
11745, 11746	Probability: 0.972 AA1: 18 AA2: 19	MKYKIIFFIAAFMAFSTLV
1177, 1178	Probability: 0.995 AA1: 20 AA2: 21	MDQKKSLSLLFLIPAVSVIA
11821, 11822	Probability: 0.663 AA1: 18 AA2: 19	MSNKSIVSTLIISIFFTA
11827, 11828	Probability: 0.727 AA1: 19 AA2: 20	MYVMKILLISILFYCLLA
11935, 11936	Probability: 1.000 AA1: 20 AA2: 21	MKKTILIASLFVAAFVIGQA
11965, 11966	Probability: 0.999 AA1: 19 AA2: 20	MKKILVLSVLLTVCLISFA
12071, 12072	Probability: 0.773 AA1: 19 AA2: 20	MNKELLSFFSIFIALFVGA
12157, 12158	Probability: 0.983 AA1: 16 AA2: 17	MRLLLLLSLLVYTVFA
12377, 12378	Probability: 0.562 AA1: 15 AA2: 16	MASTTMIVSLIVAVA
12709, 12710	Probability: 0.993 AA1: 18 AA2: 19	MNNLKQILAIVMLLSVTA
13005, 13006	Probability: 0.977 AA1: 20 AA2: 21	MFLRRLSILILLFVFFTA
13017, 13018	Probability: 0.995 AA1: 17 AA2: 18	MFKNIIMSLLLCTFLSA
13139, 13140	Probability: 0.849 AA1: 17 AA2: 18	MRVVVLVLFSLHFLFA
13307, 13308	Probability: 0.995 AA1: 19 AA2: 20	MKKLILLILGFSTNLIFS
13347, 13348	Probability: 0.788 AA1: 18 AA2: 19	MLLILICAVYSVGCALA
1343, 1344	Probability: 0.708 AA1: 18 AA2: 19	MKSIIIFSLILFFTACK
13475, 13476	Probability: 0.998 AA1: 17 AA2: 18	MKIILLIFFLLLSFSFA
13531, 13532	Probability: 0.651 AA1: 17 AA2: 18	MSHLLFSTSVLILLVVS
13543, 13544	Probability: 0.995 AA1: 19 AA2: 20	MKFILTTLMMAYLILPGMA
13603, 13604	Probability: 0.734 AA1: 18 AA2: 19	MNFKNILYSLLISGCLYG
13607, 13608	Probability: 0.840 AA1: 19 AA2: 20	MKKIILSLGVATLLLTNL
13699, 13700	Probability: 0.544 AA1: 21 AA2: 22	MMKLHTLISLIFAVLMFIFCM
13711, 13712	Probability: 0.815 AA1: 20 AA2: 21	MSNKSIVSTLIISIFFTACT
13719, 13720	Probability: 1.000 AA1: 20 AA2: 21	MKLTKIITVFMVFSLSLMA
13777, 13778	Probability: 0.682 AA1: 19 AA2: 20	MKSMRTIFISFLIILLQG
13829, 13830	Probability: 0.940 AA1: 19 AA2: 20	MKNLGLILLVFLGLISTS
13891, 13892	Probability: 0.993 AA1: 16 AA2: 17	MKYFLLLLLIITLNA
13915, 13916	Probability: 1.000 AA1: 20 AA2: 21	MKKFFLALFLTSIVTISIAA
13933, 13934	Probability: 0.962 AA1: 19 AA2: 20	MFMNKKVYISLITALVNA
14081, 14082	Probability: 0.918 AA1: 18 AA2: 19	MTYLFLAIAIGLITAASK
14133, 14134	Probability: 0.989 AA1: 20 AA2: 21	MNNLIKILLITLSFSLLS
14197, 14198	Probability: 0.995 AA1: 18 AA2: 19	MKKITLILFAIFTALSMS
14267, 14268	Probability: 0.815 AA1: 20 AA2: 21	MSNKSIVSTLIISIFFTACT
14369, 14370	Probability: 0.669 AA1: 17 AA2: 18	MKKYIIIFCIFSGLYG
14505, 14506	Probability: 0.951 AA1: 20 AA2: 21	MIRFGSSSSSILYFFRNTMA
14573, 14574	Probability: 0.992 AA1: 19 AA2: 20	MLRWFILLISVIVCLNVNA
1461, 1462	Probability: 0.908 AA1: 19 AA2: 20	MKKFLIFCLFLFNKPLIS
14655, 14656	Probability: 0.773 AA1: 22 AA2: 23	MAQAVAIISIAFFSVLLSLLFN
14705, 14706	Probability: 0.599 AA1: 21 AA2: 22	MGGLIAIILSSRTVAPLGQA
14835, 14836	Probability: 0.999 AA1: 17 AA2: 18	MVKKLLFLALAFSISFA
14857, 14858	Probability: 1.000 AA1: 21 AA2: 22	MIRQKIVLTMLLFCFSLITVA
14863, 14864	Probability: 0.990 AA1: 17 AA2: 18	MRKYFLVLLLFCTSLLS
15045, 15046	Probability: 0.984 AA1: 21 AA2: 22	MKNIILSTLAFVLALFFSGCT
15049, 15050	Probability: 0.845 AA1: 19 AA2: 20	MNFFIMPFLMFLFIGIFA
15055, 15056	Probability: 0.669 AA1: 15 AA2: 16	MKFNLNSFLMSVSLA
15111, 15112	Probability: 0.835 AA1: 17 AA2: 18	MIKRLFSIVLSGLVFN
15135, 15136	Probability: 0.853 AA1: 15 AA2: 16	MKYLLALCIFLLLTG
15173, 15174	Probability: 0.513 AA1: 19 AA2: 20	MKKLNVAIYIVILSLFS
15179, 15180	Probability: 0.645 AA1: 16 AA2: 17	MRYLFSLFIFTTLIFA
15201, 15202	Probability: 0.883 AA1: 20 AA2: 21	MKLLGIGSILLQVLLCSVSA
15235, 15236	Probability: 0.792 AA1: 19 AA2: 20	MNFKQLFLSVLLILTIVLS
15251, 15252	Probability: 0.998 AA1: 17 AA2: 18	MKIILLIFFLLLSFSFA
153, 154	Probability: 0.824 AA1: 20 AA2: 21	MIKTIXSLARCIIAFGILNA
15329, 15330	Probability: 0.557 AA1: 20 AA2: 21	MKNYKILLLSLLIISILG

1541, 1542	Probability: 1.000 AA1: 19 AA2: 20	MKRNSLLLVLLALSFTAA
15473, 15474	Probability: 0.934 AA1: 19 AA2: 20	MRGTICSILISFIFLITA
15475, 15476	Probability: 0.934 AA1: 20 AA2: 21	MAAGDFFAIFGIFMSLSLLA
15495, 15496	Probability: 0.645 AA1: 16 AA2: 17	MRYLFSLFIFTTLIFA
15521, 15522	Probability: 0.972 AA1: 18 AA2: 19	MIKVSIVVLLLSYIHA
15585, 15586	Probability: 0.993 AA1: 16 AA2: 17	MKLLLLLFLVLLNVNA
15589, 15590	Probability: 0.967 AA1: 17 AA2: 18	MNKKILILMILGLAVA
15623, 15624	Probability: 0.553 AA1: 18 AA2: 19	MSSRVFLTSFLIIVPLTA
15635, 15636	Probability: 1.000 AA1: 19 AA2: 20	MKNILSIALAVLMIGSLHS
15659, 15660	Probability: 1.000 AA1: 20 AA2: 21	MYKFITALISLFLTTTHSYA
15697, 15698	Probability: 0.561 AA1: 18 AA2: 19	MISIKTAIAIILVIVATN
15765, 15766	Probability: 0.936 AA1: 18 AA2: 19	MKFHKSLLLLLLSFIVS
15783, 15784	Probability: 0.951 AA1: 20 AA2: 21	MKIAVLGAGISGLGSAYLLS
1585, 1586	Probability: 0.668 AA1: 19 AA2: 20	MMFFTSISIXSFXPIXIXLX
15855, 15856	Probability: 0.677 AA1: 18 AA2: 19	MKKLKLILGSVLSIVAF
15873, 15874	Probability: 0.784 AA1: 16 AA2: 17	MIFFFIFVILFTFSVA
15907, 15908	Probability: 0.998 AA1: 20 AA2: 21	MSLKKYIFILTLFISNLFA
15909, 15910	Probability: 0.935 AA1: 20 AA2: 21	MKQKLLKITLTLTLLTSAIA
16005, 16006	Probability: 0.932 AA1: 20 AA2: 21	MLKNLKNILFFLFFLIFCLN
16015, 16016	Probability: 0.541 AA1: 16 AA2: 17	MIIAISALIATTIIA
16171, 16172	Probability: 0.985 AA1: 20 AA2: 21	MKLNLGKIFLLLIFPIITFA
16175, 16176	Probability: 0.957 AA1: 17 AA2: 18	MMKTFIVFCVMSISIFA
16183, 16184	Probability: 0.999 AA1: 20 AA2: 21	MKLISKILLILAITSGVLS
16237, 16238	Probability: 0.792 AA1: 19 AA2: 20	MNFKQLFLSVLLILTIVLS
16289, 16290	Probability: 0.995 AA1: 16 AA2: 17	MRISILLAVVSSIIFA
163, 164	Probability: 0.860 AA1: 20 AA2: 21	MQINRLIVLLIMISHKNFA
1633, 1634	Probability: 0.993 AA1: 19 AA2: 20	MKIYVILALLIFSSRSIYS
16339, 16340	Probability: 1.000 AA1: 18 AA2: 19	MKKLLLIYILLSTITFA
16345, 16346	Probability: 0.776 AA1: 19 AA2: 20	MGNIKVILVFISLFLIAIT
16373, 16374	Probability: 0.995 AA1: 16 AA2: 17	MRISILLAVVSSIIFA
1641, 1642	Probability: 0.879 AA1: 18 AA2: 19	MKKFILFLGFFYLISFFA
16455, 16456	Probability: 0.890 AA1: 19 AA2: 20	MKKFNKILIIIFISSLFLA
16467, 16468	Probability: 0.681 AA1: 20 AA2: 21	MERRFLKLGATILASSAVIA
1647, 1648	Probability: 0.812 AA1: 20 AA2: 21	MRLKLSLLILLFSGINGIA
16487, 16488	Probability: 0.987 AA1: 19 AA2: 20	MRIFNYLIMSILLSVTLMA
1669, 1670	Probability: 0.999 AA1: 18 AA2: 19	MRATFIVLSVLLTSSVMS
16711, 16712	Probability: 0.626 AA1: 17 AA2: 18	MFKTILFTFILITNIFS
16747, 16748	Probability: 0.628 AA1: 19 AA2: 20	MKNIFFLFIIVLILSNCKN
16825, 16826	Probability: 0.975 AA1: 18 AA2: 19	MFKKALLVFYIFLGITMA
16833, 16834	Probability: 0.857 AA1: 20 AA2: 21	MNNKTIFLPILLAMAIVLG
16885, 16886	Probability: 0.993 AA1: 16 AA2: 17	MKLLLLLFLVLLNVNA
16967, 16968	Probability: 0.888 AA1: 20 AA2: 21	MKPTKLLFGLFILIFTFTTS
17035, 17036	Probability: 0.977 AA1: 16 AA2: 17	MMKKYIIALISTFLYA
17065, 17066	Probability: 0.982 AA1: 17 AA2: 18	MKHFLLCVLLLGVLDA
171, 172	Probability: 0.956 AA1: 21 AA2: 22	MKRIIYIILLFSVAVILSSCT
17157, 17158	Probability: 0.952 AA1: 16 AA2: 17	MKILLIVLFISSLFS
17331, 17332	Probability: 0.981 AA1: 17 AA2: 18	MLKKLLILTFTTISFA
17347, 17348	Probability: 0.999 AA1: 16 AA2: 17	MSKIIILISFLIANA
17353, 17354	Probability: 0.993 AA1: 20 AA2: 21	MKLKYLIIIIITLGQFVIA
17359, 17360	Probability: 0.932 AA1: 19 AA2: 20	MKIKHFILLFLFSIALYS
17367, 17368	Probability: 0.912 AA1: 20 AA2: 21	MKKSILFLLLTLLIIMGIG
1749, 1750	Probability: 0.990 AA1: 18 AA2: 19	MNRIFLIVVLFISSTCFS
17537, 17538	Probability: 0.999 AA1: 17 AA2: 18	MKFFFILLILFMFNALS
17547, 17548	Probability: 0.959 AA1: 19 AA2: 20	MKNIIITYLFMLMSLFLLS
1771, 1772	Probability: 0.931 AA1: 20 AA2: 21	MVMKSILGIVSFLIGLSLIA

17751, 17752	Probability: 0.561 AA1: 18 AA2: 19	MKYLLILLLVFTGCNNV
17783, 17784	Probability: 0.987 AA1: 19 AA2: 20	MTKIKVVGLLVILSIALA
1785, 1786	Probability: 0.716 AA1: 17 AA2: 18	MKLLSATFFMVVFSVIS
17915, 17916	Probability: 0.898 AA1: 17 AA2: 18	MVKIFLSIILFVNIVFA
18019, 18020	Probability: 0.993 AA1: 18 AA2: 19	MKKITFLLILFVTTFSFS
18039, 18040	Probability: 0.867 AA1: 19 AA2: 20	MQKVILTLVCIITSFFFQA
18057, 18058	Probability: 0.874 AA1: 19 AA2: 20	MRFLFVLFTFLIFSCSKNS
18131, 18132	Probability: 1.000 AA1: 19 AA2: 20	MKKTQIILLILLSMASHA
18237, 18238	Probability: 0.975 AA1: 18 AA2: 19	MKKVLIFYCVLFSLQGF
18249, 18250	Probability: 0.719 AA1: 18 AA2: 19	MKTKTLLTVLTILFSLQS
18329, 18330	Probability: 0.988 AA1: 17 AA2: 18	MSKLAVLFLFLACNN
18377, 18378	Probability: 0.983 AA1: 18 AA2: 19	MKKARIILSFFIGMVAA
18403, 18404	Probability: 1.000 AA1: 19 AA2: 20	MKKTILVLICLFSISALFA
18435, 18436	Probability: 0.611 AA1: 19 AA2: 20	MKIGFILILSIAICTSCKV
18489, 18490	Probability: 0.914 AA1: 17 AA2: 18	MKKLTYLFLSITLLSFG
18495, 18496	Probability: 0.627 AA1: 19 AA2: 20	MKNSIAFLFLSLLIFTGCK
18507, 18508	Probability: 0.783 AA1: 20 AA2: 21	MKKIYLILASTIVLASCNGK
1851, 1852	Probability: 0.998 AA1: 18 AA2: 19	MKKFLAIFLFFIAFHGNA
18529, 18530	Probability: 0.999 AA1: 19 AA2: 20	MKKNITLLFGIVLVFAAYG
18587, 18588	Probability: 0.956 AA1: 19 AA2: 20	MSFFKPSFVLFFCLLGLHG
18607, 18608	Probability: 0.636 AA1: 18 AA2: 19	MHGLHSIFSLLFLCTL
18713, 18714	Probability: 1.000 AA1: 18 AA2: 19	MKKTLLFLFLSTLVVQA
18747, 18748	Probability: 0.985 AA1: 18 AA2: 19	MKKIYIFVILLSVSVSG
18825, 18826	Probability: 0.999 AA1: 18 AA2: 19	MKFILLAFFTLISNYALS
18841, 18842	Probability: 1.000 AA1: 19 AA2: 20	MLKSAIFVLVLSLVGSAFG
18919, 18920	Probability: 0.995 AA1: 20 AA2: 21	MHIFLKSFILFIFLSFILQA
18921, 18922	Probability: 0.998 AA1: 18 AA2: 19	MKNLIVLIFVVLTLQLSVA
18957, 18958	Probability: 0.719 AA1: 18 AA2: 19	MKTKTLLTVLTILFSLQS
18971, 18972	Probability: 0.775 AA1: 17 AA2: 18	MKKLIALFFLCILISCN
18977, 18978	Probability: 1.000 AA1: 17 AA2: 18	MKKLFLILMLPFSLLA
19079, 19080	Probability: 0.895 AA1: 19 AA2: 20	MKFFSALLILTLVITSCKS
19143, 19144	Probability: 0.610 AA1: 18 AA2: 19	MKKNQLSFLLLVFLISNT
1919, 1920	Probability: 0.996 AA1: 19 AA2: 20	MKTLIFFLILFFGSIPSYS
19211, 19212	Probability: 0.517 AA1: 19 AA2: 20	MFNKKQAITLFSGLLFCFT
19265, 19266	Probability: 1.000 AA1: 19 AA2: 20	MKKTILVLICLFSISALFA
19277, 19278	Probability: 0.945 AA1: 19 AA2: 20	MKFTSYLFFLFFIFMNCTA
19385, 19386	Probability: 0.835 AA1: 18 AA2: 19	MKKIIPYILSCMLLSLAA
19391, 19392	Probability: 0.999 AA1: 19 AA2: 20	MKSFLTILFSLFLTGSINS
19421, 19422	Probability: 0.998 AA1: 20 AA2: 21	MRKHQLLILILMLTSVSNS
19467, 19468	Probability: 0.994 AA1: 20 AA2: 21	MSNYLLSVILLAFILASCST
19475, 19476	Probability: 0.998 AA1: 19 AA2: 20	MKIRFYLSALFACLLFASS
19527, 19528	Probability: 0.998 AA1: 17 AA2: 18	MKKILLLLPLISILSYA
19535, 19536	Probability: 0.596 AA1: 20 AA2: 21	MKSIKKLFIFILVLYL
1955, 1956	Probability: 1.000 AA1: 19 AA2: 20	MRKIYGLLAFCLLMNTAKA
19563, 19564	Probability: 0.940 AA1: 20 AA2: 21	MKNSIAFLFLSLLIFTGCKS
19657, 19658	Probability: 0.994 AA1: 20 AA2: 21	MIAKKITLLILFVNQYVIA
19733, 19734	Probability: 0.938 AA1: 20 AA2: 21	MNITHGSGYVGLVSGTCFA
19785, 19786	Probability: 0.936 AA1: 19 AA2: 20	MRTLSFLIVTFSVLISGCA
19797, 19798	Probability: 1.000 AA1: 18 AA2: 19	MKTALFILFCTLGQMSLA
19915, 19916	Probability: 0.999 AA1: 17 AA2: 18	MKKLLILLFLFNSNLFA
19919, 19920	Probability: 0.676 AA1: 20 AA2: 21	MRISVFFYISLFIISSTKFS
19953, 19954	Probability: 1.000 AA1: 19 AA2: 20	MKKFLLFLVPLLAISGFA
19993, 19994	Probability: 0.575 AA1: 20 AA2: 21	MRTTLKRIAFLFFFSFLIFS
20001, 20002	Probability: 0.674 AA1: 18 AA2: 19	MKKIIFLLVTLLIFNSCK
2003, 2004	Probability: 1.000 AA1: 18 AA2: 19	MKVRYLLAFLIISASLA

20069, 20070	Probability: 1.000 AA1: 20 AA2: 21	MKIKIRCLLIFLTLSPFVQA
20083, 20084	Probability: 0.637 AA1: 20 AA2: 21	MILGLLLALIAIVFLFLK
20111, 20112	Probability: 1.000 AA1: 19 AA2: 20	MRKILFTCFLLILSLFSYA
20143, 20144	Probability: 0.946 AA1: 17 AA2: 18	MKKFIFSVLTLLLVGLS
20161, 20162	Probability: 0.602 AA1: 19 AA2: 20	MKSIYMAALIILSVKGTS
20187, 20188	Probability: 0.585 AA1: 20 AA2: 21	MKPMRNLLFLVLIANTSLL
20225, 20226	Probability: 1.000 AA1: 20 AA2: 21	MLQKTILVLLFLLTTSNSFS
20229, 20230	Probability: 0.522 AA1: 20 AA2: 21	MKFIINPILILLAVIILSLN
20253, 20254	Probability: 0.906 AA1: 20 AA2: 21	MKTILRLTICGLILLNASLA
203, 204	Probability: 0.824 AA1: 19 AA2: 20	MENKMKRLLTIFVFLIVFS
20301, 20302	Probability: 0.675 AA1: 19 AA2: 20	MIRIISFLLPLLFFLNCQK
20309, 20310	Probability: 0.989 AA1: 19 AA2: 20	MKMKFTFLLLIISTISIYG
20349, 20350	Probability: 0.967 AA1: 19 AA2: 20	MKKHLLFFLTILSISGYS
20371, 20372	Probability: 0.605 AA1: 18 AA2: 19	MNKLISIVLVCITLMSTG
2045, 2046	Probability: 0.906 AA1: 20 AA2: 21	MKKHLFITALLMLTVINYTG
20485, 20486	Probability: 0.951 AA1: 17 AA2: 18	MKNLFLFLTILSLSCMQ
20487, 20488	Probability: 0.951 AA1: 17 AA2: 18	MKNLFLFLTILSLSCMQ
20531, 20532	Probability: 0.895 AA1: 19 AA2: 20	MFSFLGVILIAFFGFIGFS
20569, 20570	Probability: 0.819 AA1: 19 AA2: 20	MKILLRISLLITTISCTS
20571, 20572	Probability: 0.819 AA1: 19 AA2: 20	MKILLRISLLITTISCTS
20665, 20666	Probability: 0.989 AA1: 18 AA2: 19	MRKKIFLVLIILMSLSLG
2071, 2072	Probability: 0.994 AA1: 19 AA2: 20	MKKIVSILVFLANLSQA
20735, 20736	Probability: 1.000 AA1: 18 AA2: 19	MKLFVTLVLFVFCVFATA
20743, 20744	Probability: 0.998 AA1: 19 AA2: 20	MKNVIVLFSVAMAFSCFS
20805, 20806	Probability: 0.962 AA1: 19 AA2: 20	MMLKKSILLSIAALFISSA
20881, 20882	Probability: 0.574 AA1: 18 AA2: 19	MRVFILISLFFTLFSCQ
2093, 2094	Probability: 0.641 AA1: 18 AA2: 19	MNFIIFCFVLLSGFLTG
21115, 21116	Probability: 0.990 AA1: 19 AA2: 20	MMKLYLFVFFFVIVAAGYA
21121, 21122	Probability: 0.680 AA1: 17 AA2: 18	MKPIYLIFSLLTFISLS
21133, 21134	Probability: 0.998 AA1: 19 AA2: 20	MKRTLVMVFLMTISQIQA
2115, 2116	Probability: 0.699 AA1: 20 AA2: 21	MKRHNIIYFAAILFACNGNT
2117, 2118	Probability: 0.999 AA1: 19 AA2: 20	MNKLFLSIVLILTCCQLSA
21307, 21308	Probability: 0.814 AA1: 16 AA2: 17	MRKIILSILGVLFIIA
21361, 21362	Probability: 0.856 AA1: 19 AA2: 20	MKKSLFFFTIIFCILFLSQ
21363, 21364	Probability: 0.856 AA1: 19 AA2: 20	MKKSLFFFTIIFCILFLSQ
21395, 21396	Probability: 0.698 AA1: 19 AA2: 20	MMKRVIVGLSGGVDSSVAA
21427, 21428	Probability: 0.971 AA1: 19 AA2: 20	MRNSVILSLIFVMISNQLS
21563, 21564	Probability: 0.984 AA1: 18 AA2: 19	MIRLITILLIISTNIYS
21595, 21596	Probability: 0.871 AA1: 18 AA2: 19	MNYSKLVAIFFIAMLSA
21755, 21756	Probability: 0.998 AA1: 18 AA2: 19	MKNILLTIALSFVNLFA
21773, 21774	Probability: 0.895 AA1: 19 AA2: 20	MKKKKKKKNXSGVSLSFDSA
21777, 21778	Probability: 0.845 AA1: 19 AA2: 20	MKYFVFFFSIILCSCSSSE
21845, 21846	Probability: 0.940 AA1: 19 AA2: 20	MKMILHTLFILLISIPLYA
21851, 21852	Probability: 0.976 AA1: 18 AA2: 19	MKKFFKFLGILLVVLIVA
21863, 21864	Probability: 0.818 AA1: 16 AA2: 17	MKALFFIIFVAIAVA
21939, 21940	Probability: 0.993 AA1: 18 AA2: 19	MKGIFYLLLFVSALSFS
21987, 21988	Probability: 0.875 AA1: 16 AA2: 17	MKKIMVLGILIVVFM
22293, 22294	Probability: 0.615 AA1: 20 AA2: 21	MRKSFKILFSILGILLLL
22337, 22338	Probability: 1.000 AA1: 19 AA2: 20	MKKIITLVALVFFSVSTFA
22363, 22364	Probability: 0.997 AA1: 18 AA2: 19	MKRLIMVIFLFLGVQSI
22455, 22456	Probability: 1.000 AA1: 18 AA2: 19	MKTVLLLLSILVSSYSLA
22467, 22468	Probability: 0.546 AA1: 17 AA2: 18	MARMRISVLFFMFCVFA
22491, 22492	Probability: 1.000 AA1: 18 AA2: 19	MKKKFLLLLLVTSATFA
22509, 22510	Probability: 1.000 AA1: 18 AA2: 19	MKKTLFFIAILLTFNSNA
22513, 22514	Probability: 0.542 AA1: 13 AA2: 14	MKKILTGVILTLA

22657, 22658	Probability: 1.000 AA1: 19 AA2: 20	MTKNLILLILVLIFNIGFA
22701, 22702	Probability: 0.970 AA1: 17 AA2: 18	MKKHALLVLVSLFSCG
22703, 22704	Probability: 0.984 AA1: 16 AA2: 17	MIYKKIVFLVTLAFA
22767, 22768	Probability: 0.988 AA1: 14 AA2: 15	MRLILLFTLCLAMA
22803, 22804	Probability: 0.575 AA1: 19 AA2: 20	MKKTTLIAIFLLIGLKIN
2281, 2282	Probability: 0.999 AA1: 18 AA2: 19	MKLFISLSLLFISIFVIA
22817, 22818	Probability: 0.934 AA1: 18 AA2: 19	MKKSIIISAIVLGFSLV
22903, 22904	Probability: 0.996 AA1: 20 AA2: 21	MKKLFTLLIMSLVSSCTDA
22953, 22954	Probability: 0.593 AA1: 18 AA2: 19	MTKILMVCLGNICRSPLA
22993, 22994	Probability: 1.000 AA1: 19 AA2: 20	MKNLVLSLFLIAISAFS
23055, 23056	Probability: 0.757 AA1: 18 AA2: 19	MKSIKFILVLFITVSIFS
23107, 23108	Probability: 0.782 AA1: 18 AA2: 19	MKKLFITFTLLLLIACK
23167, 23168	Probability: 0.816 AA1: 18 AA2: 19	MKKFLLIVCIGLLMFSFT
23175, 23176	Probability: 0.631 AA1: 18 AA2: 19	MNRLILLFSIFLISCYN
2321, 2322	Probability: 1.000 AA1: 20 AA2: 21	MFRKTILGGLAIIAALTINA
23253, 23254	Probability: 0.930 AA1: 19 AA2: 20	MKKIIFVLLIVLFLASCCK
23277, 23278	Probability: 0.814 AA1: 16 AA2: 17	MRKIILSILGVLFIIA
23279, 23280	Probability: 0.771 AA1: 18 AA2: 19	MKQYLVITFLLSLTLGFS
23323, 23324	Probability: 0.536 AA1: 19 AA2: 20	MKYIISILITVLITCNNHS
23339, 23340	Probability: 0.821 AA1: 18 AA2: 19	MMKKISLLILIIIGSCQT
2339, 2340	Probability: 1.000 AA1: 18 AA2: 19	MKKIFLSFCLLSSFIGFA
23415, 23416	Probability: 0.882 AA1: 19 AA2: 20	MIKSIYLLFLIFSLTIIA
23431, 23432	Probability: 0.926 AA1: 16 AA2: 17	MKNTILLSVILLLLFS
23549, 23550	Probability: 0.516 AA1: 17 AA2: 18	MNKLAVILLVVIVAFLS
23559, 23560	Probability: 0.998 AA1: 20 AA2: 21	MKKLFCILSILIFGCGSTS
23587, 23588	Probability: 0.862 AA1: 18 AA2: 19	MKKICFLFFCFMITYIavg
23631, 23632	Probability: 0.676 AA1: 18 AA2: 19	MKKLAVLIVLVCTILSCN
23635, 23636	Probability: 0.886 AA1: 16 AA2: 17	MKKIAVVFLLLIVVIS
23649, 23650	Probability: 0.993 AA1: 16 AA2: 17	MKKILTSLFFLLVLTA
23723, 23724	Probability: 0.996 AA1: 18 AA2: 19	MKLLKKILFALVILLAIA
23817, 23818	Probability: 0.635 AA1: 19 AA2: 20	MIMNKRSISVLLIAMMALL
23827, 23828	Probability: 0.871 AA1: 17 AA2: 18	MKNYILTTAALLAFLFT
23841, 23842	Probability: 0.647 AA1: 19 AA2: 20	MKKYFLIFMISALYSCGSA
23851, 23852	Probability: 0.861 AA1: 18 AA2: 19	MKKIITFLLLTIVLVSCG
23879, 23880	Probability: 0.710 AA1: 19 AA2: 20	MKEILSFILFTSVAINIIA
23913, 23914	Probability: 1.000 AA1: 19 AA2: 20	MKKSIIIVIVLIFGFSVNA
23937, 23938	Probability: 0.997 AA1: 19 AA2: 20	MKKTILLITCLLSIFSIS
23941, 23942	Probability: 0.988 AA1: 17 AA2: 18	MKYIYLCLFLFSSFTFS
23967, 23968	Probability: 0.991 AA1: 19 AA2: 20	MKKFLITLVLPFFGIAQT
24023, 24024	Probability: 0.572 AA1: 20 AA2: 21	MNKYFIILIFICFDSGSQN
24063, 24064	Probability: 1.000 AA1: 17 AA2: 18	MKKILFLLLISSTVSA
2411, 2412	Probability: 1.000 AA1: 21 AA2: 22	MKKIVVLLALITAMVPAGVFA
24141, 24142	Probability: 0.985 AA1: 20 AA2: 21	MNMMKGFLLFFLFSVHILSA
2415, 2416	Probability: 0.907 AA1: 20 AA2: 21	MIMNQRIKKIVGIMLLSVVA
24159, 24160	Probability: 0.994 AA1: 20 AA2: 21	MNKIKYFLLTITFLSLSACT
24161, 24162	Probability: 0.578 AA1: 20 AA2: 21	MNKFLQRISFTLLSCILLG
24267, 24268	Probability: 0.993 AA1: 20 AA2: 21	MKQLLALALLVFCACKSTK
2429, 2430	Probability: 0.925 AA1: 18 AA2: 19	MKYCLILFSIVNSLFTNA
24317, 24318	Probability: 0.592 AA1: 21 AA2: 22	MLFIAPLVFYILLTGTNNFA
2435, 2436	Probability: 0.594 AA1: 20 AA2: 21	MKKKINYIAFIILLICSVPA
24359, 24360	Probability: 0.943 AA1: 18 AA2: 19	MKKLIHLALILISVSFS
24367, 24368	Probability: 0.968 AA1: 20 AA2: 21	MNMKILLSILSLFLLFNCVN
24397, 24398	Probability: 1.000 AA1: 20 AA2: 21	MKLKIVLLILFVSITTLVNA
24469, 24470	Probability: 0.998 AA1: 18 AA2: 19	MKKILLIAIFLWSWVSTA
24473, 24474	Probability: 0.996 AA1: 18 AA2: 19	MKLLKKILFALVILLAIA

24525, 24526	Probability: 0.992 AA1: 19 AA2: 20	MNRIKPFLILLFLTSLTYS
24535, 24536	Probability: 1.000 AA1: 18 AA2: 19	MKKLILICALLISVFSTA
24579, 24580	Probability: 0.998 AA1: 19 AA2: 20	MRKNMLIIIFVFLTTSIFG
24607, 24608	Probability: 0.998 AA1: 19 AA2: 20	MKNVLFILIMTFGILSCNA
24633, 24634	Probability: 0.537 AA1: 19 AA2: 20	MKLKKYIALMLFCLFIGFV
24655, 24656	Probability: 1.000 AA1: 21 AA2: 22	MKKLSPALLILLFLIPNFLQA
24707, 24708	Probability: 0.704 AA1: 18 AA2: 19	MKLTTHIIILIPFXCFÄ
24719, 24720	Probability: 0.989 AA1: 19 AA2: 20	MNKRHISILMLAMTALLSG
24821, 24822	Probability: 0.945 AA1: 19 AA2: 20	MQKILLIIVMFVFTIKVYS
24823, 24824	Probability: 0.975 AA1: 18 AA2: 19	MKNSITFFILLTIIVSA
24853, 24854	Probability: 1.000 AA1: 21 AA2: 22	MRVFFINCLMVFLSSCTSYA
24879, 24880	Probability: 0.996 AA1: 18 AA2: 19	MNRLIILILIFFSQISIA
25057, 25058	Probability: 0.548 AA1: 20 AA2: 21	MTFHLKPILVFALLFMSCNT
25085, 25086	Probability: 0.900 AA1: 19 AA2: 20	MQKKLYFSSLLFFLIVSFT
25115, 25116	Probability: 0.748 AA1: 18 AA2: 19	MKNSILIFTTLFSFICGT
25169, 25170	Probability: 0.703 AA1: 19 AA2: 20	MKTLKQLLFITAFALLSFT
25203, 25204	Probability: 0.505 AA1: 18 AA2: 19	MRLTFIFTLLIIGQFSYG
25225, 25226	Probability: 0.998 AA1: 19 AA2: 20	MSKTIFLFLITTVLSAQN
25299, 25300	Probability: 0.513 AA1: 17 AA2: 18	MKKFLVGSCFSITMLMG
25307, 25308	Probability: 1.000 AA1: 19 AA2: 20	MKKHIITLLVLVFSFSAIA
25311, 25312	Probability: 0.999 AA1: 20 AA2: 21	MKKSITIIILLVFVATQSFA
25355, 25356	Probability: 0.751 AA1: 16 AA2: 17	MKKIFLLLIIVFVSCS
25361, 25362	Probability: 0.708 AA1: 18 AA2: 19	MNRLIILLIFSIFLISCYN
25395, 25396	Probability: 0.982 AA1: 18 AA2: 19	MKSCFVLIILLCSSFCIS
25449, 25450	Probability: 0.969 AA1: 19 AA2: 20	MKKLAVLIVLVCTILSCNE
25563, 25564	Probability: 0.960 AA1: 19 AA2: 20	MKPIFSFFICMSICTTIFS
25571, 25572	Probability: 0.997 AA1: 20 AA2: 21	MHSRYFIILLVLFTINSFS
25615, 25616	Probability: 0.955 AA1: 20 AA2: 21	MMSVVLLGLIASVITQYVAS
25621, 25622	Probability: 0.511 AA1: 21 AA2: 22	MIKNRPRKTYTILSLLVASYS
2571, 2572	Probability: 0.871 AA1: 20 AA2: 21	MKKLKLTLSSLAFLSTVPV
25761, 25762	Probability: 0.989 AA1: 19 AA2: 20	MNKRHISILMLAMTALLSG
25797, 25798	Probability: 0.999 AA1: 18 AA2: 19	MKNLILILALSIGFNAFS
25833, 25834	Probability: 0.998 AA1: 18 AA2: 19	MKKITLLILFTSIISFS
25865, 25866	Probability: 0.745 AA1: 15 AA2: 16	MKKIIIALATTLVFG
25867, 25868	Probability: 0.949 AA1: 18 AA2: 19	MKKTIVILLIFISCSSTK
25899, 25900	Probability: 1.000 AA1: 19 AA2: 20	MKKIITLVALVFFSVSTFA
25985, 25986	Probability: 0.776 AA1: 20 AA2: 21	MNFKASLFFVVTIFSIGLMS
26069, 26070	Probability: 0.730 AA1: 18 AA2: 19	MKKNIYRIFLTILSIALA
26081, 26082	Probability: 1.000 AA1: 18 AA2: 19	MKNLFFTAIFLFCPLALA
26085, 26086	Probability: 0.980 AA1: 17 AA2: 18	MKWSFLILFVLSFPSSA
26127, 26128	Probability: 0.985 AA1: 17 AA2: 18	MKRNLAIIILLITTVLS
26133, 26134	Probability: 0.846 AA1: 20 AA2: 21	MPMKNASFLIVLLFFSACK
26249, 26250	Probability: 0.999 AA1: 17 AA2: 18	MKQILILFSLLYFSAQA
26305, 26306	Probability: 0.998 AA1: 18 AA2: 19	MASGLLVFLALHPTQSNA
26341, 26342	Probability: 0.629 AA1: 20 AA2: 21	MKKSNSIYYLLSLTLFFSS
26431, 26432	Probability: 0.663 AA1: 18 AA2: 19	MNIVILFFLSFLALVLS
26445, 26446	Probability: 0.527 AA1: 13 AA2: 14	MKTKSLSFFMAHN
26489, 26490	Probability: 0.999 AA1: 20 AA2: 21	MKRTFSMSIILILALSFFNA
26595, 26596	Probability: 0.979 AA1: 19 AA2: 20	MKYLLFILLVGLSTTFGFS
26609, 26610	Probability: 0.997 AA1: 20 AA2: 21	MHSRYFIILLVLFTINSFS
26625, 26626	Probability: 0.901 AA1: 20 AA2: 21	MKRSTLSLFLVITLSLFQIG
26627, 26628	Probability: 0.998 AA1: 19 AA2: 20	MNKYIPLMLVLFFANLSFS
26675, 26676	Probability: 0.939 AA1: 17 AA2: 18	MKKLLICMSALAIVACK
26681, 26682	Probability: 0.715 AA1: 18 AA2: 19	MKRTVILTIVFLPLILIG
26719, 26720	Probability: 0.996 AA1: 18 AA2: 19	MNKFILLIGLCVCSNIFS

26747, 26748	Probability: 0.689 AA1: 18 AA2: 19	MIKVFKLVVALLCLACK
2675, 2676	Probability: 1.000 AA1: 18 AA2: 19	MKKTMSLLFFVSAIAFS
2683, 2684	Probability: 0.939 AA1: 19 AA2: 20	MKKIILSFLFLLYCTFVQN
26855, 26856	Probability: 0.619 AA1: 18 AA2: 19	MNKLGIIGLLIGLGLFG
26857, 26858	Probability: 0.501 AA1: 20 AA2: 21	MYVMKSIFFLFFLMCMNISON
275, 276	Probability: 0.999 AA1: 21 AA2: 22	MLKNISIFSILFILLINASNA
2761, 2762	Probability: 0.980 AA1: 17 AA2: 18	MKKIHIVFLILIVAALA
2927, 2928	Probability: 0.964 AA1: 18 AA2: 19	MLKNISIFSILFILLINA
2941, 2942	Probability: 0.997 AA1: 19 AA2: 20	MKSTLVTFILLFSQFIVA
2985, 2986	Probability: 0.957 AA1: 19 AA2: 20	MLRSKWGFLALCALLISWQ
303, 304	Probability: 0.997 AA1: 19 AA2: 20	MSKIFLAVLTVFTGIGVQA
3055, 3056	Probability: 0.545 AA1: 19 AA2: 20	MNSMNKVLIFIILLFSSVS
3113, 3114	Probability: 0.978 AA1: 19 AA2: 20	MKRAILITFIIFTNQLYA
3117, 3118	Probability: 0.623 AA1: 19 AA2: 20	MKTKTIFILFFSIVSFCFK
3119, 3120	Probability: 0.999 AA1: 20 AA2: 21	MKIILLYAAIVGSLFVSCNA
3221, 3222	Probability: 0.995 AA1: 20 AA2: 21	MIKAKIFSGLLLFISTALFS
3231, 3232	Probability: 0.992 AA1: 19 AA2: 20	MRIIAILIIVLPLISQG
3233, 3234	Probability: 1.000 AA1: 20 AA2: 21	MKKDLILTLLIFLFTVSLTA
3235, 3236	Probability: 1.000 AA1: 20 AA2: 21	MKKDLILTLLIFLXTVSLTA
3245, 3246	Probability: 0.975 AA1: 19 AA2: 20	MKTNLKFLIMLSISIEA
3277, 3278	Probability: 0.979 AA1: 20 AA2: 21	MRNSLTLLIFALLLTNCNNS
3337, 3338	Probability: 0.994 AA1: 19 AA2: 20	MKKIVSILVFVLLANLSQA
3397, 3398	Probability: 0.643 AA1: 19 AA2: 20	MEESMRLFVLLFLIFPVVA
3405, 3406	Probability: 0.534 AA1: 20 AA2: 21	MIKKGLSLLRGILSPSITWK
3471, 3472	Probability: 0.954 AA1: 19 AA2: 20	MKRIFFAFSILFISVCGFA
3515, 3516	Probability: 0.686 AA1: 19 AA2: 20	MAFIFFALVIGTMVIGISMT
3525, 3526	Probability: 0.873 AA1: 20 AA2: 21	MKRKIFFYTLMSILLAGIFA
3565, 3566	Probability: 0.646 AA1: 19 AA2: 20	MKRFSYLFLILLINQCRN
365, 366	Probability: 0.540 AA1: 21 AA2: 22	MHNSSPMKNLLILFASFILSS
3705, 3706	Probability: 0.845 AA1: 19 AA2: 20	MKPTLLIMAAGMASRYGSM
3711, 3712	Probability: 0.994 AA1: 19 AA2: 20	MKKIVSILVFVLLANLSQA
373, 374	Probability: 0.665 AA1: 20 AA2: 21	MNKRILISATVVSISLQV
3771, 3772	Probability: 0.860 AA1: 20 AA2: 21	MQINRLIVLLIMISHKNFA
3843, 3844	Probability: 1.000 AA1: 19 AA2: 20	MKSFIFFLFFVLAFSVANA
3871, 3872	Probability: 0.973 AA1: 18 AA2: 19	MNKSVLVVGAGLGGMALA
3913, 3914	Probability: 0.999 AA1: 19 AA2: 20	MNRFLIFIVICFCGTAVS
397, 398	Probability: 0.978 AA1: 18 AA2: 19	MIRFVIPVFFLLPFFSNA
4037, 4038	Probability: 0.904 AA1: 19 AA2: 20	MKKEFLKIGIAILVLFAIA
4087, 4088	Probability: 1.000 AA1: 18 AA2: 19	MRKIFAVAALFTSSQLAA
4153, 4154	Probability: 0.515 AA1: 18 AA2: 19	MLKSLFLFTSFSSFFLLV
4167, 4168	Probability: 0.784 AA1: 17 AA2: 18	MARLVLVFILLHQTIVA
419, 420	Probability: 0.708 AA1: 18 AA2: 19	MKSLIIFSLILFFTACK
4223, 4224	Probability: 0.659 AA1: 19 AA2: 20	MRSKIFLLMLXTASFYSPS
4241, 4242	Probability: 1.000 AA1: 20 AA2: 21	MKKKITILILFFICLFALS
4259, 4260	Probability: 0.788 AA1: 17 AA2: 18	MKTIILITILITSCA
4273, 4274	Probability: 0.987 AA1: 19 AA2: 20	MKAHIRIILLALFFGTAVQ
4291, 4292	Probability: 1.000 AA1: 18 AA2: 19	MKKIFLSFCLLSSFIGFA
4309, 4310	Probability: 0.924 AA1: 18 AA2: 19	MKYCLILFSIVNSLFTNA
4313, 4314	Probability: 0.834 AA1: 18 AA2: 19	MKNKVLLSFLCFFLYTHV
4319, 4320	Probability: 0.670 AA1: 15 AA2: 16	MKLAALILLIIFTQS
4337, 4338	Probability: 0.537 AA1: 20 AA2: 21	MKKLTVILFFVIGVTYQVIG
4361, 4362	Probability: 0.850 AA1: 17 AA2: 18	MKKILFSLIVCVFCLSS
4405, 4406	Probability: 0.873 AA1: 20 AA2: 21	MKRKIFFYTLMSILLAGIFA
4415, 4416	Probability: 0.923 AA1: 18 AA2: 19	MKQMLAAIFCFCFFISHS
4483, 4484	Probability: 0.575 AA1: 18 AA2: 19	MRTIVILYLVMFSLSCQQ

4623, 4624	Probability: 0.540 AA1: 21 AA2: 22	MHNSSPMKNLLILFASFILSS
463, 464	Probability: 0.643 AA1: 21 AA2: 22	MIRTKGXXXXXXXXXXXXXXXXX
4641, 4642	Probability: 0.976 AA1: 20 AA2: 21	MKRMIITGMLAFLGTTGFG
4771, 4772	Probability: 0.998 AA1: 19 AA2: 20	MSKIFLAVLTVFTGIGVQA
4903, 4904	Probability: 0.998 AA1: 17 AA2: 18	MFRFIIVSVFAISVSFA
4937, 4938	Probability: 0.977 AA1: 19 AA2: 20	MTIMKYKLITLFLLFQTLA
4939, 4940	Probability: 0.600 AA1: 19 AA2: 20	MKTTVRILCVCILVCSSVS
495, 496	Probability: 0.674 AA1: 20 AA2: 21	MGRHAVCXXXXXXXXXXXXXXXX
5031, 5032	Probability: 0.713 AA1: 18 AA2: 19	MKKSLTMTLFAGLFLINS
5037, 5038	Probability: 0.987 AA1: 19 AA2: 20	MKAHIRIILLALFFGTAVQ
5057, 5058	Probability: 0.990 AA1: 19 AA2: 20	MRNYILTILTFFFSITLFA
509, 510	Probability: 0.558 AA1: 18 AA2: 19	MKVLLSTALPIALCCLLL
5261, 5262	Probability: 0.558 AA1: 18 AA2: 19	MKVLLSTALPIALCCLLL
5289, 5290	Probability: 0.979 AA1: 15 AA2: 16	MANKYLLCCLFLVSA
5351, 5352	Probability: 0.928 AA1: 18 AA2: 19	MKFLALLIITCSDICTA
5371, 5372	Probability: 0.588 AA1: 20 AA2: 21	MKKLILLPFLALLLGFILPG
5421, 5422	Probability: 1.000 AA1: 19 AA2: 20	MLKILLAVTVAFSFLPAFS
5571, 5572	Probability: 0.836 AA1: 18 AA2: 19	MKLTVTAIFLCVAIQAIS
5573, 5574	Probability: 0.985 AA1: 20 AA2: 21	MKKYFGILLITSLICLVQLQ
5575, 5576	Probability: 0.999 AA1: 19 AA2: 20	MRTNCILLSVLLFTFSTSS
5617, 5618	Probability: 0.968 AA1: 19 AA2: 20	MKNKIIAFLPLICAGVIT
5693, 5694	Probability: 0.992 AA1: 18 AA2: 19	MKILTIVFLVGFFCFVQA
5801, 5802	Probability: 1.000 AA1: 20 AA2: 21	MKKILFIAATAVLFSTTTMA
5811, 5812	Probability: 0.875 AA1: 18 AA2: 19	MKSFYFLIAMGISLNASA
5943, 5944	Probability: 0.983 AA1: 16 AA2: 17	MTTNTILLLLLSLVIA
5951, 5952	Probability: 0.722 AA1: 20 AA2: 21	MKLKKGIIILIAFLGFGLSN
5953, 5954	Probability: 0.973 AA1: 20 AA2: 21	MMPKLKLLLGCLLILLKNA
6027, 6028	Probability: 0.682 AA1: 18 AA2: 19	MKSLIIIFSLILFFTACK
6041, 6042	Probability: 0.873 AA1: 18 AA2: 19	MTTSKTLFILFLVMTQL
6185, 6186	Probability: 0.997 AA1: 19 AA2: 20	MKSTLVTFILLFSQFIVA
6245, 6246	Probability: 0.854 AA1: 17 AA2: 18	MKYFLFIFLLSCPVTLS
6289, 6290	Probability: 0.999 AA1: 19 AA2: 20	MKKLFPVVLFLSMNVLQA
6323, 6324	Probability: 1.000 AA1: 20 AA2: 21	MKFFSLFYCFLLLGLNFALA
6469, 6470	Probability: 0.997 AA1: 19 AA2: 20	MKSTLVTFILLFSQFIVA
6667, 6668	Probability: 0.912 AA1: 18 AA2: 19	MRKNFQIVLAFAMTIATS
6719, 6720	Probability: 1.000 AA1: 18 AA2: 19	MRKVLLTMLFLSCFSGNA
6741, 6742	Probability: 0.551 AA1: 18 AA2: 19	MKKVLLTGCLLITIISTG
6755, 6756	Probability: 0.909 AA1: 19 AA2: 20	MKKFLIFCLFLFNKPLIS
6789, 6790	Probability: 0.707 AA1: 18 AA2: 19	MRAFLSITVCFFLFVNFA
6885, 6886	Probability: 0.693 AA1: 19 AA2: 20	MKILKLFFLLFILPITTLQ
6893, 6894	Probability: 0.911 AA1: 16 AA2: 17	MKYLILIALCTLTFS
6943, 6944	Probability: 1.000 AA1: 18 AA2: 19	MKKLILSLFILISLNVFA
6951, 6952	Probability: 0.903 AA1: 19 AA2: 20	MLFMKKIILLIVTAVVVS
7029, 7030	Probability: 0.852 AA1: 16 AA2: 17	MKKIFLLIFTFIYLN
711, 712	Probability: 0.936 AA1: 19 AA2: 20	MKNQIFSGFLLFIVNQVA
7357, 7358	Probability: 0.610 AA1: 16 AA2: 17	MLRVILISIFVLNIYA
7389, 7390	Probability: 0.987 AA1: 19 AA2: 20	MKYFTLIFLFTYLSLSSFG
7491, 7492	Probability: 0.682 AA1: 19 AA2: 20	MKSMRTIFISFLIILLQG
7505, 7506	Probability: 0.995 AA1: 19 AA2: 20	MRRILALMCVILLSSFVV
7543, 7544	Probability: 0.997 AA1: 19 AA2: 20	MLIKNIVLSFLFVLFAGG
759, 760	Probability: 0.711 AA1: 19 AA2: 20	MKFKLAIFALILISINLIS
7765, 7766	Probability: 0.529 AA1: 18 AA2: 19	MKICIIGLGYVGLPLAHA
7785, 7786	Probability: 0.983 AA1: 19 AA2: 20	MFKKVIGILLFLIALSLVVL
7835, 7836	Probability: 0.878 AA1: 15 AA2: 16	MRIIFLVLSISFLYA
7907, 7908	Probability: 0.926 AA1: 19 AA2: 20	MKKSSLLLLITFVVVLFQG

821, 822	Probability: 1.000 AA1: 20 AA2: 21	MKKWRFSLSIFLFVCVTCLA
8247, 8248	Probability: 0.995 AA1: 16 AA2: 17	MRISILLAVVSSIIFA
827, 828	Probability: 1.000 AA1: 19 AA2: 20	MKKFFSLIIFLIFSFAFA
8279, 8280	Probability: 0.672 AA1: 15 AA2: 16	MKFNLNSFLMSVSLA
8313, 8314	Probability: 0.992 AA1: 19 AA2: 20	MKHIKKALLILLFLFLSFS
8349, 8350	Probability: 0.562 AA1: 17 AA2: 18	MFKTILFTIVFVTNIFS
8437, 8438	Probability: 0.820 AA1: 16 AA2: 17	MKKRVMSSMKSGGVVA
8461, 8462	Probability: 0.857 AA1: 17 AA2: 18	MKKYLALFAFILLVLSS
8513, 8514	Probability: 0.993 AA1: 16 AA2: 17	MKLLLLLFLVLLNVNA
8561, 8562	Probability: 0.618 AA1: 17 AA2: 18	MKLNAGAILVLSPSGA
8585, 8586	Probability: 0.997 AA1: 17 AA2: 18	MKKFTLSILISSSLAFG
8727, 8728	Probability: 0.825 AA1: 19 AA2: 20	MKKITKILLIFALVAIFSG
8793, 8794	Probability: 0.582 AA1: 19 AA2: 20	MKNKCLLIILLRVISTFLL
8853, 8854	Probability: 0.649 AA1: 17 AA2: 18	MMKILITITTTAILCA
9021, 9022	Probability: 0.998 AA1: 19 AA2: 20	MNYKSFLALTAAVIISFSA
9039, 9040	Probability: 0.977 AA1: 19 AA2: 20	MQKAFYILILLSVSLSSFG
9213, 9214	Probability: 0.772 AA1: 17 AA2: 18	MKKKILVGGGTAGTMT
9351, 9352	Probability: 0.744 AA1: 18 AA2: 19	MIKRTTGILLIFISIFA
9373, 9374	Probability: 0.931 AA1: 17 AA2: 18	MKHILFITLFFLTSLFA
9413, 9414	Probability: 0.540 AA1: 15 AA2: 16	MSNIALSLGSCFTIA
9613, 9614	Probability: 0.998 AA1: 17 AA2: 18	MKIFSLIFILLFTSLSA
9713, 9714	Probability: 0.911 AA1: 17 AA2: 18	MKKVITLSLITLNLFA
9829, 9830	Probability: 0.768 AA1: 19 AA2: 20	MKNILKIIFILFSSCQT
9881, 9882	Probability: 0.963 AA1: 19 AA2: 20	MNKNLITAALLFVFGYTML
9925, 9926	Probability: 0.751 AA1: 18 AA2: 19	MLQKSFISILLSLLLSLS
9979, 9980	Probability: 0.799 AA1: 19 AA2: 20	MIMKDLILTLLLSVYCLV

Methods for identifying "prepro" domain sequences and signal sequences are well known in the art, see, e.g., Van de Ven (1993) Crit. Rev. Oncog. 4(2):115-136. For example, to identify a prepro sequence, the protein is purified from the extracellular space and the N-terminal protein sequence is determined and compared to the unprocessed form.

The invention includes polypeptides with or without a signal sequence and/or a prepro sequence. The invention includes polypeptides with heterologous signal sequences and/or prepro sequences. The prepro sequence (including a sequence of the invention used as a heterologous prepro domain) can be located on the amino terminal or the carboxy terminal end of the protein. The invention also includes isolated or recombinant signal sequences, prepro sequences and catalytic domains (e.g., "active sites") comprising sequences of the invention. The polypeptide comprising a signal sequence of the invention can be a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention or another polypeptide, enzyme, protein, e.g. structural or binding protein, or another enzyme or other polypeptide.

The polypeptide, enzyme, protein, e.g. structural or binding protein signal sequences (SPs) and/or prepro sequences of the invention can be isolated peptides, or,

sequences joined to another a polypeptide, enzyme, protein, e.g. structural or binding protein, or a non-polypeptide, non-enzyme, non-protein, e.g. non-structural or non-binding protein, e.g., as a fusion (chimeric) protein. In one aspect, the invention provides polypeptides comprising a polypeptide, enzyme, protein, e.g. structural or binding protein, signal sequences of the invention. In one aspect, polypeptides comprising polypeptide, enzyme, protein, e.g. structural or binding protein signal sequences SPs and/or prepro of the invention comprise sequences heterologous to a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention (e.g., a fusion protein comprising an SP and/or prepro of the invention and sequences from another a polypeptide, enzyme, protein, e.g. structural or binding protein, or a non-polypeptide, non-enzyme, non-protein, e.g. non-structural or non-binding protein). In one aspect, the invention provides a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention with heterologous SPs and/or prepro sequences, e.g., sequences with a yeast signal sequence. A polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention can comprise a heterologous SP and/or prepro in a vector, e.g., a pPIC series vector (Invitrogen, Carlsbad, CA).

In one aspect, SPs and/or prepro sequences of the invention are identified following identification of novel a polypeptide, enzyme, protein, e.g. structural or binding protein. The pathways by which proteins are sorted and transported to their proper cellular location are often referred to as protein targeting pathways. One of the most important elements in all of these targeting systems is a short amino acid sequence at the amino terminus of a newly synthesized polypeptide called the signal sequence. This signal sequence directs a protein to its appropriate location in the cell and is removed during transport or when the protein reaches its final destination. Most lysosomal, membrane, or secreted proteins have an amino-terminal signal sequence that marks them for translocation into the lumen of the endoplasmic reticulum. The signal sequences can vary in length from about 10 to 65, or more, amino acid residues. Various methods of recognition of signal sequences are known to those of skill in the art. For example, in one aspect, novel a polypeptide, enzyme, protein, e.g. structural or binding protein, signal peptides are identified by a method referred to as SignalP. SignalP uses a combined neural network which recognizes both signal peptides and their cleavage sites. (Nielsen (1997) "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites." Protein Engineering 10:1-6.

It should be understood that in some aspects a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention may not have SPs and/or prepro sequences, or "domains." In one aspect, the invention provides the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention lacking all or part of an SP and/or a prepro domain. In one aspect, the invention provides a nucleic acid sequence encoding a signal sequence (SP) and/or prepro from one a polypeptide, enzyme, protein, e.g. structural or binding protein, operably linked to a nucleic acid sequence of a different a polypeptide, enzyme, protein, e.g. structural or binding protein, or, optionally, a signal sequence (SPs) and/or prepro domain from a non-enzyme or non-protein, e.g. non-structural or non-binding protein, may be desired.

The invention also provides isolated or recombinant polypeptides comprising signal sequences (SPs), prepro domain and/or catalytic domains (CDs) of the invention and heterologous sequences. The heterologous sequences are sequences not naturally associated (e.g., to a enzyme) with an SP, prepro domain and/or CD. The sequence to which the SP, prepro domain and/or CD are not naturally associated can be on the SP's, prepro domain and/or CD's amino terminal end, carboxy terminal end, and/or on both ends of the SP and/or CD. In one aspect, the invention provides an isolated or recombinant polypeptide comprising (or consisting of) a polypeptide comprising a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention with the proviso that it is not associated with any sequence to which it is naturally associated (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, sequence). Similarly in one aspect, the invention provides isolated or recombinant nucleic acids encoding these polypeptides. Thus, in one aspect, the isolated or recombinant nucleic acid of the invention comprises coding sequence for a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention and a heterologous sequence (i.e., a sequence not naturally associated with the a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention). The heterologous sequence can be on the 3' terminal end, 5' terminal end, and/or on both ends of the SP, prepro domain and/or CD coding sequence.

Hybrid (chimeric) a polypeptide, enzyme, protein, e.g. structural or binding protein, and peptide libraries

In one aspect, the invention provides hybrid a polypeptide, enzyme, protein, e.g. structural or binding protein, and fusion proteins, including peptide libraries, comprising sequences of the invention. The peptide libraries of the invention can be used

to isolate peptide modulators (e.g., activators or inhibitors) of targets, such as a polypeptide, enzyme, protein, e.g. structural or binding protein, substrates, receptors, enzymes. The peptide libraries of the invention can be used to identify formal binding partners of targets, such as ligands, e.g., cytokines, hormones and the like. In one aspect, the invention provides chimeric proteins comprising a signal sequence (SP), prepro domain and/or catalytic domain (CD) of the invention or a combination thereof and a heterologous sequence (see above).

In one aspect, the fusion proteins of the invention (e.g., the peptide moiety) are conformationally stabilized (relative to linear peptides) to allow a higher binding affinity for targets. The invention provides fusions of a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention and other peptides, including known and random peptides. They can be fused in such a manner that the structure of the polypeptide, enzyme, protein, e.g. structural or binding proteins is not significantly perturbed and the peptide is metabolically or structurally conformationally stabilized. This allows the creation of a peptide library that is easily monitored both for its presence within cells and its quantity.

Amino acid sequence variants of the invention can be characterized by a predetermined nature of the variation, a feature that sets them apart from a naturally occurring form, e.g., an allelic or interspecies variation of a polypeptide, enzyme, protein, e.g. structural or binding protein, sequence. In one aspect, the variants of the invention exhibit the same qualitative biological activity as the naturally occurring analogue. Alternatively, the variants can be selected for having modified characteristics. In one aspect, while the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed a polypeptide, enzyme, protein, e.g. structural or binding protein, variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, as discussed herein for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants can be done using, e.g., assays of glucan hydrolysis. In alternative aspects, amino acid substitutions can be single residues; insertions can be on the order of from about 1 to 20 amino acids, although considerably larger insertions can be done. Deletions can range from about 1 to about 20, 30, 40, 50, 60, 70 residues or more. To obtain a final derivative with the optimal

properties, substitutions, deletions, insertions or any combination thereof may be used. Generally, these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances.

The invention provides a polypeptide, enzyme, protein, e.g. structural or binding protein, where the structure of the polypeptide backbone, the secondary or the tertiary structure, e.g., an alpha-helical or beta-sheet structure, has been modified. In one aspect, the charge or hydrophobicity has been modified. In one aspect, the bulk of a side chain has been modified. Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative. For example, substitutions can be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example a alpha-helical or a beta-sheet structure; a charge or a hydrophobic site of the molecule, which can be at an active site; or a side chain. The invention provides substitutions in polypeptide of the invention where (a) a hydrophilic residues, e.g. seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine. The variants can exhibit the same qualitative biological activity (i.e., an enzyme, structural or binding activity) although variants can be selected to modify the characteristics of the polypeptide, enzyme, protein, e.g. structural or binding proteins as needed.

In one aspect, a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention comprise epitopes or purification tags, signal sequences or other fusion sequences, etc. In one aspect, the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention can be fused to a random peptide to form a fusion polypeptide. By "fused" or "operably linked" herein is meant that the random peptide and the polypeptide, enzyme, protein, e.g. structural or binding protein are linked together, in such a manner as to minimize the disruption to the stability of the polypeptide, enzyme, protein, e.g. structural or binding protein structure, e.g., it retains a polypeptide, enzyme, protein, e.g. structural or binding protein, activity. The fusion polypeptide (or fusion polynucleotide encoding the fusion polypeptide) can comprise further components as well, including multiple peptides at multiple loops.

In one aspect, the peptides and nucleic acids encoding them are randomized, either fully randomized or they are biased in their randomization, e.g. in nucleotide/residue frequency generally or per position. "Randomized" means that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. In one aspect, the nucleic acids which give rise to the peptides can be chemically synthesized, and thus may incorporate any nucleotide at any position. Thus, when the nucleic acids are expressed to form peptides, any amino acid residue may be incorporated at any position. The synthetic process can be designed to generate randomized nucleic acids, to allow the formation of all or most of the possible combinations over the length of the nucleic acid, thus forming a library of randomized nucleic acids. The library can provide a sufficiently structurally diverse population of randomized expression products to affect a probabilistically sufficient range of cellular responses to provide one or more cells exhibiting a desired response. Thus, the invention provides an interaction library large enough so that at least one of its members will have a structure that gives it affinity for some molecule, protein, or other factor.

In one aspect, a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention is a multidomain enzyme that comprises a signal peptide, a carbohydrate binding module, a polypeptide, enzyme, protein, e.g. structural or binding protein, catalytic domain, a linker and/or another catalytic domain.

The invention provides a means for generating chimeric polypeptides which may encode biologically active hybrid polypeptides (e.g., hybrid a polypeptide, enzyme, protein, e.g. structural or binding protein,). In one aspect, the original polynucleotides encode biologically active polypeptides. The method of the invention produces new hybrid polypeptides by utilizing cellular processes which integrate the sequence of the original polynucleotides such that the resulting hybrid polynucleotide encodes a polypeptide demonstrating activities derived from the original biologically active polypeptides. For example, the original polynucleotides may encode a particular enzyme from different microorganisms. An enzyme encoded by a first polynucleotide from one organism or variant may, for example, function effectively under a particular environmental condition, e.g. high salinity. An enzyme encoded by a second polynucleotide from a different organism or variant may function effectively under a different environmental condition, such as extremely high temperatures. A hybrid polynucleotide containing sequences from the first and second original polynucleotides may encode an enzyme which exhibits characteristics of both enzymes encoded by the

original polynucleotides. Thus, the enzyme encoded by the hybrid polynucleotide may function effectively under environmental conditions shared by each of the enzymes encoded by the first and second polynucleotides, *e.g.*, high salinity and extreme temperatures.

A hybrid polypeptide resulting from the method of the invention may exhibit specialized enzyme activity not displayed in the original enzymes. For example, following recombination and/or reductive reassortment of polynucleotides encoding a polypeptide, enzyme, protein, *e.g.* structural or binding protein, the resulting hybrid polypeptide encoded by a hybrid polynucleotide can be screened for specialized non-enzyme, non-structural or non-binding activities, obtained from each of the original enzymes. Thus, for example, the hybrid polypeptide may be screened to ascertain those chemical functionalities which distinguish the hybrid polypeptide from the original parent polypeptides, such as the temperature, pH or salt concentration at which the hybrid polypeptide functions.

In one aspect, the invention relates to a method for producing a biologically active hybrid polypeptide and screening such a polypeptide for enhanced activity by:

- 1) introducing at least a first polynucleotide in operable linkage and a second polynucleotide in operable linkage, the at least first polynucleotide and second polynucleotide sharing at least one region of partial sequence homology, into a suitable host cell;
- 2) growing the host cell under conditions which promote sequence reorganization resulting in a hybrid polynucleotide in operable linkage;
- 3) expressing a hybrid polypeptide encoded by the hybrid polynucleotide;
- 4) screening the hybrid polypeptide under conditions which promote identification of enhanced biological activity; and
- 5) isolating the a polynucleotide encoding the hybrid polypeptide.

Isolating and discovering a polypeptide, enzyme, protein, *e.g.* structural or binding protein

The invention provides methods for isolating and discovering a polypeptide, enzyme, protein, *e.g.* structural or binding protein, and the nucleic acids that encode them. Polynucleotides or enzymes may be isolated from individual organisms ("isolates"), collections of organisms that have been grown in defined media ("enrichment cultures"), or, uncultivated organisms ("environmental samples"). The

organisms can be isolated by, e.g., *in vivo* biopanning (see discussion, below). The use of a culture-independent approach to derive polynucleotides encoding novel bioactivities from environmental samples is most preferable since it allows one to access untapped resources of biodiversity. Polynucleotides or enzymes also can be isolated from any one of numerous organisms, e.g. bacteria. In addition to whole cells, polynucleotides or enzymes also can be isolated from crude enzyme preparations derived from cultures of these organisms, e.g., bacteria.

"Environmental libraries" are generated from environmental samples and represent the collective genomes of naturally occurring organisms archived in cloning vectors that can be propagated in suitable prokaryotic hosts. Because the cloned DNA is initially extracted directly from environmental samples, the libraries are not limited to the small fraction of prokaryotes that can be grown in pure culture. Additionally, a normalization of the environmental DNA present in these samples could allow more equal representation of the DNA from all of the species present in the original sample. This can dramatically increase the efficiency of finding interesting genes from minor constituents of the sample which may be under-represented by several orders of magnitude compared to the dominant species.

For example, gene libraries generated from one or more uncultivated microorganisms are screened for an activity of interest. Potential pathways encoding bioactive molecules of interest are first captured in prokaryotic cells in the form of gene expression libraries. Polynucleotides encoding activities of interest are isolated from such libraries and introduced into a host cell. The host cell is grown under conditions which promote recombination and/or reductive reassortment creating potentially active biomolecules with novel or enhanced activities.

In vivo biopanning may be performed utilizing a FACS-based and non-optical (e.g., magnetic) based machines. Complex gene libraries are constructed with vectors which contain elements which stabilize transcribed RNA. For example, the inclusion of sequences which result in secondary structures such as hairpins which are designed to flank the transcribed regions of the RNA would serve to enhance their stability, thus increasing their half life within the cell. The probe molecules used in the biopanning process consist of oligonucleotides labeled with reporter molecules that only fluoresce upon binding of the probe to a target molecule. These probes are introduced into the recombinant cells from the library using one of several transformation methods. The probe molecules bind to the transcribed target mRNA resulting in DNA/RNA

heteroduplex molecules. Binding of the probe to a target will yield a fluorescent signal which is detected and sorted by the FACS machine during the screening process.

Additionally, subcloning may be performed to further isolate sequences of interest. In subcloning, a portion of DNA is amplified, digested, generally by restriction enzymes, to cut out the desired sequence, the desired sequence is ligated into a recipient vector and is amplified. At each step in subcloning, the portion is examined for the activity of interest, in order to ensure that DNA that encodes the structural protein has not been excluded. The insert may be purified at any step of the subcloning, for example, by gel electrophoresis prior to ligation into a vector or where cells containing the recipient vector and cells not containing the recipient vector are placed on selective media containing, for example, an antibiotic, which will kill the cells not containing the recipient vector. Specific methods of subcloning cDNA inserts into vectors are well-known in the art (Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press (1989)). In another aspect, the enzymes of the invention are subclones. Such subclones may differ from the parent clone by, for example, length, a mutation, a tag or a label.

In one aspect, the signal sequences of the invention are identified following identification of a novel polypeptide, enzyme, protein, e.g. structural or binding protein. The pathways by which proteins are sorted and transported to their proper cellular location are often referred to as protein targeting pathways. One of the most important elements in all of these targeting systems is a short amino acid sequence at the amino terminus of a newly synthesized polypeptide called the signal sequence. This signal sequence directs a protein to its appropriate location in the cell and is removed during transport or when the protein reaches its final destination. Most lysosomal, membrane, or secreted proteins have an amino-terminal signal sequence that marks them for translocation into the lumen of the endoplasmic reticulum. More than 100 signal sequences for proteins in this group have been determined. The sequences vary in length from 13 to 36 amino acid residues. Various methods of recognition of signal sequences are known to those of skill in the art. In one aspect, the peptides are identified by a method referred to as SignalP. SignalP uses a combined neural network which recognizes both signal peptides and their cleavage sites. See, e.g., Nielsen (1997) "Identification of prokaryotic and eukaryotic signal peptides and prediction of their cleavage sites." *Protein Engineering*, vol. 10, no. 1, p. 1-6. It should be understood that some of the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention may or may not

contain signal sequences. It may be desirable to include a nucleic acid sequence encoding a signal sequence from a polypeptide, enzyme, protein, e.g. structural or binding protein, operably linked to a nucleic acid sequence of a different polypeptide, enzyme, protein, e.g. structural or binding protein may be desired.

The microorganisms from which the polynucleotide may be discovered, isolated or prepared include prokaryotic microorganisms, such as *Eubacteria* and *Archaeobacteria* and lower eukaryotic microorganisms such as fungi, some algae and protozoa. Polynucleotides may be discovered, isolated or prepared from environmental samples in which case the nucleic acid may be recovered without culturing of an organism or recovered from one or more cultured organisms. In one aspect, such microorganisms may be extremophiles, such as hyperthermophiles, psychrophiles, psychrotrophs, halophiles, barophiles and acidophiles. Polynucleotides encoding enzymes isolated from extremophilic microorganisms can be used. Such enzymes may function at temperatures above 100°C in terrestrial hot springs and deep seamount vents, at temperatures below 0°C in arctic waters, in the saturated salt environment of the Dead Sea, at pH values around 0 in coal deposits and geothermal sulfur-rich springs, or at pH values greater than 11 in sewage sludge. For example, several esterases and lipases cloned and expressed from extremophilic organisms show high activity throughout a wide range of temperatures and pHs.

Polynucleotides selected and isolated as hereinabove described are introduced into a suitable host cell. A suitable host cell is any cell which is capable of promoting recombination and/or reductive reassortment. The selected polynucleotides are in one aspect already in a vector which includes appropriate control sequences. The host cell can be a higher eukaryotic cell, such as a mammalian cell, or a lower eukaryotic cell, such as a yeast cell, or in one aspect, the host cell can be a prokaryotic cell, such as a bacterial cell. Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-Dextran mediated transfection, or electroporation (Davis *et al.*, 1986).

As representative examples of appropriate hosts, there may be mentioned: bacterial cells, such as *E. coli*, *Streptomyces*, *Salmonella typhimurium*; fungal cells, such as yeast; insect cells such as *Drosophila S2* and *Spodoptera Sf9*; animal cells such as CHO, COS or Bowes melanoma; adenoviruses; and plant cells. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein.

With particular references to various mammalian cell culture systems that can be employed to express recombinant protein, examples of mammalian expression systems include the COS-7 lines of monkey kidney fibroblasts, described in "SV40-transformed simian cells support the replication of early SV40 mutants" (Gluzman, 1981) and other cell lines capable of expressing a compatible vector, for example, the C127, 3T3, CHO, HeLa and BHK cell lines. Mammalian expression vectors will comprise an origin of replication, a suitable promoter and enhancer and also any necessary ribosome binding sites, polyadenylation site, splice donor and acceptor sites, transcriptional termination sequences and 5' flanking nontranscribed sequences. DNA sequences derived from the SV40 splice and polyadenylation sites may be used to provide the required nontranscribed genetic elements.

In another aspect, it is envisioned the method of the present invention can be used to generate novel polynucleotides encoding biochemical pathways from one or more operons or gene clusters or portions thereof. For example, bacteria and many eukaryotes have a coordinated mechanism for regulating genes whose products are involved in related processes. The genes are clustered, in structures referred to as "gene clusters," on a single chromosome and are transcribed together under the control of a single regulatory sequence, including a single promoter which initiates transcription of the entire cluster. Thus, a gene cluster is a group of adjacent genes that are either identical or related, usually as to their function. An example of a biochemical pathway encoded by gene clusters are polyketides.

Gene cluster DNA can be isolated from different organisms and ligated into vectors, particularly vectors containing expression regulatory sequences which can control and regulate the production of a detectable protein or protein-related array activity from the ligated gene clusters. Use of vectors which have an exceptionally large capacity for exogenous DNA introduction are particularly appropriate for use with such gene clusters and are described by way of example herein to include the f-factor (or fertility factor) of *E. coli*. This f-factor of *E. coli* is a plasmid which affects high-frequency transfer of itself during conjugation and is ideal to achieve and stably propagate large DNA fragments, such as gene clusters from mixed microbial samples. One aspect is to use cloning vectors, referred to as "fosmids" or bacterial artificial chromosome (BAC) vectors. These are derived from *E. coli* f-factor which is able to stably integrate large segments of genomic DNA. When integrated with DNA from a mixed uncultured environmental sample, this makes it possible to achieve large genomic fragments in the

form of a stable "environmental DNA library." Another type of vector for use in the present invention is a cosmid vector. Cosmid vectors were originally designed to clone and propagate large segments of genomic DNA. Cloning into cosmid vectors is described in detail in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press (1989). Once ligated into an appropriate vector, two or more vectors containing different polyketide synthase gene clusters can be introduced into a suitable host cell. Regions of partial sequence homology shared by the gene clusters will promote processes which result in sequence reorganization resulting in a hybrid gene cluster. The novel hybrid gene cluster can then be screened for enhanced activities not found in the original gene clusters.

Methods for screening for various enzyme activities are known to those of skill in the art and are discussed throughout the present specification. Such methods may be employed when isolating the polypeptides and polynucleotides of the invention.

In one aspect, the invention provides methods for discovering and isolating polypeptides, enzymes, proteins, e.g. structural or binding proteins or compounds to modify the enzymatic activity, using a whole cell approach. Putative clones encoding polypeptides, enzymes, proteins, e.g. structural or binding proteins from genomic DNA library can be screened.

Screening Methodologies and "On-line" Monitoring Devices

In practicing the methods of the invention, a variety of apparatus and methodologies can be used to in conjunction with the polypeptides and nucleic acids of the invention, e.g., to screen polypeptides for a polypeptide, enzyme, protein, e.g. structural or binding protein, activity, to screen compounds as potential modulators, e.g., activators or inhibitors, of an enzyme, structural or binding activity, for antibodies that bind to a polypeptide of the invention, for nucleic acids that hybridize to a nucleic acid of the invention, to screen for cells expressing a polypeptide of the invention and the like. In addition to the array formats described in detail below for screening samples, alternative formats can also be used to practice the methods of the invention. Such formats include, for example, mass spectrometers, chromatographs, e.g., high-throughput HPLC and other forms of liquid chromatography, and smaller formats, such as 1536-well plates, 384-well plates and so on. High throughput screening apparatus can be adapted and used to practice the methods of the invention, see, e.g., U.S. Patent Application No. 20020001809.

Capillary Arrays

Nucleic acids or polypeptides of the invention can be immobilized to or applied to an array. Arrays can be used to screen for or monitor libraries of compositions (e.g., small molecules, antibodies, nucleic acids, etc.) for their ability to bind to or modulate the activity of a nucleic acid or a polypeptide of the invention. Capillary arrays, such as the GIGAMATRIX™, Diversa Corporation, San Diego, CA; and arrays described in, e.g., U.S. Patent Application No. 20020080350 A1; WO 0231203 A; WO 0244336 A, provide an alternative apparatus for holding and screening samples. In one aspect, the capillary array includes a plurality of capillaries formed into an array of adjacent capillaries, wherein each capillary comprises at least one wall defining a lumen for retaining a sample. The lumen may be cylindrical, square, hexagonal or any other geometric shape so long as the walls form a lumen for retention of a liquid or sample. The capillaries of the capillary array can be held together in close proximity to form a planar structure. The capillaries can be bound together, by being fused (e.g., where the capillaries are made of glass), glued, bonded, or clamped side-by-side. Additionally, the capillary array can include interstitial material disposed between adjacent capillaries in the array, thereby forming a solid planar device containing a plurality of through-holes.

A capillary array can be formed of any number of individual capillaries, for example, a range from 100 to 4,000,000 capillaries. Further, a capillary array having about 100,000 or more individual capillaries can be formed into the standard size and shape of a Microtiter® plate for fitment into standard laboratory equipment. The lumens are filled manually or automatically using either capillary action or microinjection using a thin needle. Samples of interest may subsequently be removed from individual capillaries for further analysis or characterization. For example, a thin, needle-like probe is positioned in fluid communication with a selected capillary to either add or withdraw material from the lumen.

In a single-pot screening assay, the assay components are mixed yielding a solution of interest, prior to insertion into the capillary array. The lumen is filled by capillary action when at least a portion of the array is immersed into a solution of interest. Chemical or biological reactions and/or activity in each capillary are monitored for detectable events. A detectable event is often referred to as a "hit", which can usually be distinguished from "non-hit" producing capillaries by optical detection. Thus, capillary arrays allow for massively parallel detection of "hits".

In a multi-pot screening assay, a polypeptide or nucleic acid, e.g., a ligand, can be introduced into a first component, which is introduced into at least a portion of a capillary of a capillary array. An air bubble can then be introduced into the capillary behind the first component. A second component can then be introduced into the capillary, wherein the second component is separated from the first component by the air bubble. The first and second components can then be mixed by applying hydrostatic pressure to both sides of the capillary array to collapse the bubble. The capillary array is then monitored for a detectable event resulting from reaction or non-reaction of the two components.

In a binding screening assay, a sample of interest can be introduced as a first liquid labeled with a detectable particle into a capillary of a capillary array, wherein the lumen of the capillary is coated with a binding material for binding the detectable particle to the lumen. The first liquid may then be removed from the capillary tube, wherein the bound detectable particle is maintained within the capillary, and a second liquid may be introduced into the capillary tube. The capillary is then monitored for a detectable event resulting from reaction or non-reaction of the particle with the second liquid.

Arrays, or "Biochips"

Nucleic acids or polypeptides of the invention can be immobilized to or applied to an array. Arrays can be used to screen for or monitor libraries of compositions (e.g., small molecules, antibodies, nucleic acids, etc.) for their ability to bind to or modulate the activity of a nucleic acid or a polypeptide of the invention. For example, in one aspect of the invention, a monitored parameter is transcript expression of a polypeptide, enzyme, protein, e.g. structural or binding protein, gene. One or more, or, all the transcripts of a cell can be measured by hybridization of a sample comprising transcripts of the cell, or, nucleic acids representative of or complementary to transcripts of a cell, by hybridization to immobilized nucleic acids on an array, or "biochip." By using an "array" of nucleic acids on a microchip, some or all of the transcripts of a cell can be simultaneously quantified. Alternatively, arrays comprising genomic nucleic acid can also be used to determine the genotype of a newly engineered strain made by the methods of the invention. Polypeptide arrays" can also be used to simultaneously quantify a plurality of proteins. The present invention can be practiced with any known "array," also referred to as a "microarray" or "nucleic acid array" or "polypeptide array" or "antibody array" or "biochip," or variation thereof. Arrays are generically a plurality of "spots" or "target elements," each target element comprising a defined amount of one or more biological

molecules, e.g., oligonucleotides, immobilized onto a defined area of a substrate surface for specific binding to a sample molecule, e.g., mRNA transcripts.

The terms "array" or "microarray" or "biochip" or "chip" as used herein is a plurality of target elements, each target element comprising a defined amount of one or more polypeptides (including antibodies) or nucleic acids immobilized onto a defined area of a substrate surface, as discussed in further detail, below.

In practicing the methods of the invention, any known array and/or method of making and using arrays can be incorporated in whole or in part, or variations thereof, as described, for example, in U.S. Patent Nos. 6,277,628; 6,277,489; 6,261,776; 6,258,606; 6,054,270; 6,048,695; 6,045,996; 6,022,963; 6,013,440; 5,965,452; 5,959,098; 5,856,174; 5,830,645; 5,770,456; 5,632,957; 5,556,752; 5,143,854; 5,807,522; 5,800,992; 5,744,305; 5,700,637; 5,556,752; 5,434,049; see also, e.g., WO 99/51773; WO 99/09217; WO 97/46313; WO 96/17958; see also, e.g., Johnston (1998) *Curr. Biol.* 8:R171-R174; Schummer (1997) *Biotechniques* 23:1087-1092; Kern (1997) *Biotechniques* 23:120-124; Solinas-Toldo (1997) *Genes, Chromosomes & Cancer* 20:399-407; Bowtell (1999) *Nature Genetics Supp.* 21:25-32. See also published U.S. patent applications Nos. 20010018642; 20010019827; 20010016322; 20010014449; 20010014448; 20010012537; 20010008765.

Antibodies and Antibody-based screening methods

The invention provides isolated or recombinant antibodies that specifically bind to a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention. These antibodies can be used to isolate, identify or quantify the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention or related polypeptides. These antibodies can be used to isolate other polypeptides within the scope the invention or other related a polypeptide, enzyme, protein, e.g. structural or binding protein, . The antibodies can be designed to bind to an active site of a polypeptide, enzyme, protein, e.g. structural or binding protein. Thus, the invention provides methods of inhibiting a polypeptide, enzyme, protein, e.g. structural or binding protein, using the antibodies of the invention (see discussion above regarding applications for anti-polypeptide, anti-enzyme, anti-protein, e.g., anti-structural or anti-binding protein compositions of the invention).

The invention provides fragments of the enzymes of the invention, including immunogenic fragments of a polypeptide of the invention. The invention provides

compositions comprising a polypeptide or peptide of the invention and adjuvants or carriers and the like.

The term "antibody" includes a peptide or polypeptide derived from, modeled after or substantially encoded by an immunoglobulin gene or immunoglobulin genes, or fragments thereof, capable of specifically binding an antigen or epitope, see, e.g. Fundamental Immunology, Third Edition, W.E. Paul, ed., Raven Press, N.Y. (1993); Wilson (1994) J. Immunol. Methods 175:267-273; Yarmush (1992) J. Biochem. Biophys. Methods 25:85-97. The term antibody includes antigen-binding portions, i.e., "antigen binding sites," (e.g., fragments, subsequences, complementarity determining regions (CDRs)) that retain capacity to bind antigen, including (i) a Fab fragment, a monovalent fragment consisting of the VL, VH, CL and CH1 domains; (ii) a F(ab')₂ fragment, a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region; (iii) a Fd fragment consisting of the VH and CH1 domains; (iv) a Fv fragment consisting of the VL and VH domains of a single arm of an antibody; (v) a dAb fragment (Ward et al., (1989) Nature 341:544-546), which consists of a VH domain; and (vi) an isolated complementarity determining region (CDR). Single chain antibodies are also included by reference in the term "antibody."

The antibodies can be used in immunoprecipitation, staining, immunoaffinity columns, and the like. If desired, nucleic acid sequences encoding for specific antigens can be generated by immunization followed by isolation of polypeptide or nucleic acid, amplification or cloning and immobilization of polypeptide onto an array of the invention. Alternatively, the methods of the invention can be used to modify the structure of an antibody produced by a cell to be modified, e.g., an antibody's affinity can be increased or decreased. Furthermore, the ability to make or modify antibodies can be a phenotype engineered into a cell by the methods of the invention.

Methods of immunization, producing and isolating antibodies (polyclonal and monoclonal) are known to those of skill in the art and described in the scientific and patent literature, see, e.g., Coligan, CURRENT PROTOCOLS IN IMMUNOLOGY, Wiley/Greene, NY (1991); Stites (eds.) BASIC AND CLINICAL IMMUNOLOGY (7th ed.) Lange Medical Publications, Los Altos, CA ("Stites"); Goding, MONOCLONAL ANTIBODIES: PRINCIPLES AND PRACTICE (2d ed.) Academic Press, New York, NY (1986); Kohler (1975) Nature 256:495; Harlow (1988) ANTIBODIES, A LABORATORY MANUAL, Cold Spring Harbor Publications, New York. Antibodies also can be generated *in vitro*, e.g., using recombinant antibody binding site expressing

phage display libraries, in addition to the traditional *in vivo* methods using animals. See, e.g., Hoogenboom (1997) *Trends Biotechnol.* 15:62-70; Katz (1997) *Annu. Rev. Biophys. Biomol. Struct.* 26:27-45.

The polypeptides of the invention or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof, may also be used to generate antibodies which bind specifically to the polypeptides or fragments. The resulting antibodies may be used in immunoaffinity chromatography procedures to isolate or purify the polypeptide or to determine whether the polypeptide is present in a biological sample. In such procedures, a protein preparation, such as an extract, or a biological sample is contacted with an antibody capable of specifically binding to one of the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof.

In immunoaffinity procedures, the antibody is attached to a solid support, such as a bead or other column matrix. The protein preparation is placed in contact with the antibody under conditions in which the antibody specifically binds to one of the polypeptides of the invention, or fragment thereof. After a wash to remove non-specifically bound proteins, the specifically bound polypeptides are eluted.

The ability of proteins in a biological sample to bind to the antibody may be determined using any of a variety of procedures familiar to those skilled in the art. For example, binding may be determined by labeling the antibody with a detectable label such as a fluorescent agent, an enzymatic label, or a radioisotope. Alternatively, binding of the antibody to the sample may be detected using a secondary antibody having such a detectable label thereon. Particular assays include ELISA assays, sandwich assays, radioimmunoassays and Western Blots.

Polyclonal antibodies generated against the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof can be obtained by direct injection of the polypeptides into an animal or by administering the polypeptides to an animal, for example, a nonhuman. The antibody so obtained can bind the polypeptide itself. In this manner, even a sequence encoding only a fragment of the polypeptide can be used to generate antibodies which may bind to the whole native polypeptide. Such antibodies can then be used to isolate the polypeptide from cells expressing that polypeptide.

For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the

hybridoma technique (Kohler and Milstein, *Nature*, 256:495-497, 1975), the trioma technique, the human B-cell hybridoma technique (Kozbor *et al.*, *Immunology Today* 4:72, 1983) and the EBV-hybridoma technique (Cole, *et al.*, 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96).

Techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof. Alternatively, transgenic mice may be used to express humanized antibodies to these polypeptides or fragments thereof.

Antibodies generated against the polypeptides of the invention, or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof may be used in screening for similar polypeptides from other organisms and samples. In such techniques, polypeptides from the organism are contacted with the antibody and those polypeptides which specifically bind the antibody are detected. Any of the procedures described above may be used to detect antibody binding. One such screening assay is described in "Methods for Measuring Cellulase Activities", *Methods in Enzymology*, Vol 160, pp. 87-116.

Kits

The invention provides kits comprising the compositions, e.g., nucleic acids, expression cassettes, vectors, cells, transgenic seeds or plants or plant parts, polypeptides and/or antibodies of the invention. The kits also can contain instructional material teaching the methodologies and uses of the enzymes of the invention (see, e.g., Table 3), including the industrial, experimental, food and feed processing and medical uses of the compositions and methods of the invention, as described herein.

Whole cell engineering and measuring metabolic parameters

The methods of the invention provide whole cell evolution, or whole cell engineering, of a cell to develop a new cell strain having a new phenotype, e.g., a new or modified a polypeptide, enzyme, protein, e.g. structural or binding protein, activity, by modifying the genetic composition of the cell. The genetic composition can be modified by addition to the cell of a nucleic acid of the invention, e.g., a coding sequence for an enzyme of the invention. See, e.g., WO0229032; WO0196551.

To detect the new phenotype, at least one metabolic parameter of a modified cell is monitored in the cell in a "real time" or "on-line" time frame. In one aspect, a plurality

of cells, such as a cell culture, is monitored in "real time" or "on-line." In one aspect, a plurality of metabolic parameters is monitored in "real time" or "on-line." Metabolic parameters can be monitored using the polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention.

Metabolic flux analysis (MFA) is based on a known biochemistry framework. A linearly independent metabolic matrix is constructed based on the law of mass conservation and on the pseudo-steady state hypothesis (PSSH) on the intracellular metabolites. In practicing the methods of the invention, metabolic networks are established, including the:

- identity of all pathway substrates, products and intermediary metabolites
- identity of all the chemical reactions interconverting the pathway metabolites, the stoichiometry of the pathway reactions,
- identity of all the enzymes catalyzing the reactions, the enzyme reaction kinetics,
- the regulatory interactions between pathway components, e.g. allosteric interactions, enzyme-enzyme interactions etc,
- intracellular compartmentalization of enzymes or any other supramolecular organization of the enzymes, and,
- the presence of any concentration gradients of metabolites, enzymes or effector molecules or diffusion barriers to their movement.

Once the metabolic network for a given strain is built, mathematic presentation by matrix notion can be introduced to estimate the intracellular metabolic fluxes if the on-line metabolome data is available. Metabolic phenotype relies on the changes of the whole metabolic network within a cell. Metabolic phenotype relies on the change of pathway utilization with respect to environmental conditions, genetic regulation, developmental state and the genotype, etc. In one aspect of the methods of the invention, after the on-line MFA calculation, the dynamic behavior of the cells, their phenotype and other properties are analyzed by investigating the pathway utilization. For example, if the glucose supply is increased and the oxygen decreased during the yeast fermentation, the utilization of respiratory pathways will be reduced and/or stopped, and the utilization of the fermentative pathways will dominate. Control of physiological state of cell cultures will become possible after the pathway analysis. The methods of the invention can help determine how to manipulate the fermentation by determining how to change the substrate supply, temperature, use of inducers, etc. to control the physiological state of cells to move along desirable direction. In practicing the methods of the invention, the

MFA results can also be compared with transcriptome and proteome data to design experiments and protocols for metabolic engineering or gene shuffling, etc.

In practicing the methods of the invention, any modified or new phenotype can be conferred and detected, including new or improved characteristics in the cell. Any aspect of metabolism or growth can be monitored.

Monitoring expression of an mRNA transcript

In one aspect of the invention, the engineered phenotype comprises increasing or decreasing the expression of an mRNA transcript (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein, message) or generating new (e.g., polypeptide, enzyme, protein, e.g. structural or binding protein) transcripts in a cell. This increased or decreased expression can be traced by testing for the presence of a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention or by a polypeptide, enzyme, protein, e.g. structural or binding protein, activity assays. Such assays are well known in the art. mRNA transcripts, or messages, also can be detected and quantified by any method known in the art, including, e.g., Northern blots, quantitative amplification reactions, hybridization to arrays, and the like. Quantitative amplification reactions include, e.g., quantitative PCR, including, e.g., quantitative reverse transcription polymerase chain reaction, or RT-PCR; quantitative real time RT-PCR, or "real-time kinetic RT-PCR" (see, e.g., Kreuzer (2001) *Br. J. Haematol.* 114:313-318; Xia (2001) *Transplantation* 72:907-914).

In one aspect of the invention, the engineered phenotype is generated by knocking out expression of a homologous gene. The gene's coding sequence or one or more transcriptional control elements can be knocked out, e.g., promoters or enhancers. Thus, the expression of a transcript can be completely ablated or only decreased.

In one aspect of the invention, the engineered phenotype comprises increasing the expression of a homologous gene. This can be effected by knocking out of a negative control element, including a transcriptional regulatory element acting in cis- or trans-, or, mutagenizing a positive control element. One or more, or, all the transcripts of a cell can be measured by hybridization of a sample comprising transcripts of the cell, or, nucleic acids representative of or complementary to transcripts of a cell, by hybridization to immobilized nucleic acids on an array.

Monitoring expression of a polypeptides, peptides and amino acids

In one aspect of the invention, the engineered phenotype comprises increasing or decreasing the expression of a polypeptide (e.g., a polypeptide, enzyme, protein, e.g. structural or binding protein,) or generating new polypeptides in a cell. This increased or decreased expression can be traced by determining the amount of a polypeptide, enzyme, protein, e.g. structural or binding protein, present or by a polypeptide, enzyme, protein, e.g. structural or binding protein, activity assays.

Polypeptides, peptides and amino acids also can be detected and quantified by any method known in the art, including, e.g., nuclear magnetic resonance (NMR), spectrophotometry, radiography (protein radiolabeling), electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, various immunological methods, e.g. immunoprecipitation, immunodiffusion, immuno-electrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, gel electrophoresis (e.g., SDS-PAGE), staining with antibodies, fluorescent activated cell sorter (FACS), pyrolysis mass spectrometry, Fourier-Transform Infrared Spectrometry, Raman spectrometry, GC-MS, and LC-Electrospray and cap-LC-tandem-electrospray mass spectrometries, and the like. Novel bioactivities can also be screened using methods, or variations thereof, described in U.S. Patent No. 6,057,103. Furthermore, as discussed below in detail, one or more, or, all the polypeptides of a cell can be measured using a protein array.

Pharmaceutical Compositions and Dietary Supplements

The invention provides pharmaceutical compositions, e.g., formulations, comprising a composition (including polypeptide, nucleic acid, or antibody) of the invention and a pharmaceutically acceptable excipient. The invention provides enteral and parenteral formulations comprising compositions of the invention. For example, the invention provides oral formulations (including or dietary supplements) comprising a composition of the invention. The invention provides formulations and methods for treating, ameliorating, diagnosing or preventing disease of condition of interest; e.g., in one aspect the invention provides methods comprising providing a pharmaceutical composition or dietary supplement comprising a composition of the invention; and administering an effective amount of the pharmaceutical composition or dietary supplement to a subject in need thereof.

The compositions and methods of the invention can also be practiced *ex vivo* or *in vitro*, or on a non-biological fluid or substance. In one aspect, the compositions and methods comprise providing a pharmaceutical composition or dietary supplement comprising a formulation of the invention; and administering an effective amount of the pharmaceutical composition or dietary supplement to a subject in need thereof.

The pharmaceutical compositions and dietary supplements used in the methods of the invention can be administered by any means known in the art, e.g., parenterally, topically, orally, or by local administration, such as by aerosol or transdermally. The compositions and dietary supplements of the invention can be formulated as a tablet, gel, gellab, pill, implant, liquid, spray, powder, food, feed pellet, as an injectable formulation or as an encapsulated formulation. The pharmaceutical compositions and dietary supplements can be formulated in any way and can be administered in a variety of unit dosage forms depending upon the condition or disease and the degree of illness, the general medical condition of each patient, the resulting preferred method of administration and the like. Details on techniques for formulation and administration are well described in the scientific and patent literature, see, e.g., the latest edition of Remington's Pharmaceutical Sciences, Maack Publishing Co, Easton PA ("Remington's") (e.g., Remington, The Science and Practice of Pharmacy, 21st Edition, by University of the Sciences in Philadelphia, Editor).

Pharmaceutical formulations and dietary supplements can be prepared according to any method known to the art for the manufacture of pharmaceuticals and dietary supplements. Such drugs and dietary supplements can contain sweetening agents, flavoring agents, coloring agents and preserving agents. A formulation (which includes "dietary supplements") can be admixed with nontoxic pharmaceutically or orally acceptable excipients which are suitable for manufacture. Formulations may comprise one or more diluents, emulsifiers, preservatives, buffers, excipients, etc. and may be provided in such forms as liquids, powders, emulsions, lyophilized powders, sprays, creams, lotions, controlled release formulations, tablets, pills, gels, on patches, in implants, etc.

Pharmaceutical formulations and dietary supplements for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in appropriate and suitable dosages. Such carriers enable the pharmaceuticals and dietary supplements to be formulated in unit dosage forms as tablets, pills, powder, dragees, capsules, liquids, lozenges, gels, syrups, slurries, suspensions, etc., suitable for ingestion

by the patient. Pharmaceutical preparations and dietary supplements for oral use can be formulated as a solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable additional compounds, if desired, to obtain tablets or dragee cores. Suitable solid excipients are carbohydrate or protein fillers include, e.g., sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxy-methylcellulose; and gums including arabic and tragacanth; and proteins, e.g., gelatin and collagen. Disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

Dragee cores are provided with suitable coatings such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound (i.e., dosage). Pharmaceutical preparations and dietary supplements of the invention can also be used orally using, e.g., push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating such as glycerol or sorbitol. Push-fit capsules can contain active agents mixed with a filler or binders such as lactose or starches, lubricants such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active agents can be dissolved or suspended in suitable liquids, such as fatty oils, liquid paraffin, or liquid polyethylene glycol with or without stabilizers.

Aqueous suspensions can contain an active agent (e.g., an enzyme or peptidomimetic of the invention) in admixture with excipients suitable for the manufacture of aqueous suspensions. Such excipients include a suspending agent, such as sodium carboxymethylcellulose, methylcellulose, hydroxypropylmethylcellulose, sodium alginate, polyvinylpyrrolidone, gum tragacanth and gum acacia, and dispersing or wetting agents such as a naturally occurring phosphatide (e.g., lecithin), a condensation product of an alkylene oxide with a fatty acid (e.g., polyoxyethylene stearate), a condensation product of ethylene oxide with a long chain aliphatic alcohol (e.g., heptadecaethylene oxycetanol), a condensation product of ethylene oxide with a partial ester derived from a fatty acid and a hexitol (e.g., polyoxyethylene sorbitol mono-oleate), or a condensation product of ethylene oxide with a partial ester derived from fatty acid and a hexitol anhydride (e.g., polyoxyethylene sorbitan mono-oleate). The aqueous

suspension can also contain one or more preservatives such as ethyl or n-propyl p-hydroxybenzoate, one or more coloring agents, one or more flavoring agents and one or more sweetening agents, such as sucrose, aspartame or saccharin. Formulations can be adjusted for osmolarity.

Oil-based pharmaceuticals are particularly useful for administration of hydrophobic formulations or active agents of the invention. Oil-based suspensions can be formulated by suspending an active agent (e.g., a composition of the invention) in a vegetable oil, such as arachis oil, olive oil, sesame oil or coconut oil, or in a mineral oil such as liquid paraffin; or a mixture of these. See e.g., U.S. Patent No. 5,716,928 describing using essential oils or essential oil components for increasing bioavailability and reducing inter- and intra-individual variability of orally administered hydrophobic pharmaceutical compounds (see also U.S. Patent No. 5,858,401). The oil suspensions can contain a thickening agent, such as beeswax, hard paraffin or cetyl alcohol. Sweetening agents can be added to provide a palatable oral preparation, such as glycerol, sorbitol or sucrose. These formulations and dietary supplements can be preserved by the addition of an antioxidant such as ascorbic acid. As an example of an injectable oil vehicle, see Minto (1997) *J. Pharmacol. Exp. Ther.* 281:93-102.

The pharmaceutical formulations and dietary supplements of the invention can also be in the form of oil-in-water emulsions. The oily phase can be a vegetable oil or a mineral oil, described above, or a mixture of these. Suitable emulsifying agents include naturally-occurring gums, such as gum acacia and gum tragacanth, naturally occurring phosphatides, such as soybean lecithin, esters or partial esters derived from fatty acids and hexitol anhydrides, such as sorbitan mono-oleate, and condensation products of these partial esters with ethylene oxide, such as polyoxyethylene sorbitan mono-oleate. The emulsion can also contain sweetening agents and flavoring agents, as in the formulation of syrups and elixirs. Such formulations can also contain a demulcent, a preservative, or a coloring agent.

In the methods of the invention, the pharmaceutical compounds and dietary supplements can also be administered by intranasal, intraocular and intravaginal routes including suppositories, insufflation, powders and aerosol formulations (for examples of steroid inhalants, see Rohatagi (1995) *J. Clin. Pharmacol.* 35:1187-1193; Tjwa (1995) *Ann. Allergy Asthma Immunol.* 75:107-111). Suppositories formulations can be prepared by mixing the drug with a suitable non-irritating excipient which is solid at ordinary temperatures but liquid at body temperatures and will therefore melt in the body

to release the drug. Such materials are cocoa butter and polyethylene glycols.

In the methods of the invention, the pharmaceutical compounds and dietary supplements can be delivered by transdermally, by a topical route, formulated as applicator sticks, solutions, suspensions, emulsions, gels, creams, ointments, pastes, jellies, paints, powders, and aerosols.

In the methods of the invention, the pharmaceutical compounds and dietary supplements can also be delivered as microspheres for slow release in the body. For example, microspheres can be administered via intradermal injection of drug which slowly release subcutaneously; see Rao (1995) *J. Biomater Sci. Polym. Ed.* 7:623-645; as biodegradable and injectable gel formulations, see, e.g., Gao (1995) *Pharm. Res.* 12:857-863 (1995); or, as microspheres for oral administration, see, e.g., Eyles (1997) *J. Pharm. Pharmacol.* 49:669-674.

In the methods of the invention, the pharmaceutical compounds can be parenterally administered, such as by intravenous (IV) administration or administration into a body cavity or lumen of an organ. These formulations can comprise a solution of active agent dissolved in a pharmaceutically acceptable carrier. Acceptable vehicles and solvents that can be employed are water and Ringer's solution, an isotonic sodium chloride. In addition, sterile fixed oils can be employed as a solvent or suspending medium. For this purpose any bland fixed oil can be employed including synthetic mono- or diglycerides. In addition, fatty acids such as oleic acid can likewise be used in the preparation of injectables. These solutions are sterile and generally free of undesirable matter. These formulations may be sterilized by conventional, well known sterilization techniques. The formulations may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight, and the like, in accordance with the particular mode of administration selected and the patient's needs. For IV administration, the formulation can be a sterile injectable preparation, such as a sterile injectable aqueous or oleaginous suspension. This suspension can be formulated using those suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation can also be a suspension in a nontoxic parenterally-acceptable diluent or solvent, such as a solution of 1,3-butanediol. The administration can be by bolus or continuous infusion (e.g.,

substantially uninterrupted introduction into a blood vessel for a specified period of time).

The pharmaceutical compounds, formulations and dietary supplements of the invention can be lyophilized. The invention provides a stable lyophilized formulation comprising a composition of the invention, which can be made by lyophilizing a solution comprising a pharmaceutical of the invention and a bulking agent, e.g., mannitol, trehalose, raffinose, and sucrose or mixtures thereof. A process for preparing a stable lyophilized formulation can include the equivalent of lyophilizing a solution about 2.5 mg/mL protein, about 15 mg/mL sucrose, about 19 mg/mL NaCl, and a sodium citrate buffer having a pH greater than 5.5 but less than 6.5. See, e.g., U.S. patent app. no. 20040028670.

The compositions (e.g., formulations, including dietary supplements) of the invention can be delivered by the use of liposomes. By using liposomes, particularly where the liposome surface carries ligands specific for target cells, or are otherwise preferentially directed to a specific organ, one can focus the delivery of the active agent into target cells *in vivo*. See, e.g., U.S. Patent Nos. 6,063,400; 6,007,839; Al-Muhammed (1996) *J. Microencapsul.* 13:293-306; Chonn (1995) *Curr. Opin. Biotechnol.* 6:698-708; Ostro (1989) *Am. J. Hosp. Pharm.* 46:1576-1587.

The compositions (e.g., formulations, including dietary supplements) of the invention can be administered for prophylactic and/or therapeutic treatments. In therapeutic applications, compositions are administered to a subject already suffering from a condition, infection or disease of interest in an amount sufficient to cure, alleviate or partially arrest the clinical manifestations of the condition, infection or disease and its complications (a "therapeutically effective amount"). In the methods of the invention, a pharmaceutical composition is administered in an amount sufficient to treat (e.g., ameliorate) or prevent a disease-related condition, a diseases or a symptoms, or to decrease or increase the amount of substance in a body fluid such as blood, serum, CSF and the like. The amount of composition (e.g., pharmaceutical compositions, formulations, including dietary supplements) adequate to accomplish this is defined as a "therapeutically effective dose." The dosage schedule and amounts effective for this use, i.e., the "dosing regimen," will depend upon a variety of factors, including the stage of the disease or condition, the severity of the disease or condition, the general state of the patient's health, the patient's physical status, age and the like. In calculating the dosage regimen for a patient, the mode of administration also is taken into consideration.

The dosage regimen also takes into consideration pharmacokinetics parameters

well known in the art, i.e., the active agents' rate of absorption, bioavailability, metabolism, clearance, and the like (see, e.g., Hidalgo-Aragones (1996) *J. Steroid Biochem. Mol. Biol.* 58:611-617; Groning (1996) *Pharmazie* 51:337-341; Fotherby (1996) *Contraception* 54:59-69; Johnson (1995) *J. Pharm. Sci.* 84:1144-1146; Rohatagi (1995) *Pharmazie* 50:610-613; Brophy (1983) *Eur. J. Clin. Pharmacol.* 24:103-108; the latest Remington's, *supra*). The state of the art allows the clinician to determine the dosage regimen for each individual patient, active agent and disease or condition treated. Guidelines provided for similar compositions used as pharmaceuticals can be used as guidance to determine the dosage regiment, i.e., dose schedule and dosage levels, administered practicing the methods of the invention are correct and appropriate.

Single or multiple administrations of compositions (e.g., pharmaceutical compositions, formulations, including dietary supplements) of the invention can be given depending on the dosage and frequency as required and tolerated by the patient. The compositions should provide a sufficient quantity of active agent to effectively treat, ameliorate or prevent PKU or other PKU-related conditions, diseases or symptoms. For example, an exemplary pharmaceutical formulation for oral administration of a protein of the invention is in a daily amount of between about 0.1 to 0.5 to about 20, 50, 100 or 1000 or more μg per kilogram of body weight per day. In an alternative embodiment, dosages are from about 1 mg to about 4 mg per kg of body weight per patient per day are used. Lower dosages can be used, in contrast to administration orally, into the blood stream, into a body cavity or into a lumen of an organ. Substantially higher dosages can be used in topical or oral administration or administering by powders, spray or inhalation. Actual methods for preparing parenterally or non-parenterally administrable formulations will be known or apparent to those skilled in the art and are described in more detail in such publications as Remington's, *supra*.

The compositions (e.g., pharmaceutical compositions, formulations, including dietary supplements) of the invention can further comprise other drugs or pharmaceuticals, e.g., compositions for treating a disease of interest and related symptoms or conditions. The methods of the invention can further comprise co-administration with other drugs or pharmaceuticals, e.g., compositions for treating septic shock, infection, fever, pain and related symptoms or conditions. For example, the methods and/or compositions and formulations of the invention can be co-formulated with and/or co-administered with antibiotics (e.g., antibacterial or bacteriostatic peptides or proteins), particularly those effective against bacteria or toxins, e.g., germ warfare

agents, gram negative bacteria, fluids, cytokines, immunoregulatory agents, anti-inflammatory agents, complement activating agents, such as peptides or proteins comprising collagen-like domains or fibrinogen-like domains (e.g., a ficolin), carbohydrate-binding domains, and the like and combinations thereof.

In one aspect, the polypeptide (e.g., including a pharmaceutical composition or dietary supplement) of the invention is chemically modified. For example, the polypeptide can be chemically modified to produce a protected form that possesses better specific activity, prolonged half-life, and/or reduced immunogenicity *in vivo*. A polypeptide of the invention can be modified by any means known in the art, for example, by glycosylation, pegylation or a combination thereof.

In one aspect, the polypeptide (e.g., including a pharmaceutical composition or dietary supplement) of the invention is formulated by encapsulation in a liposome, or a micro- or nano-structure, such as a nanotubule or a nano- or microcapsule.

In one aspect, the polypeptide is formulated in a matrix stabilized enzyme crystal. The invention also provides matrix stabilized enzyme crystals comprising a polypeptide of the invention for use as pharmaceutical composition or dietary supplement, e.g., to treat or ameliorate a disease or condition of interest, e.g., as described in U.S. Patent App. No. 20020182201; for example, the formulation can be a cross-linked crystalline enzyme and a polymer with a reactive moiety effective to adhere to the crystal layer of the crystalline enzyme. The invention also provides polypeptides of the invention as polymers in the form of multimerized (e.g., multi-functional) cross-linking forms; which in one aspect comprise a matrix stabilized enzyme crystal, e.g., a form resistant to degradation by proteolytic enzymes; and in alternative aspects, the cross-linking reagents comprise a dialdehyde cross-linking reagent, such as a linear or branched dialdehyde, or a substituted or unsubstituted glutaraldehyde (1,5-pentanedial), malonaldehyde (1,3-propanedial), succinaldehyde (1,4-butanedial), adipaldehyde (1,6-hexanedial), pimelaldehyde (1,7-heptanedial), or, glutaraldehyde; in other alternative aspects, the cross-linking reagents comprise carbodiimides, isoxazolium derivatives, chloroformates, carbonyldiimidazole, bis-imidoesters, bis-succinimidyl derivatives, di-isocyanates, di-isothiocyanates, di-sulfonyl halides, bis-nitrophenyl esters, dialdehydes, diacylazides, bis-maleimides, bis-haloacetyl derivatives, di-alkyl halides and bis-oxiranes (e.g., as described in U.S. Pat. No. 5,753,487).

The compositions of the invention can also be manufactured into biocompatible matrices, e.g., sol-gels, for encapsulating a polypeptide of the invention for use as

pharmaceutical composition or dietary supplement, e.g., to treat or ameliorate a disease or condition of interest. In one aspect, compositions of the invention are manufactured as silica-based (e.g., oxysilane) sol-gel matrices, e.g., as described in U.S. Pat. No. 6,395,299, Pat. App. No. 20040241205. The invention also provides nano- or microcapsules comprising a composition of the invention for use as pharmaceutical composition or dietary supplement, e.g., to treat or ameliorate a disease or condition of interest, e.g., as described in U.S. Patent App. No. 20030157181.

The pharmaceutical compositions of the invention can be manufactured using any conventional method, e.g., mixing, dissolving, granulating, dragée-making, levigating, emulsifying, encapsulating, entrapping, melt-spinning, spray-drying, or lyophilizing processes. Alternative pharmaceutical formulations can be determined depending on the patient (e.g., adult or pediatric), condition, route of administration (e.g., oral) and the desired dosage.

Applications – Industrial, Medical, Experimental, Food and Feed Processing

Polypeptides (including enzymes and antibodies) and nucleic acids of the invention can be used for a variety of industrial, experimental, food and feed processing, nutritional and pharmaceutical applications, e.g., for food and feed supplements, colorants, nutraceuticals, cosmetic and pharmaceutical needs.

Polypeptides of the invention (e.g., having enzyme, structural or binding activity) can be highly selective catalysts. The invention provides methods using enzymes of the invention in the food and feed industries, e.g., in methods for making food and feed products and food and feed additives. In one aspect, the invention provides processes using enzymes of the invention in the medical industry, e.g., to make pharmaceuticals.

The enzymes of the invention can catalyze reactions with exquisite stereo-, regio- and chemo- selectivities. The polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention can be engineered to function in various solvents, operate at extreme pHs (for example, high pHs and low pHs) extreme temperatures (for example, high temperatures and low temperatures), extreme salinity levels (for example, high salinity and low salinity) and catalyze reactions with compounds that are structurally unrelated to their natural, physiological substrates.

Animal feeds and food or feed additives

The invention provides compositions (e.g., enzymes of the invention, as those described in Tables 1, 2, and 3) methods for treating animal feeds and foods and food or

feed additives using a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention, and/or the antibodies of the invention. The invention provides animal feeds, foods, and additives comprising a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention, antibodies of the invention. The animal can be any farm animal or any animal raised for its meat, e.g., a pig, goat, cattle, sheep, horse and the like.

The animal feed additive of the invention may be a granulated enzyme product that may readily be mixed with feed components. Alternatively, feed additives of the invention can form a component of a pre-mix. The granulated enzyme product of the invention may be coated or uncoated. The particle size of the enzyme granulates can be compatible with that of feed and pre-mix components. This provides a safe and convenient mean of incorporating enzymes into feeds. Alternatively, the animal feed additive of the invention may be a stabilized liquid composition. This may be an aqueous or oil-based slurry. See, e.g., U.S. Patent No. 6,245,546.

A polypeptide, enzyme, protein, e.g. structural or binding protein, of the present invention, in the modification of animal feed or a food, can process the food or feed either *in vitro* (by modifying components of the feed or food) or *in vivo*. Polypeptides of the invention can be added to animal feed or food compositions.

In one aspect, an enzyme of the invention has any of the following enzyme activities, or is added in combination with another enzyme, e.g., beta-galactosidases, catalases, laccases, cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylo-laccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, cellobiohydrolases and/or transglutaminases. These enzyme digestion products are more digestible by the animal. Thus, a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention can contribute to the available energy of the feed or food. Also, a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention can improve the digestibility and uptake of carbohydrate and non-carbohydrate feed or food constituents such as protein, fat and minerals.

In another aspect, a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention can be supplied by expressing the enzymes directly in transgenic feed crops (as, e.g., transgenic plants, seeds and the like), such as grains, cereals, corn, soy bean, rape seed, lupin and the like. As discussed above, the invention provides transgenic plants, plant parts and plant cells comprising a nucleic acid sequence encoding a polypeptide of the invention. In one aspect, the nucleic acid is expressed such that the polypeptide, enzyme, protein, e.g. structural or binding protein of the invention is produced in recoverable quantities. The polypeptide, enzyme, protein, e.g. structural or binding protein can be recovered from any plant or plant part. Alternatively, the plant or plant part containing the recombinant polypeptide can be used as such for improving the quality of a food or feed, e.g., improving nutritional value, palatability, etc.

The enzyme delivery matrix of the invention is in the form of discrete plural particles, pellets or granules. By "granules" is meant particles that are compressed or compacted, such as by a pelletizing, extrusion, or similar compacting to remove water from the matrix. Such compression or compacting of the particles also promotes intraparticle cohesion of the particles. For example, the granules can be prepared by pelletizing the grain-based substrate in a pellet mill. The pellets prepared thereby are ground or crumbled to a granule size suitable for use as an adjuvant in animal feed. Since the matrix is itself approved for use in animal feed, it can be used as a diluent for delivery of enzymes in animal feed.

The polypeptide, enzyme, protein, e.g. structural or binding protein contained in the invention enzyme delivery matrix and methods is in one aspect thermostable polypeptide, enzyme, protein, e.g. structural or binding protein, as described herein, so as to resist inactivation of the polypeptide, enzyme, protein, e.g. structural or binding protein during manufacture where elevated temperatures and/or steam may be employed to prepare the palletized enzyme delivery matrix. During digestion of feed containing the invention enzyme delivery matrix, aqueous digestive fluids will cause release of the active enzyme. Other types of thermostable enzymes and nutritional supplements that are thermostable can also be incorporated in the delivery matrix for release under any type of aqueous conditions.

A coating can be applied to the invention enzyme matrix particles for many different purposes, such as to add a flavor or nutrition supplement to animal feed, to delay release of animal feed supplements and enzymes in gastric conditions, and the like. Or, the coating may be applied to achieve a functional goal, for example, whenever it is

desirable to slow release of the enzyme from the matrix particles or to control the conditions under which the enzyme will be released. The composition of the coating material can be such that it is selectively broken down by an agent to which it is susceptible (such as heat, acid or base, enzymes or other chemicals). Alternatively, two or more coatings susceptible to different such breakdown agents may be consecutively applied to the matrix particles.

The invention is also directed towards a process for preparing an enzyme-releasing matrix. In accordance with the invention, the process comprises providing discrete plural particles of a grain-based substrate in a particle size suitable for use as an enzyme-releasing matrix, wherein the particles comprise a polypeptide, enzyme, protein, e.g. structural or binding protein, encoded by an amino acid sequence of the invention. In one aspect, the process includes compacting or compressing the particles of enzyme-releasing matrix into granules, which most in one aspect is accomplished by pelletizing. The mold inhibitor and cohesiveness agent, when used, can be added at any suitable time, and in one aspect are mixed with the grain-based substrate in the desired proportions prior to pelletizing of the grain-based substrate. Moisture content in the pellet mill feed in one aspect is in the ranges set forth above with respect to the moisture content in the finished product, and in one aspect is about 14-15%. In one aspect, moisture is added to the feedstock in the form of an aqueous preparation of the enzyme to bring the feedstock to this moisture content. The temperature in the pellet mill in one aspect is brought to about 82°C with steam. The pellet mill may be operated under any conditions that impart sufficient work to the feedstock to provide pellets. The pelleting process itself is a cost-effective process for removing water from the enzyme-containing composition.

The compositions and methods of the invention can be practiced in conjunction with various nutritional and environmental factors including, e.g., (1) manipulation of gut microflora by supplementing feed with prebiotics and/or antibiotics, (2) low fiber diet (low energy and low purine diet), (3) restricting feed for 48 hours and withholding feed for 12 hours before slaughter, (4) increasing consumption of water, and/or (5) keeping animals clean.

The compositions and methods of the invention can be practiced in conjunction with administration of prebiotics, which are high molecular weight sugars, e.g., fructo-oligosaccharides (FOS); galacto-oligosaccharides (GOS), GRAS (Generally Recognized As Safe) material. These prebiotics can be metabolized by some probiotic lactic acid bacteria (LAB). They are non-digestible by the majority of intestinal microbes.

Treating foods and food processing

The polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention, e.g., as described in Tables 1, 2, and 3, have numerous applications in food processing industry. The invention provides treatment compositions, including, e.g., a plant cell, a bacterial cell, a yeast cell, an insect cell, or an animal cell, or any plant or plant part, or any food or feed, a waste product and the like.

The invention provides feeds or foods comprising a polypeptide, enzyme, protein, e.g. structural or binding protein, the invention, e.g., a feed, a liquid, e.g., a beverage (such as a fruit juice or a beer), a bread or a dough or a bread product, or a beverage precursor (e.g., a wort).

The food treatment processes of the invention can comprise use of any enzyme of the invention, which can have the following enzymatic activities, and also include the use of any combination of any enzyme, including lyases, laccases, catalases, laccases, cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipoxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylolaccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, cellobiohydrolases and/or transglutaminases.

Confectionaries, cacao butter and foods

In one aspect, the compositions and methods of the invention can be used to make and process hard butters, such as cacao butter (cocoa butter). The compositions and methods of the invention can be used to make cocoa butter alternatives by "structured" synthetic techniques using the enzymes of the invention, e.g., as described in Tables 1, 2, and 3, including esterases, acylases, lipases, phospholipases or proteases of the invention. For example, in one aspect, the methods of the invention process or synthesize triacylglycerides, diacylglycerides and/or monoacylglycerides for use as, e.g., cocoa butter alternatives. In one aspect, the methods of the invention generate a hard butter with a defined "plastic region" to maintain sufficient hardness below or at room temperature. In one aspect, the processed or synthesized lipid is designed to have a very narrow "plastic region," e.g., in one aspect, where it rapidly melts at about body temperature. Natural cacao butter begins to soften at approximately 30°C to 32°C, and

completely melts at approximately 36°C. Natural cacao butter can contain 70 wt % or more of three 1,3-disaturated -2-oleoyl glycerols, which are 1,3-dipalmitoyl-2-oleoyl glycerol (POP), 1-palmitoyl-2-oleoyl glycerol (POSt) and 1,3-distearoyl-2-oleoyl glycerol (StOSt). These three glycerols show a similar melting behavior to each other and are responsible for melting properties of the cacao butter, exhibiting a very narrow plastic region. The invention provides synthetic cacao butters or processed cacao butters (synthesized or processed using a hydrolase of the invention, all possible composition are referred to as cocoa-butter alternatives) with varying percentages of 1,3-dipalmitoyl-2-oleoyl glycerol (POP), 1-palmitoyl-2-oleoyl glycerol (POSt) and 1,3-distearoyl-2-oleoyl glycerol (StOSt), depending on the desired properties of the synthetic cacao butter, and, synthetic cacao butters with more or less than 70 wt % of the three 1,3-disaturated -2-oleoyl glycerols. The synthetic cacao butters of the invention can partially or completely replace natural or unprocessed cacao butters and can maintain or improve essential hard butter properties.

The invention provides synthetic cacao butters or processed cacao butters (synthesized or processed using a hydrolase of the invention) with desired properties for use in confectionary, bakery and pharmaceutical products. In one aspect, the invention provides confectionary, bakery and pharmaceutical products comprising a hydrolase of the invention. In one aspect, the methods of the invention make or process a lipid (a fat) from a confection (e.g., a chocolate) or to be used in a confection. In one aspect, a lipid is made or processed such that the chocolate shows less finger-imprinting than chocolate made from natural cocoa butter, while still having sharp melting characteristics in the mouth. In one aspect, a lipid is made or processed such that a confection (e.g., chocolate) can be made at a comparatively high ambient temperature, or, be made using a cooling water at a comparatively high temperature. In one aspect, the lipid is made or processed such that a confection (e.g., chocolate) can be stored under relatively warmer conditions, e.g., tropical or semi-tropical conditions or in centrally heated buildings. In one aspect, the lipids are made or processed such that a confection (e.g., chocolate) will have a lipid (fat) content of consistent composition and quality. The enzymes of the invention can be used to provide a substitute composition for cacao butter which can significantly improve its thermal stability and replace it in a wide range of applications.

Margarine and shortening production

The invention provides synthetic or processed fats, e.g., margarine and shortening synthesized or processed using an enzyme of the invention, e.g., as described in Tables 1,

2, and 3, such as a hydrolase of the invention. In one aspect, the invention provides processed fats comprising a vegetable oil, such as soybean oil, corn oil, rapeseed oil, palm oil or lauric type oils synthesized or processed using a hydrolase of the invention. The synthetic or processed fats, e.g., margarine and shortening, are designed to have a desired "plasticity." Many of the plastic fat products, such as margarine and shortening, are produced from hard stocks and liquid oils as raw materials. For example, liquid oils such as soybean oil, corn oil, palm oil and rapeseed oil, are blended with their hardened oils (hard stocks), and the blend is adjusted to have an appropriate consistency (plasticity). The plastic fat products such as margarine and shortening so produced tend to cause the formation of relatively coarse crystallines because fats and oils used as the raw materials are composed of fatty acids having almost the same carbon chain length. In other words, they have a highly-unified composition of fatty acids. For this reason, the plasticity of these products can be maintained at an appropriate degree only within a narrow temperature range, so that the liquid oils contained therein have a tendency to exude. In one aspect, the invention provides methods of making or processing fats designed such that they have a varied (and defined) composition of fatty acids. The resultant oil, e.g., margarine or shortening, can have a broader range of plasticity.

In one aspect, the methods and compositions of the invention are used to make or process vegetable oils, such as soybean oil, corn oil, rapeseed oil, palm oil or lauric type oils using the hydrolases of the invention, including inter-esterification and enzymatic transesterification, see e.g., U.S. Patent No. 5,288,619. The methods and compositions of the invention can be used in place of random inter-esterification as described in, e.g., U.S. Patent No. 3,949,105. In one aspect, the methods and compositions of the invention are used to in enzymatic transesterification for preparing an oil, e.g., a margarine oil, having both low trans- acid and low intermediate chain fatty acid content.

In one aspect, the symmetric structure of an oil, e.g., a palm or lauric type oils is modified, e.g., into a random structure. Thus, the methods of the invention can be used to modify the properties of plastic fat products. In one aspect, the modification of oils by the methods of the invention can be designed to prevent or slow gradually hardening of the oil with time, particularly when the products are being stored.

In one aspect, the methods and compositions of the invention in a trans-esterification reaction mixture comprising a stearic acid source material and an edible liquid vegetable oil, trans-esterifying the stearic acid source material and the vegetable oil using a 1-, 3-positionally specific lipase of the invention, and then hydrogenating the fatty

acid mixture to provide a recycle stearic acid source material for a recyclic reaction with the vegetable oil. See e.g., U.S. Patent No. 5,288,619.

In one aspect, an inter-esterification reaction is conducted with a lipase of the invention. In one aspect, the lipase of the invention has a selectivity for the 1- and 3-positions of triglyceride to slow or inhibit an increase in the amount of tri-saturated triglycerides in the oil. In this reaction of the invention, deficiencies of conventional random inter-esterification and the difficulty of inter-esterification with a non-specific lipase can be overcome because the inter-esterification is conducted by an enzyme of the invention having a specificity for the 1- and 3- positions of triglycerides. In one aspect, the exudation of liquid oils contained in the products is slowed or prevented with a temperature increase in the reaction to inhibit a rise in the melting point caused by an increase in the amount of tri-saturated triglycerides. This addresses the problem of hardening of products during long-term storage.

Brewing and fermenting

The invention provides methods of brewing (e.g., fermenting) beer comprising hydrolases of the invention. In one exemplary process, starch-containing raw materials are disintegrated and processed to form a malt. A hydrolase of the invention is used at any point in the fermentation process. For example, hydrolases (e.g., proteases) of the invention can be used in the processing of barley malt. The major raw material of beer brewing is barley malt. This can be a three stage process. First, the barley grain can be steeped to increase water content, e.g., to around about 40%. Second, the grain can be germinated by incubation at 15 to 25°C for 3 to 6 days when enzyme synthesis is stimulated under the control of gibberellins. In one aspect, hydrolases of the invention are added at this (or any other) stage of the process. The action of hydrolases results in an increase in fermentable reducing sugars. This can be expressed as the diastatic power, DP, which can rise from around 80 to 190 in 5 days at 12°C. Hydrolases (e.g., proteases) of the invention can be used in any beer or alcoholic beverage producing process, as described, e.g., in U.S. Patent No. 5,762,991; 5,536,650; 5,405,624; 5,021,246; 4,788,066.

Waste treatment

The polypeptide, enzyme, protein, e.g. structural or binding proteins of the invention, e.g., as described in Tables 1, 2, and 3, can be used in a variety of other industrial applications, e.g., in waste treatment (in addition to, e.g., biomass conversion to

fuels). For example, in one aspect, the invention provides a solid waste digestion process using a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention. The methods can comprise reducing the mass and volume of substantially untreated solid waste. Solid waste can be treated with an enzymatic digestive process in the presence of an enzymatic solution (including a polypeptide, enzyme, protein, e.g. structural or binding protein, of the invention) at a controlled temperature. This results in a reaction without appreciable bacterial fermentation from added microorganisms. The solid waste is converted into a liquefied waste and any residual solid waste. The resulting liquefied waste can be separated from said any residual solidified waste. See e.g., U.S. Patent No. 5,709,796.

In one aspect, the compositions and methods of the invention are used for odor removal or odor reduction in animal waste lagoons, e.g., on swine farms, and other animal waste management systems.

The waste treatment processes of the invention can comprise use of any enzyme of the invention, which can have the following enzymatic activities, and also include the use of any combination of any enzyme or protein, including e.g. structural or binding protein, catalases, lyases, laccases, cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, phytases, arabinanases, hemicellulases, mannanases, xylolaccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, cellobiohydrolases and/or transglutaminases.

Increasing the flow of production fluids from a subterranean formation

The invention also includes a method using an enzyme of the invention, e.g., as described in Tables 1, 2, and 3, wherein the method increases the flow of production fluids from a subterranean formation by removing viscous (e.g., starch-containing) damaging fluids formed during production operations; these fluids can be found within the subterranean formation which surrounds a completed well bore. Thus, this method of the invention results in production fluids being able to flow from the well bore. This method of the invention also addresses the problem of damaging fluids reducing the flow of production fluids from a formation below expected flow rates. In one aspect, the

invention provides for formulating an enzyme treatment (using an enzyme of the invention) by blending together an aqueous fluid and a polypeptide of the invention; pumping the enzyme treatment to a desired location within the well bore; allowing the enzyme treatment to degrade the viscous (e.g., starch-containing) damaging fluid, whereby the fluid can be removed from the subterranean formation to the well surface; and wherein the enzyme treatment is effective to attack linkages in the viscous (e.g., starch-containing) fluid.

The subterranean formation enzyme treatment processes of the invention can comprise use of any enzyme of the invention, which can have the following enzymatic activities, and also include the use of any combination of any enzyme, including tryptophanases or tyrosine decarboxylases, laccases, catalases, lyases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylolaccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Latex processing

The methods and compositions (e.g., enzymes of the invention, e.g., as described in Tables 1, 2, and 3, including esterases, acylases, lipases, phospholipases or proteases of the invention) of the invention can be used to selectively hydrolyze saturated esters over unsaturated esters into acids or alcohols. In one aspect, the invention provides for the selective hydrolysis of ethyl propionate over ethyl acrylate. In one aspect, these methods are used to remove undesired esters from monomer feeds used in latex polymerization and from the latexes after polymerization. The methods and compositions (hydrolases) of the invention can be used to treat latexes for a variety of purposes, e.g., to treat latexes used in hair fixative compositions to remove unpleasant odors. Latexes treated by the methods and compositions of the invention include, e.g., polymers containing acrylic, vinyl and unsaturated acid monomers, including alkyl acrylate monomers such as methyl acrylate, ethyl acrylate, propyl acrylate and butyl acrylate, and acrylate acids such as acrylic acid, methacrylic acid, crotonic acid, itaconic acid and mixtures thereof. See, e.g.,

U.S. Patent No. 5,856,150.

Biomass conversion and production of clean bio fuels

The invention provides enzymes, e.g., as described in Tables 1, 2, and 3 (including mixtures, or "cocktails" of enzymes) and methods for the conversion of a biomass or any lignocellulosic material (e.g., any composition comprising cellulose, hemicellulose and lignin), to fuels (e.g., bioethanol, biodiesel), in addition to feeds, foods and chemicals. Thus, the compositions and methods of the invention provide effective and sustainable alternatives or adjuncts to use of petroleum-based products, e.g., as a mixture of bioethanol and gasoline. The invention provides organisms expressing enzymes of the invention for participation in chemical cycles involving natural biomass conversion. In one aspect, enzymes and methods for the conversion are used in enzyme ensembles for the efficient depolymerization of cellulosic and hemicellulosic polymers to metabolizeable carbon moieties. The invention provides methods for discovering and implementing the most effective of enzymes to enable these important new "biomass conversion" and alternative energy industrial processes.

The methods of the invention also include taking the converted lignocellulosic material (processed by enzymes of the invention) and making it into a fuel (e.g. a bioethanol, a biodiesel) by fermentation and/or by chemical synthesis. In one aspect, the produced sugars are fermented and/or the non-fermentable products are gasified.

The enzymes of the invention (including, for example, organisms, such as microorganisms, e.g., fungi, yeast or bacteria, making and in some aspects secreting recombinant enzymes of the invention) can be used in or included/ integrated at any stage of any biomass conversion process, e.g., at any one step, several steps, or included in all of the steps, or all of the following methods of biomass conversion processes, or all of these biofuel alternatives:

- Direct combustion: the burning of material by direct heat and is the simplest biomass technology; can be very economical if a biomass source is nearby.
- Pyrolysis: is the thermal degradation of biomass by heat in the absence of oxygen. In one aspect, biomass is heated to a temperature between about 800 and 1400 degrees Fahrenheit, but no oxygen is introduced to support combustion resulting in the creation of gas, fuel oil and charcoal.
- Gasification: biomass can be used to produce methane through heating or anaerobic digestion. Syngas, a mixture of carbon monoxide and hydrogen, can be derived from biomass.
 - Landfill Gas: is generated by the decay (anaerobic digestion) of buried garbage in landfills. When the organic waste decomposes, it generates gas consisting of approximately 50% methane, the major component of natural gas.

- Anaerobic digestion: converts organic matter to a mixture of methane, the major component of natural gas, and carbon dioxide. In one aspect, biomass such as wastewater (sewage), manure, or food processing waste, is mixed with water and fed into a digester tank without air.
- Fermentation
 - Alcohol Fermentation: fuel alcohol is produced by converting starch to sugar, fermenting the sugar to alcohol, then separating the alcohol water mixture by distillation. Feedstocks such as wheat, barley, potatoes, and waste paper, sawdust, and straw containing sugar, starch, or cellulose can be converted to alcohol by fermentation with yeast.
- Transesterification: An exemplary reaction for converting oil to biodiesel is called transesterification. The transesterification process reacts an alcohol (like methanol) with the triglyceride oils contained in vegetable oils, animal fats, or recycled greases, forming fatty acid alkyl esters (biodiesel) and glycerin. The reaction requires heat and a strong base catalyst, such as sodium hydroxide or potassium hydroxide.
 - Biodiesel: Biodiesel is a mixture of fatty acid alkyl esters made from vegetable oils, animal fats or recycled greases. Biodiesel can be used as a fuel for vehicles in its pure form, but it is usually used as a petroleum diesel additive to reduce levels of particulates, carbon monoxide, hydrocarbons and air toxics from diesel-powered vehicles.
- Hydrolysis: includes hydrolysis of a compound, e.g., a biomass, such as a lignocellulosic material, catalyzed using an enzyme of the instant invention.
- Cogeneration: is the simultaneous production of more than one form of energy using a single fuel and facility. In one aspect, biomass cogeneration has more potential growth than biomass generation alone because cogeneration produces both heat and electricity.

In one aspect, the polypeptides of the invention have cellulolytic activity, e.g., cellulases activity, such as endoglucanase, cellobiohydrolase and/or β -glucosidase (beta-glucosidase) activity, or other enzymatic activity for generating biodiesel or bioethanol from an organic material, e.g., a biomass, such as compositions derived from plants and animals, including any agricultural crop or other renewable feedstock, an agricultural residue or an animal waste, or the organic components of municipal and industrial wastes, or microorganisms such as algae or yeast. In one aspect, polypeptides of the invention are used in processes for converting lignocellulosic biomass to ethanol, or otherwise are used in processes for hydrolyzing or digesting biomaterials such that they can be used as a biofuel (including biodiesel or bioethanol), or for making it easier for the biomass to be processed into a fuel. In an alternative aspect, polypeptides of the invention are used in processes for a transesterification process reacting an alcohol (like methanol) with a triglyceride oil contained in a vegetable oil, animal fat or recycled greases, forming fatty acid alkyl esters (biodiesel) and glycerin. In one aspect, biodiesel is made from soybean

oil or recycled cooking oils. Animal's fats, other vegetable oils, and other recycled oils can also be used to produce biodiesel, depending on their costs and availability. In another aspect, blends of all kinds of fats and oils are used to produce a biodiesel fuel of the invention.

Enzymes of the invention can also be used in glycerin refining. The glycerin by-product contains unreacted catalyst and soaps that are neutralized with an acid. Water and alcohol are removed to produce 50% to 80% crude glycerin. The remaining contaminants include unreacted fats and oils, which can be processed using the polypeptides of the invention. In a large biodiesel plant of the invention, the glycerin can be further purified, e.g., to 99% or higher purity, for the pharmaceutical and cosmetic industries.

Both bioethanol and biodiesel made using the polypeptides of the invention can be used with fuel oxygenates to improve combustion characteristics. Adding oxygen results in more complete combustion, which reduces carbon monoxide emissions. This is another environmental benefit of replacing petroleum fuels with biofuels (e.g., a fuel of the invention). A bioethanol made using the compositions and/or methods of this invention can be blended with gasoline to form an E10 blend (about 5% to 10% ethanol and about 90% to 95% gasoline), but it can be used in higher concentrations such as E85 or in its pure form. A bioethanol made using the compositions and/or methods of this invention can be blended with petroleum diesel to form a B20 blend (20% biodiesel and 80% petroleum diesel), although other blend levels can be used up to B100 (pure biodiesel).

The invention also provides processes for making ethanol ("bioethanol") from compositions comprising lignocellulosic biomass. The lignocellulose biomass material can be obtained from agricultural crops, as a byproduct of food or feed production, or as lignocellulosic waste products, such as plant residues and waste paper. Examples of suitable plant sources or plant residues for treatment with polypeptides of the invention include kelp, algae, grains, seeds, stems, leaves, hulls, husks, corn cobs, corn stover, straw, grasses (e.g., Indian grass, such as *Sorghastrum nutans*; or, switch grass, e.g., *Panicum* species, such as *Panicum virgatum*), and the like, as well as wood, wood chips, wood pulp, and sawdust. Examples of paper waste suitable for treatment with polypeptides of the invention include discard photocopy paper, computer printer paper, notebook paper, notepad paper, typewriter paper, and the like, as well as newspapers, magazines, cardboard, and paper-based packaging materials.

In one aspect, the enzymes and methods of the invention can be used in conjunction with more "traditional" means of making ethanol from biomass, e.g., as methods comprising hydrolyzing lignocellulosic materials by subjecting dried lignocellulosic material in a reactor to a catalyst comprised of a dilute solution of a strong acid and a metal salt; this can lower the activation energy, or the temperature, of cellulose hydrolysis to obtain higher sugar yields; see, e.g., U.S. Patent Nos. 6,660,506; 6,423,145.

Another exemplary method that incorporated use of enzymes of the invention comprises hydrolyzing lignocellulosic material containing hemicellulose, cellulose and lignin by subjecting the material to a first stage hydrolysis step in an aqueous medium at a temperature and a pressure chosen to effect primarily depolymerization of hemicellulose without major depolymerization of cellulose to glucose. This step results in a slurry in which the liquid aqueous phase contains dissolved monosaccharides resulting from depolymerization of hemicellulose and a solid phase containing cellulose and lignin. A second stage hydrolysis step can comprise conditions such that at least a major portion of the cellulose is depolymerized, such step resulting in a liquid aqueous phase containing dissolved/ soluble depolymerization products of cellulose. See, e.g., U.S. Patent No. 5,536,325. Enzymes of the invention can be added at any stage of this exemplary process.

Another exemplary method that incorporated use of enzymes of the invention comprises processing a lignocellulose-containing biomass material by one or more stages of dilute acid hydrolysis with about 0.4% to 2% strong acid; and treating an unreacted solid lignocellulosic component of the acid hydrolyzed biomass material by alkaline delignification to produce precursors for biodegradable thermoplastics and derivatives. See, e.g., U.S. Patent No. 6,409,841. Enzymes of the invention can be added at any stage of this exemplary process.

Another exemplary method that incorporated use of enzymes of the invention comprises prehydrolyzing lignocellulosic material in a prehydrolysis reactor; adding an acidic liquid to the solid lignocellulosic material to make a mixture; heating the mixture to reaction temperature; maintaining reaction temperature for time sufficient to fractionate the lignocellulosic material into a solubilized portion containing at least about 20% of the lignin from the lignocellulosic material and a solid fraction containing cellulose; removing a solubilized portion from the solid fraction while at or near reaction temperature wherein the cellulose in the solid fraction is rendered more amenable to enzymatic digestion; and recovering a solubilized portion. See, e.g., U.S. Patent No.

5,705,369. Enzymes of the invention can be added at any stage of this exemplary process.

The invention provides methods for making motor fuel compositions (e.g., for spark ignition motors) based on liquid hydrocarbons blended with a fuel grade alcohol made by using an enzyme or a method of the invention. In one aspect, the fuels made by use of an enzyme of the invention comprise, e.g., coal gas liquid- or natural gas liquid-ethanol blends. In one aspect, a co-solvent is biomass-derived 2-methyltetrahydrofuran (MTHF). See, e.g., U.S. Patent No. 6,712,866.

In one aspect, methods of the invention for the enzymatic degradation of lignocellulose, e.g., for production of ethanol from lignocellulosic material, can also comprise use of ultrasonic treatment of the biomass material; see, e.g., U.S. Patent No. 6,333,181.

In another aspect, methods of the invention for producing bioethanol from a cellulosic substrate comprise providing a reaction mixture in the form of a slurry comprising cellulosic substrate, an enzyme of this invention and a fermentation agent (e.g., within a reaction vessel, such as a semi-continuously solids-fed bioreactor), and the reaction mixture is reacted under conditions sufficient to initiate and maintain a fermentation reaction (as described, e.g., in U.S. Pat. App. No. 20060014260). In one aspect, experiment or theoretical calculations can determine an optimum feeding frequency. In one aspect, additional quantities of the cellulosic substrate and the enzyme are provided into the reaction vessel at an interval(s) according to the optimized feeding frequency.

One exemplary process for making a biofuels and biodiesels of the invention is described in U.S. Pat. App. Pub. Nos. 20050069998; 20020164730; and in one aspect comprises stages of grinding the lignocellulosic biomass (e.g., to a size of 15-30 mm), subjecting the product obtained to steam explosion pre-treatment (e.g., at a temperature of 190-230°C) for between 1 and 10 minutes in a reactor; collecting the pre-treated material in a cyclone or related product of manufacture; and separating the liquid and solid fractions by filtration in a filter press, introducing the solid fraction in a fermentation deposit and adding one or more enzymes of the invention, e.g., a cellulase and/or beta-glucosidase enzyme (e.g., dissolved in citrate buffer pH 4.8).

Another exemplary process for making a biofuels and biodiesels of the invention comprising ethanol using enzymes of the invention comprises pretreating a starting material comprising a lignocellulosic feedstock comprising at least hemicellulose and

cellulose. In one aspect, the starting material comprises potatoes, soybean (rapeseed), barley, rye, corn, oats, wheat, beets or sugar cane or a component or waste or food or feed production byproduct. The starting material ("feedstock") is reacted at conditions which disrupt the plant's fiber structure to effect at least a partial hydrolysis of the hemicellulose and cellulose. Disruptive conditions can comprise, e.g., subjecting the starting material to an average temperature of 180°C to 270°C at pH 0.5 to 2.5 for a period of about 5 seconds to 60 minutes; or, temperature of 220°C to 270°C, at pH 0.5 to 2.5 for a period of 5 seconds to 120 seconds, or equivalent. This generates a feedstock with increased accessibility to being digested by an enzyme, e.g., a cellulase enzyme of the invention. U.S. Patent No. 6,090,595.

Exemplary conditions for cellulase hydrolysis of lignocellulosic material include reactions at temperatures between about 30°C and 48°C, and/or a pH between about 4.0 and 6.0. Other exemplary conditions include a temperature between about 30°C and 60°C and a pH between about 4.0 and 8.0.

Detergent Compositions

The invention provides detergent compositions comprising one or more polypeptides of the invention (e.g., enzymes as described in Tables 1, 2, and 3, e.g., having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity) and methods of making and using these compositions. The invention incorporates all methods of making and using detergent compositions, see, e.g., U.S. Patent No. 6,413,928; 6,399,561; 6,365,561; 6,380,147. The detergent compositions can be a one and two part aqueous composition, a non-aqueous liquid composition, a cast solid, a granular form, a particulate form, a compressed tablet, a gel and/or a paste and a slurry form. The invention also provides methods capable of a rapid removal of gross food soils, films of food residue and other minor food compositions using these detergent compositions. Enzymes of the invention can facilitate the removal of starchy stains by means of catalytic hydrolysis of the starch polysaccharide. Enzymes of the invention can be used in dishwashing detergents in textile laundering detergents.

The actual active enzyme content depends upon the method of manufacture of a detergent composition and is not critical, assuming the detergent solution has the desired enzymatic activity. In one aspect, the amount of glucosidase present in the final solution ranges from about 0.001 mg to 0.5 mg per gram of the detergent composition. The particular enzyme chosen for use in the process and products of this invention depends upon the conditions of final utility, including the physical product form, use pH, use

temperature, and soil types to be degraded or altered. The enzyme can be chosen to provide optimum activity and stability for any given set of utility conditions. In one aspect, the polypeptides of the present invention are active in the pH ranges of from about 4 to about 12 and in the temperature range of from about 20°C to about 95°C. The detergents of the invention can comprise cationic, semi-polar nonionic or zwitterionic surfactants; or, mixtures thereof.

Enzymes of the present invention (e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity) can be formulated into powdered and liquid detergents having pH between 4.0 and 12.0 at levels of about 0.01 to about 5% (preferably 0.1% to 0.5%) by weight. These detergent compositions can also include other enzymes such as known proteases, cellulases, lipases or endoglycosidases, as well as builders and stabilizers. The addition of enzymes of the invention to conventional cleaning compositions does not create any special use limitation. In other words, any temperature and pH suitable for the detergent is also suitable for the present compositions as long as the pH is within the above range, and the temperature is below the described enzyme's denaturing temperature. In addition, the polypeptides of the invention can be used in a cleaning composition without detergents, again either alone or in combination with builders and stabilizers.

The present invention provides cleaning compositions including detergent compositions for cleaning hard surfaces, detergent compositions for cleaning fabrics, dishwashing compositions, oral cleaning compositions, denture cleaning compositions, and contact lens cleaning solutions.

In one aspect, the invention provides a method for washing an object comprising contacting the object with a polypeptide of the invention under conditions sufficient for washing. A polypeptide of the invention may be included as a detergent additive. The detergent composition of the invention may, for example, be formulated as a hand or machine laundry detergent composition comprising a polypeptide of the invention. A laundry additive suitable for pre-treatment of stained fabrics can comprise a polypeptide of the invention. A fabric softener composition can comprise a polypeptide of the invention. Alternatively, a polypeptide of the invention can be formulated as a detergent composition for use in general household hard surface cleaning operations. In alternative aspects, detergent additives and detergent compositions of the invention may comprise one or more other enzymes such as a protease, a lipase, a cutinase, another glucosidase, a carbohydrase, another cellulase, a pectinase, a mannanase, an arabinase, a galactanase, a

xylanase, an oxidase, e.g., a lactase, and/or a peroxidase. The properties of the enzyme(s) of the invention are chosen to be compatible with the selected detergent (i.e. pH-optimum, compatibility with other enzymatic and non-enzymatic ingredients, etc.) and the enzyme(s) is present in effective amounts. In one aspect, enzymes of the invention are used to remove malodorous materials from fabrics. Various detergent compositions and methods for making them that can be used in practicing the invention are described in, e.g., U.S. Patent Nos. 6,333,301; 6,329,333; 6,326,341; 6,297,038; 6,309,871; 6,204,232; 6,197,070; 5,856,164.

The detergents and related processes of the invention can also include the use of any combination of other enzymes such as tryptophanases or tyrosine decarboxylases, laccases, catalases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylo-laccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Treating fabrics and textiles

The invention provides compositions and methods of treating fabrics and textiles using one or more polypeptides of the invention, e.g., enzymes as described in Tables 1, 2, and 3, including enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity. The polypeptides of the invention can be used in any fabric-treating method, which are well known in the art, see, e.g., U.S. Patent No. 6,077,316. For example, in one aspect, the feel and appearance of a fabric is improved by a method comprising contacting the fabric with an enzyme of the invention in a solution. In one aspect, the fabric is treated with the solution under pressure.

In one aspect, the enzymes of the invention are applied during or after the weaving of textiles, or during the desizing stage, or one or more additional fabric processing steps. During the weaving of textiles, the threads are exposed to considerable mechanical strain. Prior to weaving on mechanical looms, warp yarns are often coated with sizing starch or starch derivatives in order to increase their tensile strength and to prevent breaking. The enzymes of the invention can be applied to remove these sizing

starch or starch derivatives. After the textiles have been woven, a fabric can proceed to a desizing stage. This can be followed by one or more additional fabric processing steps. Desizing is the act of removing size from textiles. After weaving, the size coating must be removed before further processing the fabric in order to ensure a homogeneous and wash-proof result. The invention provides a method of desizing comprising enzymatic hydrolysis of the size by the action of an enzyme of the invention.

The enzymes of the invention (e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity) can be used to desize fabrics, including cotton-containing fabrics, as detergent additives, e.g., in aqueous compositions. The invention provides methods for producing a stonewashed look on indigo-dyed denim fabric and garments. For the manufacture of clothes, the fabric can be cut and sewn into clothes or garments, which is afterwards finished. In particular, for the manufacture of denim jeans, different enzymatic finishing methods have been developed. The finishing of denim garment normally is initiated with an enzymatic desizing step, during which garments are subjected to the action of amylolytic enzymes in order to provide softness to the fabric and make the cotton more accessible to the subsequent enzymatic finishing steps. The invention provides methods of finishing denim garments (e.g., a "bio-stoning process"), enzymatic desizing and providing softness to fabrics using the Enzymes of the invention. The invention provides methods for quickly softening denim garments in a desizing and/or finishing process.

The invention also provides disinfectants comprising enzymes of the invention (e.g., enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity).

The fabric or textile treatment processes of the invention can also include the use of any combination of other enzymes such as tryptophanases or tyrosine decarboxylases, laccases, catalases, laccases, other cellulases, endoglycosidases, endo-beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipooxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylo-laccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Paper or pulp treatment

The enzymes of the invention e.g., enzymes as described in Tables 1, 2, and 3, including enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity) can be in paper or pulp treatment or paper deinking. For example, in one aspect, the invention provides a paper treatment process using enzymes of the invention. In one aspect, the enzymes of the invention can be used to modify starch in the paper thereby converting it into a liquefied form. In another aspect, paper components of recycled photocopied paper during chemical and enzymatic deinking processes. In one aspect, Enzymes of the invention can be used in combination with other enzymes, including other cellulases (including other endoglucanases, cellobiohydrolases and/or beta-glucosidases). The wood, paper, paper product or pulp can be treated by the following three processes: 1) disintegration in the presence of an enzyme of the invention, 2) disintegration with a deinking chemical and an enzyme of the invention, and/or 3) disintegration after soaking with an enzyme of the invention. The recycled paper treated with an enzyme of the invention can have a higher brightness due to removal of toner particles as compared to the paper treated with just cellulase. While the invention is not limited by any particular mechanism, the effect of an enzyme of the invention may be due to its behavior as surface-active agents in pulp suspension.

The invention provides methods of treating paper and paper pulp using one or more polypeptides of the invention. The polypeptides of the invention can be used in any paper- or pulp-treating method, which are well known in the art, see, e.g., U.S. Patent No. 6,241,849; 6,066,233; 5,582,681. For example, in one aspect, the invention provides a method for deinking and decolorizing a printed paper containing a dye, comprising pulping a printed paper to obtain a pulp slurry, and dislodging an ink from the pulp slurry in the presence of an enzyme of the invention (other enzymes can also be added). In another aspect, the invention provides a method for enhancing the freeness of pulp, e.g., pulp made from secondary fiber, by adding an enzymatic mixture comprising an enzyme of the invention (can also include other enzymes, e.g., pectinase enzymes) to the pulp and treating under conditions to cause a reaction to produce an enzymatically treated pulp. The freeness of the enzymatically treated pulp is increased from the initial freeness of the secondary fiber pulp without a loss in brightness.

The paper, wood or pulp treatment or recycling processes of the invention can also include the use of any combination of other enzymes such as tryptophanases or tyrosine decarboxylases, laccases, catalases, laccases, other cellulases, endoglycosidases, endo-

beta-1,4-laccases, amyloglucosidases, other glucosidases, glucose isomerases, glycosyltransferases, lipases, phospholipases, lipoxygenases, beta-laccases, endo-beta-1,3(4)-laccases, cutinases, peroxidases, amylases, glucoamylases, pectinases, reductases, oxidases, decarboxylases, phenoloxidases, ligninases, pullulanases, arabinanases, hemicellulases, mannanases, xylolaccases, xylanases, pectin acetyl esterases, rhamnogalacturonan acetyl esterases, proteases, peptidases, proteinases, polygalacturonases, rhamnogalacturonases, galactanases, pectin lyases, transglutaminases, pectin methylesterases, other cellobiohydrolases and/or transglutaminases.

Repulping: treatment of lignocellulosic materials

The invention also provides a method for the treatment of lignocellulosic fibers, wherein the fibers are treated with a polypeptide of the invention e.g., enzymes as described in Tables 1, 2, and 3, including enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity), in an amount which is efficient for improving the fiber properties. The enzymes of the invention may also be used in the production or recycling of lignocellulosic materials such as pulp, paper and cardboard, from starch reinforced waste paper and cardboard, especially where repulping or recycling occurs at pH above 7 and where the enzymes of the invention can facilitate the disintegration of the waste material through degradation of the reinforcing starch. The enzymes of the invention can be useful in a process for producing a papermaking pulp from starch-coated printed paper. The process may be performed as described in, e.g., WO 95/14807. An exemplary process comprises disintegrating the paper to produce a pulp, treating with a starch-degrading enzyme before, during or after the disintegrating, and separating ink particles from the pulp after disintegrating and enzyme treatment. See also U.S. Patent No. 6,309,871 and other US patents cited herein. Thus, the invention includes a method for enzymatic deinking of recycled paper pulp, wherein the polypeptide is applied in an amount which is efficient for effective de-inking of the fiber surface.

Brewing and fermenting

The invention provides compositions for and methods of brewing (e.g., fermenting) beer comprising an enzyme of the invention, e.g., enzymes as described in Tables 1, 2, and 3, including enzymes having cellulase, endoglucanase, cellobiohydrolase, mannanase and/or beta-glucosidase activity. In one exemplary process, starch-containing

raw materials are disintegrated and processed to form a malt. An enzyme of the invention is used at any point in the fermentation process. For example, enzymes of the invention can be used in the processing of barley malt. The major raw material of beer brewing is barley malt. This can be a three stage process. First, the barley grain can be steeped to increase water content, e.g., to around about 40%. Second, the grain can be germinated by incubation at 15-25°C for 3 to 6 days when enzyme synthesis is stimulated under the control of gibberellins. During this time enzyme levels rise significantly. In one aspect, enzymes of the invention are added at this (or any other) stage of the process. The action of the enzyme results in an increase in fermentable reducing sugars. This can be expressed as the diastatic power, DP, which can rise from around 80 to 190 in 5 days at 12°C.

Enzymes of the invention can be used in any beer producing process, as described, e.g., in U.S. Patent No. 5,762,991; 5,536,650; 5,405,624; 5,021,246; 4,788,066.

Pharmaceutical compositions and dietary supplements

The invention also provides pharmaceutical compositions and dietary supplements (e.g., dietary aids) comprising an enzyme of the invention (e.g., an exemplary enzyme of the invention, including those described in Tables 1, 2, and 3). In one aspect, the pharmaceutical compositions and dietary supplements (e.g., dietary aids) are formulated for oral ingestion, e.g., to improve the digestibility of foods and feeds having a high cellulose or lignocellulosic component. See also discussion, above.

Periodontal treatment compounds can comprise an enzyme of the invention, e.g., as described in U.S. patent no. 6,776,979. Compositions and methods for the treatment or prophylaxis of acidic gut syndrome can comprise an enzyme of the invention, e.g., as described in U.S. patent no. 6,468,964.

In another aspect, wound dressings, implants and the like comprise antimicrobial (e.g., antibiotic-acting) enzymes, including an enzyme of the invention (including, e.g., exemplary sequences of the invention). Enzymes of the invention can also be used in alginate dressings, antimicrobial barrier dressings, burn dressings, compression bandages, diagnostic tools, gel dressings, hydro-selective dressings, hydrocellular (foam) dressings, hydrocolloid dressings, I.V dressings, incise drapes, low adherent dressings, odor absorbing dressings, paste bandages, post operative dressings, scar management, skin care, transparent film dressings and/or wound closure. Enzymes of the invention can be used in wound cleansing, wound bed preparation, to treat pressure ulcers, leg ulcers, burns, diabetic foot ulcers, scars, IV fixation, surgical wounds and minor wounds.

Enzymes of the invention can be used to in sterile enzymatic debriding compositions, e.g., ointments. In various aspects, the cellulase is formulated as a tablet, gel, pill, implant, liquid, spray, powder, food, feed pellet or as an encapsulated formulation.

The polypeptides of the invention, such as those having hydrolases activity (e.g., lipases, esterase, protease and/or phospholipases) of the invention can be used in detoxification processes, e.g., for the detoxification of endotoxins, e.g., compositions comprising lipopolysaccharides (LPS), and, the invention provides detoxification processes using at least one enzyme of the invention. In one aspect, a lipase and/or an esterase of the invention is used to detoxify a lipopolysaccharide (LPS). In one aspect, this detoxification is by deacylation of 2' and/or 3' fatty acid chains from lipid A. In one aspect, a hydrolase (e.g., a lipase and/or an esterase) of the invention is used to hydrolyze a 2'-lauroyl and/or a 3'-myristoyl chain from a lipid, e.g., a lipid A (e.g., from a bacterial endotoxin). In one aspect, the process of the invention is used to destroy an endotoxin, e.g., a toxin from a gram negative bacteria, as from *E. coli*. In one aspect, a hydrolase (e.g., a lipase and/or an esterase) of the invention is used to ameliorate the effects of toxin poisoning (e.g., from an on-going gram negative infection), or, to prophylactically to prevent the effects of endotoxin during an infection (e.g., an infection in an animal or a human). Accordingly, the invention provides a pharmaceutical composition comprising a hydrolase (e.g., a lipase and/or an esterase) of the invention, and method using a hydrolase of the invention, for the amelioration or prevention of lipopolysaccharide (LPS) toxic effects, e.g., during sepsis.

Biodefense applications

In other aspects, an enzyme of the invention (e.g., an exemplary enzyme of the invention, including those described in Tables 1, 2, and 3) can be used in biodefense (e.g., destruction of spores or bacteria comprising a lignocellulosic material). Use of enzymes of the invention in biodefense applications offer a significant benefit, in that they can be very rapidly developed against any currently unknown or biological warfare agents of the future. In addition, enzymes of the invention can be used for decontamination of affected environments. In aspect, the invention provides a biodefense or bio-detoxifying agent comprising a polypeptide of the invention (including, e.g., exemplary sequences of the invention), or a polypeptide encoded by a nucleic acid of the invention (including, e.g., exemplary sequences of the invention).

Nutraceuticals

In one aspect, the compositions, e.g., an exemplary enzyme of the invention, including those described in Tables 1, 2, and 3, and methods of the invention can be used to make nutraceuticals by processing or synthesizing lipids and oils using the enzymes of the invention, e.g., esterases, acylases, lipases, phospholipases or proteases of the invention. In one aspect, the processed or synthesized lipids or oils include polyunsaturated fatty acids (PUFAs), diacylglycerides, e.g., 1,3-diacyl glycerides (DAGs), monoacylglycerides, e.g., 2-monoacylglycerides (MAGs) and triacylglycerides (TAGs). In one aspect, the nutraceuticals is made by processing diacylglycerides, e.g., 1,3-diacyl glycerides (DAGs), monoacylglycerides, e.g., 2-monoacylglycerides (MAGs) and/or triacylglycerides (TAGs) from plant (e.g., oilseed) sources or from animal (e.g., fish oil) sources.

In one aspect, the compositions and methods of the invention can be used to fortify dietary compositions, especially cow's milk based products, e.g., cow's milk-based infant formulas, with bile salt-activated hydrolases. The compositions made by the methods and compositions of the invention can be used to feed newborn and premature infants, including administration of a bile salt-activated hydrolase of the invention to increase fat digestion and therefore growth rate. Similarly, the invention provides compositions and methods for treating subjects for inadequate pancreatic enzyme production by administration of bile salt-activated hydrolase in conjunction with ingestion of fats; see also discussion, below.

In one aspect, the invention provides a dietary composition comprising a hydrolase of the invention, e.g., bile salt-activated hydrolase of the invention. In one aspect, the invention provides a dietary composition comprising a nutritional base comprising a fat and an effective amount of bile salt-activated hydrolase of the invention. In one aspect, the invention provides a cow's milk-based infant formula comprising a hydrolase of the invention, e.g., bile salt-activated hydrolase of the invention. In one aspect, the hydrolase of the invention is active in the digestion of long chain fatty acids, e.g., C₁₂ to C₂₂, which make up a very high percentage of most milks, e.g., 99% of human breast milk. See, e.g., U.S. Patent No. 5,000,975.

In one aspect, the invention provides a dietary composition comprising a vegetable oil fat and a hydrolase of the invention. The invention provides methods of processing milk based products and/or vegetable oil-comprising compositions to make dietary compositions. In one aspect, the processed compositions comprise a lauric acid oil, an oleic acid oil, a palmitic acid oil and/or a linoleic acid oil. In one aspect, a rice

bran oil, sunflower oleic oil and/or canola oil may be used as oleic acids oils. In one aspect, fats and oils, e.g., oilseeds, from plants, including, e.g., rice, canola, sunflower, olive, palm, soy or lauric type oils for use in the nutraceuticals and dietary compositions are processed or made using a hydrolase of the invention. See, e.g., U.S. Patent No. 4,944,944.

In one aspect, the enzymes of the invention are provided in a form that is stable to storage in the formula and/or the stomach, but active when the formulation reaches the portion of the gastrointestinal tract where the formula would normally be digested. Formulations (e.g., microcapsules) for release in the intestine are well known in the art, e.g., biodegradable polymers such as polylactide and polyglycolide, as described, e.g., in U.S. Patent. Nos. 4,767,628; 4,897,268; 4,925,673; 5,902,617.

A number of aspects of the invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the invention. Accordingly, other aspects are within the scope of the following claims.

SEQ ID NO:	NR or Geneseq Protein Accession Code	% Id	Evalue	Organism	Genbank Definition	Geneseq Definition	% Id	Evalue	EC No.
1, 2	15794814	60	2.00E-34	Neisseria meningitidis Z2491	DNA-3-methyladenine glycosylase I [Neisseria meningitidis Z2491] emb CAB85151.1 DNA-3-methyladenine glycosylase I [Neisseria meningitidis Z2491] pir A81821 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) NMA1931 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)			3.2.2.20	
10001, 10002	48855446	36	7.00E-10	Cytophaga hutchinsonii	COG1173: ABC-type dipeptide/oligopeptide/nickel transport systems, permease components [Cytophaga hutchinsonii]				
10003, 10004	34557261	45	5.00E-34	Wolinella succinogenes DSM 1740	GLUCOSE INHIBITED DIVISION PROTEIN B [Wolinella succinogenes DSM 1740] emb CAE09976.1 GLUCOSE INHIBITED DIVISION PROTEIN B [Wolinella succinogenes] sp Q7M9J8 GIDB_WOLSU Methyltransferase gidB (Glucose inhibited division protein B)				
10005, 10006	17936493	44	5.00E-30	Agrobacterium tumefaciens str. C58	methyl-accepting chemotaxis protein [Agrobacterium tumefaciens str. C58] gb AAL43599.1 methyl-accepting chemotaxis protein [Agrobacterium tumefaciens str. C58] pir A12897 methyl-accepting chemotaxis protein cheD [imported] - Agrobacterium tumefaciens (strain C58, Dupont)			2.7.3.-	
10007, 10008	21229884	24	3.00E-07	Xanthomonas campestris pv. campestris str. ATCC 33913	hypothetical protein XCC0407 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM39725.1 conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913]				
10009, 10010	34557182	49	4.00E-58	Wolinella succinogenes DSM 1740	PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09897.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes]				
1001, 1002	29348342	36	4.00E-27	Bacteroides thetaiotaomicron VPI-5482	Methionyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78039.1 Methionyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482]	Mus musculus cDNA clone IMAGE:30025832	82	9.00E-09	6.1.1.10
10011, 10012	34557182	39	6.00E-41	Wolinella succinogenes DSM 1740	PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09897.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes]				
10015, 10016	53713997	40	1.00E-44	Bacteroides fragilis YCH46	two-component system sensor histidine kinase [Bacteroides fragilis YCH46] dbj BAD49455.1 two-component system sensor histidine kinase [Bacteroides fragilis YCH46]			2.7.3.-	
10019, 10020	34558361	32	4.00E-48	Wolinella succinogenes DSM 1740	conserved hypothetical protein-PREDICTED PEMEASE [Wolinella succinogenes DSM 1740] emb CAE11076.1 conserved hypothetical protein-PREDICTED PEMEASE [Wolinella succinogenes]				

10021,	48831352	31	2.00E-27	Magnetococcus sp. MC-1	COG0842: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			
10022,								
10023,				Cytophaga hutchinsonii	hypothetical protein Chut02001797 [Cytophaga hutchinsonii]			
10024,	48855460	26	3.00E-20	hutchinsonii	putative transcriptional regulator [Bacteroides fragilis YCH46]			
10025,				Bacteroides fragilis	dbj BAD48817.1 putative transcriptional regulator [Bacteroides fragilis YCH46]			
10026,	53713359	38	4.00E-13	YCH46		Wolinella succinogenes, complete genome; segment 4/7	89	5.00E-07
10027,				Wolinella succinogenes DSM 1740	hypothetical protein WS1135 [Wolinella succinogenes DSM 1740]			
10028,	34557509	60	1.00E-68	1740	emb CAE10224.1 hypothetical protein [Wolinella succinogenes]			
10029,				Wolinella succinogenes DSM 1740	REPLICATIVE DNA HELICASE EC 3.6.1. [Wolinella succinogenes DSM 1740] emb CAE09503.1 REPLICATIVE DNA HELICASE EC 3.6.1. [Wolinella succinogenes]			3.6.1.-
10030,	34556788	58	7.00E-21	1740				
10031,				Wolinella succinogenes DSM 1740	DNA TRANSFER PROTEIN [Wolinella succinogenes DSM 1740]			
10032,	34556789	36	1.00E-15	1740	emb CAE09504.1 DNA TRANSFER PROTEIN [Wolinella succinogenes]			
10033,				Wolinella succinogenes DSM 1740	HSR PROTEIN PROBABLE TYPE I RESTRICTION ENZYME	Wolinella succinogenes, complete genome; segment 4/7		
10034,	34557504	77	1.00E-120	1740	RESTRICTIONCHAIN [Wolinella succinogenes DSM 1740]			
10035,				Bacteroides fragilis	emb CAE10219.1 HSDR PROTEIN PROBABLE TYPE I RESTRICTION ENZYME RESTRICTIONCHAIN [Wolinella succinogenes]		80	2.00E-19 3.1.21.3
10036,	53713554	53	9.00E-89	YCH46	putative carbon-nitrogen hydrolase [Bacteroides fragilis YCH46]			
10037,				Leptospira borgpetersenii	dbj BAD49012.1 putative carbon-nitrogen hydrolase [Bacteroides fragilis YCH46]			
10038,	467673	26	5.00E-08	borgpetersenii	transposase [Leptospira borgpetersenii] pir S43117 transposase -			
10039,				Porphyromonas gingivalis W83	Leptospira borgpetersenii			
10040,	34397330	69	1.00E-92	gingivalis W83	PhoH family protein [Porphyromonas gingivalis W83] ref NP_905494.1			
10041,				Wolinella succinogenes DSM 1740	PhoH family protein [Porphyromonas gingivalis W83]			
10042,	34556764	49	2.00E-74	1740	POTASSIUM CHANNEL PROTEIN [Wolinella succinogenes DSM 1740]			
10043,				uncultured archaeon	emb CAE09479.1 POTASSIUM CHANNEL PROTEIN [Wolinella succinogenes]			
10044,	52549174	31	6.00E-23	GZfos26B2	hypothetical protein sensory transduction histidine kinase [uncultured archaeon GZfos26B2]			2.7.3.-
10051,				Glostridium perfringens str. 13	hypothetical protein CPE1884 [Clostridium perfringens str. 13]			
10052,	18310866	26	1.00E-11	perfringens str. 13	dbj BAB81590.1 hypothetical protein [Clostridium perfringens str. 13]			3.1.11.-
10055,				Cytophaga hutchinsonii	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii]			2.7.3.-
10056,	48855091	42	6.00E-47	hutchinsonii	hydrogenase expression/formation protein HypA [Shewanella oneidensis MR-1]			
10057,				Shewanella oneidensis MR-1	1 gb AA55136.1 hydrogenase expression/formation protein HypA [Shewanella oneidensis MR-1]			
10058,	24373649	57	4.00E-31	oneidensis MR-1	[Shewanella oneidensis MR-1]			

10059, 10060	48844993	31	4.00E-20	Geobacter metallireducens GS-15	COG2068: Uncharacterized MobA-related protein [Geobacter metallireducens GS-15]			
10061, 10062	39998151	29	2.00E-14	Geobacter sulfurreducens PCA	transcriptional regulator, TetR family [Geobacter sulfurreducens PCA] gb AAR36452.1 transcriptional regulator, TetR family [Geobacter sulfurreducens PCA]			
10063, 10064	50122251	50	5.00E-37	Erwinia carotovora subsp. atroseptica SCRI1043	putative acetyltransferase [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG76227.1 putative acetyltransferase [Erwinia carotovora subsp. atroseptica SCRI1043]			2.3.1.-
10065, 10066	56460369	40	3.00E-26	Idiomarina loihlensis L2TR	Response regulator of the LytR/AigR family [Idiomarina loihlensis L2TR] gb AAV82101.1 Response regulator of the LytR/AigR family [Idiomarina loihlensis L2TR]			
10067, 10068	15611919	46	2.00E-26	Helicobacter pylori J99	hypothetical protein jhp0852 [Helicobacter pylori J99] gb AAD06430.1 putative [Helicobacter pylori J99] pir G71880 hypothetical protein jhp0852 - Helicobacter pylori (strain J99)			
10069, 10070	34558359	55	1.00E-51	Wolinella succinogenes DSM 1740	PUTATIVE RIBOFLAVIN SYNTHASE ALPHA CHAIN [Wolinella succinogenes DSM 1740] emb CAE11074.1 PUTATIVE RIBOFLAVIN SYNTHASE ALPHA CHAIN [Wolinella succinogenes]			2.5.1.9
1007, 1008	ABB8477 1	45	9.00E-57		Desc:DNA polymerase III holoenzyme delta subunit related protein SEQ ID:144. Org:Cytophaga hutchinsonii			2.7.7.7
10071, 10072	56461220	47	9.00E-28	Idiomarina loihlensis L2TR	Signal transduction histidine kinase [Idiomarina loihlensis L2TR] gb AAV82952.1 Signal transduction histidine kinase [Idiomarina loihlensis L2TR]			2.7.3.-
10075, 10076	53759861	49	7.00E-31	Methylobacillus flagellatus KT	COG0582: Integrase [Methylobacillus flagellatus KT]			
10077, 10078	48832286	38	4.00E-36	Magnetococcus sp. MC-1	COG0470: ATPase Involved in DNA replication [Magnetococcus sp. MC-1] hypothetical protein PG2214 [Porphyromonas gingivalis W83]			2.7.7.7
10079, 10080	34398094	38	2.00E-18	Porphyromonas gingivalis W83	ref NP_906255.1 hypothetical protein PG2214 [Porphyromonas gingivalis W83]			
10081, 10082	29347582	32	2.00E-33	Bacteroides thetaiotaomicron VPI-5482	putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] gb AAO77279.1 putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482]			
10087, 10088	53713780	38	2.00E-42	Bacteroides fragilis YCH46	cobalamin biosynthesis protein CobD [Bacteroides fragilis YCH46] dbj BAD49238.1 cobalamin biosynthesis protein CobD [Bacteroides fragilis YCH46]			
10089, 10090	34557782	43	9.00E-32	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]			2.7.3.-

1009, 1010	ABP6072 2	48	1.00E-21			Desc: Cyanidium caldarium thiorodoxin SEQ ID NO:71. Org: Cyanidium caldarium			1.6.4.5
10095, 10096	57167613	50	2.00E-21	Campylobacter coli RM2228		probable periplasmic protein Cj1275c [Campylobacter coli RM2228] gb EAL57399.1 probable periplasmic protein Cj1275c [Campylobacter coli RM2228]			
10097, 10098	21668035	38	6.00E-30	Bacteroides fragilis uncultured		hypothetical transposase [Bacteroides fragilis]			
10099, 10100	31790367	32	5.00E-25	Acidobacteria bacterium		hypothetical protein [uncultured Acidobacteria bacterium]			
10101, 10102	57240514	40	7.00E-35	Campylobacter lari RM2100		DNA-binding response regulator CiaR [Campylobacter lari RM2100] gb EAL55628.1 DNA-binding response regulator CiaR [Campylobacter lari RM2100]			2.7.3.-
10103, 10104	57240513	33	3.00E-27	Campylobacter lari RM2100		signal-transducing protein, histidine kinase, putative [Campylobacter lari RM2100] gb EAL55627.1 signal-transducing protein, histidine kinase, putative [Campylobacter lari RM2100]			2.7.3.-
10105, 10106	17549582	28	6.00E-07	Ralstonia solanacearum GM11000		PROBABLE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER TRANSMEMBRANE PROTEIN [Ralstonia solanacearum GM11000] emb CAD18514.1 PROBABLE METHYL-ACCEPTING CHEMOTAXIS TRANSDUCER TRANSMEMBRANE PROTEIN [Ralstonia solanacearum]			
10107, 10108	42628871	43	5.00E-57	Haemophilus influenzae R2846		COG0147: Anthranilate/para-aminobenzoate synthases component I [Haemophilus influenzae R2846]			4.1.3.-
10109, 10110	34557081	59	3.00E-63	Wolinella succinogenes DSM 1740		hypothetical protein WS0668 [Wolinella succinogenes DSM 1740] emb CAE09796.1 conserved hypothetical protein [Wolinella succinogenes]			2.1.1.64
1011, 1012	16802005	37	3.00E-22	Listeria innocua Clp11262		hypothetical protein lin2946 [Listeria innocua Clp11262] emb CAC98171.1 lin2946 [Listeria innocua] pir AC1800 hypothetical protein lin2946 [Imported] Listeria innocua (strain Clp11262)			
10111, 10112	42628859	44	5.00E-30	Haemophilus influenzae R2846		COG1793: ATP-dependent DNA ligase [Haemophilus influenzae R2846]			6.5.1.1
10113, 10114	21226270	30	3.00E-09	Methanosarcina mazei Go1		hypothetical sensory transduction histidine kinase [Methanosarcina mazei Go1] gb AAM29864.1 hypothetical sensory transduction histidine kinase [Methanosarcina mazei Go1]			2.7.3.-
10115, 10116	39997412	45	8.00E-73	Geobacter sulfurreducens PCA		sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] gb AAR35690.1 sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA]			2.7.3.-
10117, 10118	54309594	27	4.00E-16	Photobacterium profundum SS9		Hypothetical enzyme of sugar metabolism [Photobacterium profundum SS9] emb CAG20812.1 Hypothetical enzyme of sugar metabolism [Photobacterium profundum]			

10119, 10120	20090576	40	3.00E-43	Methanosarcina acetivorans C2A	hypothetical protein MA1724 [Methanosarcina acetivorans C2A] gb AAM05131.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A]			
10123, 10124	56420550	30	9.00E-20	Geobacillus kaustophilus HTA426	transcriptional regulator [Geobacillus kaustophilus HTA426] dbj BAD76300.1 transcriptional regulator [Geobacillus kaustophilus HTA426]			
10125, 10126	34763623	33	5.00E-21	Fusobacterium nucleatum subsp. vincentii ATCC 49256	Autolysin sensor kinase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA23843.1 Autolysin sensor kinase [Fusobacterium nucleatum subsp. vincentii ATCC 49256]			2.7.3.-
10127, 10128	48855074	30	8.00E-15	Cytophaga hutchinsonii	COG4276: Uncharacterized conserved protein [Cytophaga hutchinsonii]			
10139, 10140	46201277	27	2.00E-18	Magnetospirillum magnetotacticum MS-1	COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1]			
10141, 10142	45656100	46	1.00E-66	Leptospira interrogans serovar Copenhageni str. Floeruz L1-130	photoproduct lyase [Leptospira interrogans serovar Copenhageni str. Floeruz L1-130] gb AAS68823.1 photoproduct lyase [Leptospira interrogans serovar Copenhageni str. Floeruz L1-130]			4.1.99.-
10143, 10144	20095132	79	1.00E-122	Providencia rettgeri	putative ATPase [Providencia rettgeri]			
10149, 10150	6939919	68	1.00E-87	Cytophaga fermentans	DNA gyrase subunit B [Cytophaga fermentans]	Polaribacter filamentus gyrB gene for DNA gyrase B subunit, partial cds	89	1.00E-17 5.99.1.3
1015, 1016	AAE1852	29	4.00E-28		Desc: Melon constitutive triple response (CTR) homologue. Org: Cucumis melo			2.7.1.37
10151, 10152	57169090	35	1.00E-12	Campylobacter coli RM2228	N-terminal HTH domain of molybdenum-binding protein family [Campylobacter coli RM2228] gb EAL56239.1 N-terminal HTH domain of molybdenum-binding protein family [Campylobacter coli RM2228]			
10153, 10154	15678768	42	7.00E-49	Methanothermobacter thermautotrophicus str. Delta H	phenylalanyl-tRNA synthetase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85246.1 phenylalanyl-tRNA synthetase [Methanothermobacter thermautotrophicus str. Delta H] sp O26837 SYFA_METTH Phenylalanyl-tRNA synthetase alpha chain (Phenylalanine--tRNA ligase alpha chain) (PheRS) pif C69199 phenylalanyl-tRNA ligase (EC 6.1.1.20) - Methanothermobacter thermautotrophicus (strain Delta H)			6.1.1.20

10155, 10156	17229117	26	1.00E-18	Nostoc sp. PCC 7120	serine/threonine kinase with two-component sensor domain [Nostoc sp. PCC 7120] pir AC2009 serine/threonine kinase with two-component sensor domain ali1625 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB77991.1 serine/threonine kinase with two-component sensor domain [Nostoc sp. PCC 7120]	2.7.3.-
10159, 10160	34557161	54	2.00E-27	Wollinella succinogenes DSM 1740	PUTATIVE ARSENATE REDUCTASE [Wollinella succinogenes DSM 1740] emb CAE09876.1 PUTATIVE ARSENATE REDUCTASE [Wollinella succinogenes]	1.97.1.5
10161, 10162	48855564	54	7.00E-35	Cytophaga hutchinsonii	COG2801: Transposase and inactivated derivatives [Cytophaga hutchinsonii]	
10163, 10164	53715139	42	5.00E-30	Bacteroides fragilis YCH46	putative acetyltransferase [Bacteroides fragilis YCH46] dbj BAD50597.1 putative acetyltransferase [Bacteroides fragilis YCH46]	2.3.1.-
10167, 10168	ABU0070	31	3.00E-26		Desc:S. pneumoniae type 4 strain protein from coding region #267. Org:Streptococcus pneumoniae type 4 strain	2.4.1.-
10169, 10170	421666	50	3.00E-58	Acholeplasma laidlawii	probable nucleotide-binding protein - Acholeplasma laidlawii emb CAA80494.1 hypothetical nucleotide binding protein [Acholeplasma laidlawii]	5.1.3.13
1017, 1018	1076839	34	9.00E-18	Dictyostelium discoideum	protein kinase - slime mold [Dictyostelium discoideum] emb CAA86053.1 protein kinase [Dictyostelium discoideum]	2.7.1.-
10171, 10172	56461419	35	3.00E-21	Idiomarina loihiensis L2TR	Predicted glycosyltransferase [Idiomarina loihiensis L2TR] gb AAV83151.1 Predicted glycosyltransferase [Idiomarina loihiensis L2TR]	
10173, 10174	34557616	29	4.00E-20	Wollinella succinogenes DSM 1740	HELICASE [Wollinella succinogenes DSM 1740] emb CAE10331.1 HELICASE [Wollinella succinogenes]	
10175, 10176	57238505	31	2.00E-44	Campylobacter jejuni RM1221	hypothetical protein CJE1655 [Campylobacter jejuni RM1221] gb AAW36088.1 conserved hypothetical protein [Campylobacter jejuni RM1221]	
10177, 10178	34557335	38	4.00E-18	Wollinella succinogenes DSM 1740	PHOSPHATE TRANSPORT PERMEASE [Wollinella succinogenes DSM 1740] emb CAE10050.1 PHOSPHATE TRANSPORT PERMEASE [Wollinella succinogenes]	
10179, 10180	34556892	59	8.00E-72	Wollinella succinogenes DSM 1740	DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wollinella succinogenes DSM 1740] emb CAE09607.1 DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wollinella succinogenes] sp Q7MA56 RPBC_WOLSU Bifunctional DNA-directed RNA polymerase, beta and beta' chain [includes: DNA-directed RNA polymerase beta chain (Transcriptase beta chain) (RNA polymerase beta subunit); DNA-directed RNA polymerase beta' chain (Transcriptase beta' chain) (RNA polymerase beta' subunit)]	2.7.7.6

10181,	46202599	33	5.00E-27	Magnetospirillum magnetotacticum MS-1	hypothetical protein Magn03007449 [Magnetospirillum magnetotacticum MS-1]				
10182									
10185,	40062812	44	1.00E-50	uncultured bacterium 440	amino transferase, DegT/DntJ/ErYc1/StrS family [uncultured bacterium 440]				
10186									
10189,				Bacteroides thetaiotaomicron	hypothetical protein BT2505 [Bacteroides thetaiotaomicron VPI-5482]				
10190	29347915	38	1.00E-51	VPI-5482	gb AAO77612.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
1019,				Bacteroides thetaiotaomicron	signal peptidase I [Bacteroides thetaiotaomicron VPI-5482]				3.4.21.8
1020	29348728	44	3.00E-53	VPI-5482	signal peptidase I [Bacteroides thetaiotaomicron VPI-5482]				9
10193,				Wolinella succinogenes DSM 1740	CARBOXYNORSPERMIDINE DECARBOXYLASE (NSPC) [Wolinella succinogenes DSM 1740] emb CAE09329.1 CARBOXYNORSPERMIDINE DECARBOXYLASE (NSPC) [Wolinella succinogenes]				4.1.1.-
10194	34556614	56	2.00E-66		putative ribonuclease [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281814.1 putative ribonuclease [Campylobacter jejuni subsp. jejuni NCTC 11168] pir F81411 probable ribonuclease C 0631c [imported] - Campylobacter jejuni (strain NCTC 11168)				
10195,	6968098	31	2.00E-08	NCTC 11168	COG3210: Large exoproteins involved in heme utilization or adhesion				
10196				Cytophaga hutchinsonii	[Cytophaga hutchinsonii]				
10197,	48856713	34	1.00E-17						
10198				Shewanella oneidensis MR-1	hypothetical protein SO0527 [Shewanella oneidensis MR-1] gb AAN53608.1 conserved hypothetical protein [Shewanella oneidensis MR-1]				
10207,	24372121	39	9.00E-16						
10208									
10209,				Nostoc punctiforme PCC 73102	COG0732: Restriction endonuclease S subunits [Nostoc punctiforme PCC 73102]				3.1.21.3
10210	23130207	33	1.00E-18						
1021,				Symbiobacterium thermophilum IAM 14863	RNA polymerase alpha subunit [Symbiobacterium thermophilum IAM 14863] dbj BAD42029.1 RNA polymerase alpha subunit [Symbiobacterium thermophilum IAM 14863]				2.7.7.6
1022	51894182	52	1.00E-72		putative 32.7 kDa rhodanese-like thiosulfate sulfurtransferase [Bacillus pseudofirmus] pir T52549 probable thiosulfate sulfurtransferase (EC 2.8.1.1) [imported] - Bacillus firmus				2.8.1.1
10217,				Bacillus pseudofirmus					
10218	2654483	30	2.00E-20		hypothetical sensory box/GGDEF family protein [Photobacterium profundum SS9] emb CAG21805.1 hypothetical sensory box/GGDEF family protein [Photobacterium profundum]				
10219,				Photobacterium profundum SS9					
10220	54310587	33	1.00E-24		COG0152: Phosphoribosylaminoimidazole succinocarboxamide (SAICAR) synthase [Cytophaga hutchinsonii]				6.3.2.6
10223,				Cytophaga hutchinsonii					
10224	48856499	71	4.00E-81						
10225,									
10226	21668035	38	2.00E-21	Bacteroides fragilis	hypothetical transposase [Bacteroides fragilis]				

10227, 10228	16945757	26	4.00E-14	Photobacterium damselae subsp. placidia	capsular polysaccharide [Photobacterium damsela subsp. placida]				
10229, 10230	15898433	35	6.00E-09	Sulfolobus solfataricus P2	hypothetical protein SSO1613 [Sulfolobus solfataricus P2] gb AAK41828.1 Hypothetical protein SSO1613 [Sulfolobus solfataricus P2] pir E90321 hypothetical protein SSO1613 [imported] - Sulfolobus solfataricus				
10231, 10232	4234793	37	2.00E-24	Leptospira borgpetersenii	unknown [Leptospira borgpetersenii]				
10235, 10236	57504674	46	1.00E-31	Campylobacter coli RM2228	citrate synthase I [Campylobacter coli RM2228] gb EAL56138.1 citrate synthase I [Campylobacter coli RM2228]				4.1.3.7
10237, 10238	34557509	62	1.00E-60	Wolinella succinogenes DSM 1740	hypothetical protein WS1135 [Wolinella succinogenes DSM 1740] emb CAE10224.1 hypothetical protein [Wolinella succinogenes] probable membrane protein Cj1484c [Campylobacter upsallensis RM3195] gb EAL53642.1 probable membrane protein Cj1484c [Campylobacter upsallensis RM3195]				
10239, 10240	57242574	30	2.00E-14	Pseudomonas fluorescens PfO-1	COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Pseudomonas fluorescens PfO-1]				6.2.1.3
10241, 10242	48730607	47	4.00E-30	Methanocaldococ- cus jannaschii DSM 2661	putative mRNA 3'-end processing factor 1 [Methanocaldococcus jannaschii DSM 2661] gb AAB98027.1 putative mRNA 3'-end processing factor 1 [Methanocaldococcus jannaschii DSM 2661] sp Q60355 Y047_METJA				
10243, 10244	15668217	35	1.00E-23	Bacteroides thetaiotaomicron VPI-5482	Hypothetical protein MJ0047 chloromuconate cycloisomerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79808.1 chloromuconate cycloisomerase [Bacteroides thetaiotaomicron VPI-5482]				4.2.1.-
10249, 10250	48846045	42	3.00E-46	Geobacter metallireducens GS- 15	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]				2.7.3.-
1025, 1026	20089441	35	3.00E-29	Methanosarcina acetivorans C2A	sensory transduction histidine kinase [Methanosarcina acetivorans C2A] gb AAM03996.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A]				2.7.3.-
10251, 10252	57237341	44	5.00E-15	Campylobacter jejuni RM1221	hypothetical protein CJE0334 [Campylobacter jejuni RM1221] gb AAW34924.1 conserved hypothetical protein [Campylobacter jejuni RM1221]				
10253, 10254	34556562	56	2.00E-46	Wolinella succinogenes DSM 1740	PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes DSM 1740] emb CAE09277.1 PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes]				
10255, 10256	34556562	80	1.00E-108	Wolinella succinogenes DSM 1740	PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes DSM 1740] emb CAE09277.1 PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes]				

10259, 10260	37719606	59	3.00E-73	Campylobacter jejuni	putative GDP-fucose synthase [Campylobacter jejuni]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 5/6	86	8.00E-09	5.1.3.-
10261, 10262	57167870	50	5.00E-29	Campylobacter coli RM2228	thioesterase family protein, putative [Campylobacter coli RM2228] gb EAL57656.1 thioesterase family protein, putative [Campylobacter coli RM2228]				
10263, 10264	34557419	31	4.00E-17	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]				
10265, 10266	34556810	38	4.00E-32	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09525.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]				2.7.3.-
10267, 10268	29349340	61	1.00E-101	Bacteroides thetaiotaomicron VPI-5482	DNA primase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79037.1 DNA primase [Bacteroides thetaiotaomicron VPI-5482]				2.7.7.-
10269, 10270	48854613	32	6.00E-35	Cytophaga hutchinsonii	COG0842: Signal transduction histidine kinase [Cytophaga hutchinsonii]				2.7.3.-
1027, 1028	30249488	37	2.00E-19	Nitrosomonas europaea ATCC 19718	6-pyruvoyl tetrahydropterin synthase [Nitrosomonas europaea ATCC 19718] emb CAD85428.1 6-pyruvoyl tetrahydropterin synthase [Nitrosomonas europaea ATCC 19718]				4.6.1.10
10273, 10274	34396339	63	6.00E-65	Porphyromonas gingivalis W83	peptidyl-tRNA hydrolase [Porphyromonas gingivalis W83] ref NP_904507.1 peptidyl-tRNA hydrolase [Porphyromonas gingivalis W83] sp Q7MXK9 PTH_PORGI Peptidyl-tRNA hydrolase (PTH)				3.1.1.29
10275, 10276	45358149	51	6.00E-55	Methanococcus maripaludis S2	uncharacterized endonuclease III related protein [Methanococcus maripaludis S2] emb CAF30142.1 uncharacterized endonuclease III related protein [Methanococcus maripaludis S2]				4.2.99.1 8
10279, 10280	57169064	41	4.00E-26	Campylobacter coli RM2228	conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228]				
10281, 10282	57241406	54	3.00E-43	Campylobacter lari RM2100	ATP-dependent Clp protease, ATP-binding subunit ClpX [Campylobacter lari RM2100] gb EAL54518.1 ATP-dependent Clp protease, ATP-binding subunit ClpX [Campylobacter lari RM2100]				
10283, 10284	34558260	57	1.00E-93	Wolinella succinogenes DSM 1740	PUTATIVE ATP-DEPENDENT PROTEASE LA PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10975.1 PUTATIVE ATP-DEPENDENT PROTEASE LA PROTEIN [Wolinella succinogenes]				3.4.21.5 3
10285, 10286	57167957	65	2.00E-99	Campylobacter coli RM2228	ATP-dependent protease La [Campylobacter coli RM2228] gb EAL57000.1 ATP-dependent protease La [Campylobacter coli RM2228]				3.4.21.5 3

10287, 10288	39997199	60	1.00E-70	Geobacter sulfurreducens PCA	formate acetyltransferase [Geobacter sulfurreducens PCA] gb AAR35477.1 formate acetyltransferase [Geobacter sulfurreducens PCA]				2.3.1.54	
10289, 10290	29346832	32	3.00E-12	Bacteroides thetataoomicron VPI-5482	hypothetical protein BT1422 [Bacteroides thetataoomicron VPI-5482] gb AAO76529.1 conserved hypothetical protein [Bacteroides thetataoomicron VPI-5482]					
10291, 10292	57241378	50	8.00E-25	Campylobacter lari RM2100	molybdopterin cofactor biosynthesis protein A [Campylobacter lari RM2100] gb EAL54490.1 molybdopterin cofactor biosynthesis protein A [Campylobacter lari RM2100]					
10293, 10294	48846592	31	5.00E-15	Geobacter metallireducens GS-15	COG4753: Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain [Geobacter metallireducens GS-15] Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] gb AAK81185.1 Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] pir F97299 sensory transduction protein containing HD_GYP domain [Imported] - Clostridium acetobutylicum			2.7.3.-		
10295, 10296	15896496	37	1.00E-40	Clostridium acetobutylicum ATCC 824	phosphoenolpyruvate synthase [Pyrococcus horikoshii OT3] dbj BAA29161.1 821aa long hypothetical phosphoenolpyruvate synthase [Pyrococcus horikoshii OT3] pir B71229 pyruvate, water dikinase (EC 2.7.9.2) - Pyrococcus horikoshii sp O57830 PPSA_PYRHO Probable phosphoenolpyruvate synthase (Pyruvate, water dikinase) (PEP synthase) Phosphoenolpyruvate synthase/pyruvate phosphate dikinase [Methanopyrus kandleri AV19] gb AAM01469.1 Phosphoenolpyruvate synthase/pyruvate phosphate dikinase [Methanopyrus kandleri AV19] hypothetical protein [Encephalitozoon cuniculi] emb CAD25326.1 hypothetical protein [Encephalitozoon cuniculi] GB-M1]			2.7.9.2		
10297, 10298	14590043	33	4.00E-31	Pyrococcus horikoshii OT3	peptidase, M42 family [Enterococcus faecalis V583] gb AAO82426.1 peptidase, M42 family [Enterococcus faecalis V583] COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii]					
10299, 10300	20093692	31	1.00E-32	Methanopyrus kandleri AV19	two-component response regulator [Synecococcus elongatus PCC 6301] dbj BAD78390.1 two-component response regulator [Synecococcus elongatus PCC 6301] ref ZP_00202158.1 COG2200: FOG: EAL domain [Synecococcus elongatus PCC 7942]					
10301, 10302	29377202	45	4.00E-57	Enterococcus faecalis V583	hypothetical protein aq_988 [Aquifex aeolicus VF5] gb AAC07080.1 hypothetical protein [Aquifex aeolicus VF5] pir F70385 conserved hypothetical protein aq_988 - Aquifex aeolicus				3.2.1.4	
10303, 10304	48853783	34	2.00E-30	Cytophaga hutchinsonii						
10307, 10308	56750209	43	9.00E-57	Synechococcus elongatus PCC 6301						
10309, 10310	15606297	27	7.00E-07	Aquifex aeolicus VF5						

10311, 10312	29348867	49	1.00E-43	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3458 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78564.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
10313, 10314	48862374	37	7.00E-20	Microbulbifer degradans 2-40	COG0501: Zn-dependent protease with chaperone function [Microbulbifer degradans 2-40]				
10317, 10318	48832341	33	4.00E-11	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]				
10321, 10322	48863739	32	7.00E-26	Microbulbifer degradans 2-40	COG2202: FOG: PAS/PAC domain [Microbulbifer degradans 2-40]				2.7.3.-
10323, 10324	15611181	61	4.00E-98	Helicobacter pylori J99	PHOSPHOENOLPYRUVATE SYNTHASE [Helicobacter pylori J99] gb AAD05690.1 PHOSPHOENOLPYRUVATE SYNTHASE [Helicobacter pylori J99] pir E71972 pyruvate, water dikinase (EC 2.7.9.2) - Helicobacter pylori (strain J99) sp Q9ZMV4 PPSA_HELP J Phosphoenolpyruvate synthase (Pyruvate, water dikinase) (PEP synthase)				2.7.9.2
10325, 10326	21233748	39	2.00E-54	Proteus vulgaris	transposase [Proteus vulgaris] dbj BAB93648.1 transposase [Proteus vulgaris]				
10327, 10328	32261558	35	4.00E-25	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_859542.1 hypothetical protein HH0011 [Helicobacter hepaticus ATCC 51449]				
10335, 10336	48832337	37	2.00E-29	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]				2.7.3.-
10339, 10340	48890583	32	1.00E-15	Trichodesmium erythraeum IMS101	COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101]				
10341, 10342	4234794	38	5.00E-09	Leptospira borgpetersenii	unknown [Leptospira borgpetersenii]				
10343, 10344	45657980	38	9.00E-25	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAK19901.1 unknown [Leptospira interrogans] gb AAD52180.1 unknown [Leptospira interrogans] gb AAS70703.1 glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				
10345, 10346	48853652	52	1.00E-69	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]			Nostoc sp. PCC 7120 DNA, complete genome 95	1.00E-08 2.7.3.-
10347, 10348	48853652	47	6.00E-55	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]				2.7.3.-
10349, 10350	48856677	50	4.00E-33	Trichodesmium erythraeum IMS101	COG0778: Nitroreductase [Trichodesmium erythraeum IMS101]				1.-.-.-

10351, 10352	19704257	29	4.00E-11	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Homoserine kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95118.1 Homoserine kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] transcriptional regulator, AraC/XylS family [Bacillus clausii dbj BAD63749.1 transcriptional regulator, AraC/XylS family [Bacillus clausii KSM-K16]				2.7.1.39
10353, 10354	56962983	24	2.00E-11	Bacillus clausii KSM-K16					
10355, 10356	48858010	33	3.00E-09	Clostridium thermocellum ATCC 27405	COG0367: Asparagine synthase (glutamine-hydrolyzing) [Clostridium thermocellum ATCC 27405]				
10357, 10358	48855327	82	1.00E-119	Cytophaga hutchinsonii	COG0086: DNA-directed RNA polymerase, beta' subunit/160 kD subunit [Cytophaga hutchinsonii]	Cyanophora paradoxa cyanelle, complete genome	83	4.00E-20	2.7.7.6
10359, 10360	57240881	41	3.00E-32	Campylobacter lari RM2100	molybdenum cofactor biosynthesis protein [Campylobacter lari RM2100] gb EAL55274.1 molybdenum cofactor biosynthesis protein [Campylobacter lari RM2100]				
10361, 10362	34558237	40	1.00E-43	Wolinella succinogenes DSM 1740	hypothetical protein WS1946 [Wolinella succinogenes DSM 1740] emb CAE10952.1 hypothetical protein [Wolinella succinogenes]				
10363, 10364	18309906	54	6.00E-32	Clostridium perfringens str. 13	hypothetical protein CPE0924 [Clostridium perfringens str. 13] dbj BAB80630.1 conserved hypothetical protein [Clostridium perfringens str. 13]				
10365, 10366	56750582	21	4.00E-12	Synechococcus elongatus PCC 6301	similar to phytoene dehydrogenase [Synechococcus elongatus PCC 6301] dbj BAD78763.1 similar to phytoene dehydrogenase [Synechococcus elongatus PCC 6301] ref ZP_00164110.1 COG1233: Phytoene dehydrogenase and related proteins [Synechococcus elongatus PCC 7942]				
10369, 10370	46135061	31	2.00E-26	Anabaena variabilis ATCC 29413	COG0438: Glycosyltransferase [Anabaena variabilis ATCC 29413] related to transcription regulator [Desulfotalea psychrophila LSV54] emb CAG36428.1 related to transcription regulator [Desulfotalea psychrophila LSV54]				
10371, 10372	51245551	24	1.00E-09	Desulfotalea psychrophila LSV54					
10375, 10376	41722683	41	1.00E-16	Dechloromonas aromatica RCB	hypothetical protein Daro03003755 [Dechloromonas aromatica RCB]				
10379, 10380	33602582	42	1.00E-18	Bordetella bronchiseptica RB50	modification methylase [Bordetella bronchiseptica RB50] emb CAE35580.1 modification methylase [Bordetella bronchiseptica RB50]				

10381, 10382	34557728	38	3.00E-34	Wollinella succinogenes DSM 1740	CHEY AND CHEB GENES (CHEMOTAXIS PROTEIN) [Wollinella succinogenes DSM 1740] emb CAE10443.1 CHEY AND CHEB GENES (CHEMOTAXIS PROTEIN) [Wollinella succinogenes]			
10383, 10384	34557728	34	2.00E-15	Wollinella succinogenes DSM 1740	CHEY AND CHEB GENES (CHEMOTAXIS PROTEIN) [Wollinella succinogenes DSM 1740] emb CAE10443.1 CHEY AND CHEB GENES (CHEMOTAXIS PROTEIN) [Wollinella succinogenes]			
10385, 10386	29608580	31	3.00E-18	Streptomyces avermitilis MA-4680	hypothetical protein [Streptomyces avermitilis MA-4680] ref NP_826099.1 hypothetical protein SAV4922 [Streptomyces avermitilis MA-4680]			
10389, 10390	57242734	44	9.00E-44	Campylobacter upsaliensis RM3195	response regulator, putative [Campylobacter upsaliensis RM3195] gb EAL53447.1 response regulator, putative [Campylobacter upsaliensis RM3195]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 4/6	87	7.00E-12 2.7.3.-
1039, 1040	48839656	88	2.00E-99	Methanosarcina barkeri str. fusaro	COG4742: Predicted transcriptional regulator [Methanosarcina barkeri str. fusaro]	Methanosarcina mazei strain Goe1, section 117 of 379 of the complete genome	80	8.00E-58
10391, 10392	57238514	28	4.00E-23	Campylobacter jejuni RM1221	DNA-binding response regulator [Campylobacter jejuni RM1221] gb AAW36097.1 DNA-binding response regulator [Campylobacter jejuni RM1221]			2.7.3.-
10399, 10400	9656845	44	1.00E-54	Vibrio cholerae O1 biovar eltor str. N16961	conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_231913.1 hypothetical protein VC2282 [Vibrio cholerae O1 biovar eltor str. N16961] pir F82096 conserved hypothetical protein VC2282 [Imported] - Vibrio cholerae (strain N16961 serogroup O1)			
10401, 10402	34558071	68	1.00E-121	Wollinella succinogenes DSM 1740	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN [Wollinella succinogenes DSM 1740] emb CAE10786.1 RIBONUCLEOSIDE- DIPHOSPHATE REDUCTASE LARGE CHAIN [Wollinella succinogenes]			1.17.4.1
10403, 10404	34556560	35	3.00E-51	Wollinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes]			
10405, 10406	32262256	66	5.00E-35	Helicobacter hepaticus ATCC 51449	guanylate kinase [Helicobacter hepaticus ATCC 51449] ref NP_860238.1 guanylate kinase [Helicobacter hepaticus ATCC 51449] sp Q7VIA1 KGUA_HELHP Guanylate kinase (GMP kinase)			2.7.4.8
10407, 10408	58461322	33	1.00E-22	Idiomarina lolhiensis L2TR	Predicted PhoH-related ATPase [Idiomarina lolhiensis L2TR] gb AAV83054.1 Predicted PhoH-related ATPase [Idiomarina lolhiensis L2TR]			

10409, 10410	34557146	45	2.00E-58	Wollinella succinogenes DSM 1740	A/G-SPECIFIC ADENINE GLYCOSYLASE EC 3.2.2. [Wollinella succinogenes DSM 1740] emb CAE09861.1 A/G-SPECIFIC ADENINE GLYCOSYLASE EC 3.2.2. [Wollinella succinogenes]	3.2.2.-
1041, 1042	53721029	37	3.00E-16	Burkholderia pseudomallei K96243	putative adenylate cyclase [Burkholderia pseudomallei K96243] ref YP_104436.1 adenylate cyclase, putative [Burkholderia mallei ATCC 23344] gb AAU48007.1 adenylate cyclase, putative [Burkholderia mallei ATCC 23344] emb CAH37434.1 putative adenylate cyclase [Burkholderia pseudomallei K96243]	4.6.1.1
10411, 10412	48478360	30	4.00E-12	Picrophilus torridus DSM 9790	thiamin-phosphate pyrophosphorylase [Picrophilus torridus DSM 9790] gb AAT43873.1 thiamin-phosphate pyrophosphorylase [Picrophilus torridus DSM 9790]	2.5.1.3
10415, 10416	57226131	50	1.00E-66	Cryptococcus neoformans var. neoformans JEC21	dehydrogenase, putative [Cryptococcus neoformans var. neoformans JEC21] gb EAL21937.1 hypothetical protein CNBC0770 [Cryptococcus neoformans var. neoformans B-3501A]	
10419, 10420	48847450	79	1.00E-107	Geobacter metallireducens GS-15	COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00301665.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00301374.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00300257.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00300170.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00298468.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00298384.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15]	Geobacter metallireducens putative ferredoxin gene, partial cds; hypothetical protein gene, complete cds; and putative transposase gene, partial cds
10423, 10424	56708541	33	6.00E-14	Francisella tularensis subsp. tularensis Schu 4	Integrase/recombinase XerC [Francisella tularensis subsp. tularensis Schu 4] emb CAG46136.1 Integrase/recombinase XerC [Francisella tularensis subsp. tularensis]	81 5.00E-41
10425, 10426	52143555	35	1.00E-18	Bacillus cereus ZK	acetyltransferase, GNAT family [Bacillus cereus ZK] gb AAU18574.1	
10427, 10428	57241016	33	3.00E-28	Campylobacter lari RM2100	acetyltransferase, GNAT family [Bacillus cereus ZK] methyl-accepting chemotaxis protein (tipB), putative [Campylobacter lari RM2100] gb EAL54712.1 methyl-accepting chemotaxis protein (tipB), putative [Campylobacter lari RM2100]	
10429, 10430	53692808	33	6.00E-19	Haemophilus sommus 129PT	hypothetical protein Hsom02000323 [Haemophilus sommus 129PT]	
1043, 1044	28854897	36	1.00E-22	Pseudomonas syringae pv. tomato str. DC3000	ISPsy11, transposase OrfB [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794264.1 ISPsy11, transposase OrfB [Pseudomonas syringae pv. tomato str. DC3000]	

10431, 10432	46120923	34	9.00E-32	Methylobacillus flagellatus KT	COG0438: Glycosyltransferase [Methylobacillus flagellatus KT]			2.4.1.-
10433, 10434	93830	33	1.00E-22		regulatory protein cII - phage phi-R73			
10435, 10436	23003026	33	1.00E-15	Lactobacillus gasseri	COG0553: Superfamily II DNA/RNA helicases, SNF2 family [Lactobacillus gasseri]			3.6.1.3
10437, 10438	AAG8151	26	6.00E-11		Desc:S. epidermidis open reading frame protein sequence SEQ ID NO:130. Org:Staphylococcus epidermidis			
10445, 10446	34558393	45	7.00E-30	Wolinnella succinogenes DSM 1740	THREONINE SYNTHASE [Wolinnella succinogenes DSM 1740] emb CAE11108.1 THREONINE SYNTHASE [Wolinnella succinogenes]			4.2.99.2
10447, 10448	42525591	33	6.00E-11	Treponema denticola ATCC 35405	methyl-accepting chemotaxis protein [Treponema denticola ATCC 35405] gb AAS10570.1 methyl-accepting chemotaxis protein [Treponema denticola ATCC 35405]			
10449, 10450	56476606	21	9.00E-07	Azoarcus sp. EbN1	hemin receptor precursor, TonB-dependent outer membrane uptake protein [Azoarcus sp. EbN1]			
1045, 1046	48833013	33	3.00E-35	Magnetococcus sp. MC-1	COG0842: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			2.7.3.-
10451, 10452	45657583	36	2.00E-46	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	nucleotide excision repair subunit A UVRABC [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_712393.1 Excinuclease ABC subunit A [Leptospira interrogans serovar Lai str. 56601] gb AAN4941.1 Excinuclease ABC subunit A [Leptospira interrogans serovar lai str. 56601] gb AAS70306.1 nucleotide excision repair subunit A UVRABC [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			
10453, 10454	27380846	40	2.00E-17	Bradyrhizobium japonicum USDA 110	transcriptional regulatory protein [Bradyrhizobium japonicum USDA 110] dbj BAC51000.1 transcriptional regulatory protein [Bradyrhizobium japonicum USDA 110]			
10455, 10456	15606172	45	3.00E-33	Aquifex aeolicus VF5	hydrogenase large subunit [Aquifex aeolicus VF5] gb AAC06945.1 hydrogenase large subunit [Aquifex aeolicus VF5] pir A70370 hydrogenase large subunit - Aquifex aeolicus			1.18.99.1
10459, 10460	48834391	24	1.00E-07	Magnetococcus sp. MC-1	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Magnetococcus sp. MC-1]			
10461, 10462	54302734	30	5.00E-23	Photobacterium profundum SS9	hypothetical dinitrification protein NorD [Photobacterium profundum SS9] emb CAG22927.1 hypothetical dinitrification protein NorD [Photobacterium profundum]			1.7.99.7

10463, 10464	20808390	30	1.00E-12	Thermoanaerobacter tengcongensis MB4	hypothetical protein TTE1987 [Thermoanaerobacter tengcongensis MB4] gb AAM25165.1 conserved hypothetical protein [Thermoanaerobacter tengcongensis MB4]			
10465, 10466	56418878	58	3.00E-47	Geobacillus kaustophilus HTA426	type I restriction modification system M subunit (site-specific DNA-methyltransferase subunit) [Geobacillus kaustophilus HTA426] dbj BAD74628.1 type I restriction modification system M subunit (site-specific DNA-methyltransferase subunit) [Geobacillus kaustophilus HTA426]			2.1.1.72
10467, 10468	34557088	43	2.00E-41	Wolinella succinogenes DSM 1740	hypothetical protein WS0675 [Wolinella succinogenes DSM 1740] emb CAE09803.1 conserved hypothetical protein [Wolinella succinogenes] tRNA pseudouridine synthase A [Campylobacter lari RM2100] gb EAL55500.1 tRNA pseudouridine synthase A [Campylobacter lari RM2100]			4.2.1.70
1047, 1048	17231815	32	7.00E-27	Nostoc sp. PCC 7120	hypothetical protein alr4323 [Nostoc sp. PCC 7120] pir AD2346 hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB76022.1 alr4323 [Nostoc sp. PCC 7120]			2.4.2.26
10471, 10472	48864587	37	2.00E-34	Microbulbifer degradans 2-40	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Microbulbifer degradans 2-40] putative transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD48817.1 putative transcriptional regulator [Bacteroides fragilis YCH46]			
10473, 10474	53713359	38	8.00E-34	Wolinella succinogenes DSM 1740	hypothetical protein WS1398 [Wolinella succinogenes DSM 1740] emb CAE10464.1 conserved hypothetical protein [Wolinella succinogenes]			1.1.1.21
10477, 10478	45546445	28	7.00E-14	Rubrobacter xylanophilus DSM 9941	COG4770: Acetyl/propionyl-CoA carboxylase, alpha subunit [Rubrobacter xylanophilus DSM 9941] polypeptide deformylase [Campylobacter upsaliensis RM3195] gb EAL53559.1 polypeptide deformylase [Campylobacter upsaliensis RM3195]			4.1.1.3
10483, 10484	57242491	60	3.00E-52	uncultured archaeon	mannosyl-3-phosphoglycerate phosphatase [uncultured archaeon GZfos9E5]			3.5.1.88
10489, 10490	39995815	38	8.00E-17	Geobacter sulfurreducens PCA	hypothetical protein GSU0709 [Geobacter sulfurreducens PCA] gb AAR34039.1 hypothetical protein GSU0709 [Geobacter sulfurreducens PCA]			
1049, 1050	48855421	33	5.00E-43	Cytophaga hutchinsonii	COG0210: Superfamily I DNA and RNA helicases [Cytophaga hutchinsonii]			3.6.1.-

10491,	57242338	30	9.00E-23	Campylobacter upsaliensis RM3195	conserved hypothetical protein [Campylobacter upsaliensis RM3195]			
10492					gb EAL53800.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195]			
10495,	40062476	36	2.00E-41	uncultured bacterium 105	hypothetical protein EBAC750-01A01.2 [uncultured bacterium 105]			
10496					putative transcriptional regulator [Bacteroides fragilis YCH46]			
105,					dbj BAD50718.1 putative transcriptional regulator [Bacteroides fragilis YCH46]			
106	53715260	46	2.00E-32	Bacteroides fragilis YCH46	PUTATIVE TWO-COMPONENT REGULATOR [Wollinella succinogenes DSM 1740] emb CAE11047.1 PUTATIVE TWO-COMPONENT REGULATOR [Wollinella succinogenes]			
10501,					conserved hypothetical protein-PREDICTED PEMEASE [Wollinella succinogenes DSM 1740] emb CAE11076.1 conserved hypothetical protein-PREDICTED PEMEASE [Wollinella succinogenes]			
10502	34558332	30	7.00E-10	Wollinella succinogenes DSM 1740	formyltetrahydrofolate deformylase VC1992 [Campylobacter lari RM2100]			2.7.7.25
10503,					gb EAL55533.1 formyltetrahydrofolate deformylase VC1992 [Campylobacter lari RM2100]			
10504	34558361	32	2.00E-42	Wollinella succinogenes DSM 1740	tRNA nucleotidyltransferase [Campylobacter upsaliensis RM3195]			2.7.7.25
10507,					gb EAL53338.1 tRNA nucleotidyltransferase [Campylobacter upsaliensis RM3195]			
10508	57240419	41	1.00E-30	Campylobacter lari RM2100	COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Microbulifer degradans 2-40]			
10509,					Microbulifer degradans 2-40			
10510	57242625	41	3.00E-21	Campylobacter upsaliensis RM3195	DIAMINOBTYRIC ACID AMINOTRANSFERASE [Wollinella succinogenes DSM 1740] emb CAE09865.1 DIAMINOBTYRIC ACID AMINOTRANSFERASE [Wollinella succinogenes]			2.6.1.46
10511,	48861334	48	4.00E-23	Microbulifer degradans 2-40	hypothetical protein SAR0197 [Staphylococcus aureus subsp. aureus MRSA252] emb CAG39224.1 hypothetical protein [Staphylococcus aureus subsp. aureus MRSA252]			
10512					sensory transduction histidine kinase [Methanosarcina acetivorans C2A]			
10513,	34557250	38	1.00E-15	Wollinella succinogenes DSM 1740	gb AAM04570.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A]			2.7.3.-
10514					ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wollinella succinogenes DSM 1740] emb CAE10562.1 ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wollinella succinogenes]			3.4.24.-
10515,					bleomycin resistance protein [Xanthomonas axonopodis pv. citri str. 306]			
10516	49482438	26	7.00E-14	Staphylococcus aureus subsp. aureus MRSA252	gb AAM39068.1 bleomycin resistance protein [Xanthomonas axonopodis pv. citri str. 306]			
10517,					COG0445: NAD/FAD-utilizing enzyme apparently involved in cell division [Chloroflexus aurantiacus]			
10518	20090015	36	9.00E-12	Methanosarcina acetivorans C2A	Desc:H. pylori HPC095 protein. Org:Helicobacter pylori			
10519,								
10520	34557847	35	2.00E-29	Wollinella succinogenes DSM 1740				
10521,								
10522	21244950	36	7.00E-12	Xanthomonas axonopodis pv. citri str. 306				
10523,								
10524	53795632	42	2.00E-18	Chloroflexus aurantiacus				
10525,	AAB4639							
10526	8	26	1.00E-11					

10527, 10528	46201536	50	4.00E-63	Magnetospirillum magnetotacticum MS-1	COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Magnetospirillum magnetotacticum MS-1]			2.7.3.-
10529, 10530	34558265	46	2.00E-53	Wolinella succinogenes DSM 1740	PUTATIVE HEMOLYSIN [Wolinella succinogenes DSM 1740] emb CAE10980.1 PUTATIVE HEMOLYSIN [Wolinella succinogenes]			
1053, 1054	53711426	42	3.00E-67	Bacteroides fragilis YCH46	hypothetical protein BF0135 [Bacteroides fragilis YCH46] dbj BAD46884.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
10531, 10532	57241759	41	2.00E-31	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54429.1 conserved hypothetical protein [Campylobacter lari RM2100]			
10533, 10534	34558271	68	5.00E-99	Wolinella succinogenes DSM 1740	DNA POLYMERASE III ALPHA SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10986.1 DNA POLYMERASE III ALPHA SUBUNIT [Wolinella succinogenes]			2.7.7.7
10535, 10536	19705092	37	2.00E-09	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Tetratricopeptide repeat family protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93886.1 Tetratricopeptide repeat family protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			
10537, 10538	32262177	34	6.00E-13	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860160.1 hypothetical protein HH0629 [Helicobacter hepaticus ATCC 51449]			
10539, 10540	34556616	37	3.00E-41	Wolinella succinogenes DSM 1740	CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes]			
10541, 10542	34557806	37	4.00E-24	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10521.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes]			

10543, 10544									Zebrafish DNA sequence from clone CH211- 286J13 in linkage group 4 Contains the gene for a novel protein containing a T-complex protein 11 domain (zgc:73347) and the 5' end of a novel gene, complete sequence	## 7.00E-15		
10545, 10546	1230584	70	3.00E-84		Vibrio cholerae O139	nucleotide sugar dehydrogenase [Vibrio cholerae O139] pir[S70888 nucleotide sugar dehydrogenase homolog - Vibrio cholerae dbj[BAA33612.1] probable nucleotide sugar dehydrogenase [Vibrio cholerae] prfj[2209416H nucleotide sugar dehydrogenase	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 5/6	87	8.00E-09	1.1.1.22		
10547, 10548	57238687	39	1.00E-20		Campylobacter jejuni RM1221	UDP-N-acetylenolpyruvoylglucosamine reductase [Campylobacter jejuni RM1221] gb AAW36270.1 UDP-N-acetylenolpyruvoylglucosamine reductase [Campylobacter jejuni RM1221]				1.1.1.15 8		
10549, 10550	48856129	37	3.00E-18		Cytophaga hutchinsonii	COG1011: Predicted hydrolase (HAD superfamily) [Cytophaga hutchinsonii]						
1055, 1056	48856079	66	1.00E-60		Cytophaga hutchinsonii	COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii]				1.8.-.-		
10551, 10552	41725960	47	6.00E-34		Dechloromonas aromatica RCB	COG4232: Thiol:disulfide Interchange protein [Dechloromonas aromatica RCB]				5.3.4.1		
10553, 10554	34557246	33	2.00E-22		Wolinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]					2.7.3.-	
10555, 10556	15611164	50	2.00E-27		Helicobacter pylori J99	hypothetical protein jhp0094 [Helicobacter pylori J99] gb AAD05675.1 putative [Helicobacter pylori J99] pir E71975 hypothetical protein jhp0094 - Helicobacter pylori (strain J99)	Bacteroides fragilis YCH46 DNA, complete genome	95	2.00E-09	2.4.-.-		

10559, 10560	9656923	55	3.00E-34	Vibrio cholerae O1 biovar eltor str. N16961	conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_231985.1 hypothetical protein VC2355 [Vibrio cholerae O1 biovar eltor str. N16961] pir C82088 conserved hypothetical protein VC2355 [imported] - Vibrio cholerae (strain N16961 serogroup O1) sp Q9KPL2 YN55_VIBCH Hypothetical UPF0246 protein VC2355			
10561, 10562	34557623	60	3.00E-28	Wolinella succinogenes DSM 1740	hypothetical protein WS1259 [Wolinella succinogenes DSM 1740] emb CAE10338.1 conserved hypothetical protein [Wolinella succinogenes]			
10565, 10566	20809022	26	5.00E-12	Thermoanaerobact er tengcongensis MB4	hypothetical protein TTE2678 [Thermoanaerobacter tengcongensis MB4] gb AAM25797.1 hypothetical protein TTE2678 [Thermoanaerobacter tengcongensis MB4]			4.1.99.-
10569, 10570	53715826	52	3.00E-57	Bacteroides fragilis YCH46	carboxy-terminal processing protease precursor [Bacteroides fragilis YCH46] db BAD51284.1 carboxy-terminal processing protease precursor [Bacteroides fragilis YCH46]			3.4.21.-
1057, 1058	48855421	32	1.00E-34	Cytophaga hutchinsonii	COG0210: Superfamily I DNA and RNA helicases [Cytophaga hutchinsonii]			3.6.1.-
10571, 10572	48855898	48	1.00E-26	Cytophaga hutchinsonii	hypothetical protein Chut02001116 [Cytophaga hutchinsonii]			
10581, 10582	48858979	43	4.00E-26	Clostridium thermocellum ATCC 27405	hypothetical protein Chte02001700 [Clostridium thermocellum ATCC 27405]			
10583, 10584	23003026	34	8.00E-30	Lactobacillus gasser	COG0553: Superfamily II DNA/RNA helicases, SNF2 family [Lactobacillus gasser]			3.6.1.3
10585, 10586	34557291	47	2.00E-40	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]			2.7.3.-
10587, 10588	46317983	60	7.00E-64	Burkholderia cepacia R18194	COG0720: 6-pyruvoyl-tetrahydropterin synthase [Burkholderia cepacia R18194]			
1059, 1060	13491145	47	1.00E-34	Aneurinibacillus thermoaerophilus	D-glycero-D-manno-heptose 1-phosphate guanosyltransferase [Aneurinibacillus thermoaerophilus]			2.7.7.13
10593, 10594	34557314	38	3.00E-23	Wolinella succinogenes DSM 1740	hypothetical protein WS0925 [Wolinella succinogenes DSM 1740] emb CAE10029.1 hypothetical protein [Wolinella succinogenes]			
10599, 10600	51245638	55	7.00E-19	Desulfotalea psychrophila LSV54	hypothetical protein DP1786 [Desulfotalea psychrophila LSV54] emb CAG36515.1 unknown protein [Desulfotalea psychrophila LSV54]			
10601, 10602	52425046	31	1.00E-10	Mannheimia succiniciproducens MBEL55E	hypothetical protein MS0991 [Mannheimia succiniciproducens MBEL55E] gb AAU37598.1 unknown [Mannheimia succiniciproducens MBEL55E]			

10603, 10604	7592813	52	1.00E-68	Actinobacillus actinomycetemcomitans	GDP-mannose pyrophosphorylase homolog [Actinobacillus actinomycetemcomitans]			2.7.7.22
10605, 10606	32262161	64	9.00E-56	Helicobacter hepaticus ATCC 51449	phosphohexosemutase [Helicobacter hepaticus ATCC 51449] ref NP_860144.1 phosphohexosemutase [Helicobacter hepaticus ATCC 51449]			5.4.2.8
10607, 10608	32263402	44	1.00E-46	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861381.1 hypothetical protein HH1850 [Helicobacter hepaticus ATCC 51449]			
10609, 10610	34557341	45	7.00E-34	Wolinella succinogenes DSM 1740	hypothetical protein WS0953 [Wolinella succinogenes DSM 1740] emb CAE10056.1 conserved hypothetical protein [Wolinella succinogenes]			
1061, 1062	29349972	61	1.00E-66	Bacteroides thetaiotaomicron VPI-5482	putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79669.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.4.1.83
10613, 10614	57506236	67	3.00E-13	Campylobacter upsallensis RM3195	malate:quinone oxidoreductase, putative [Campylobacter upsallensis RM3195] gb EAL52259.1 malate:quinone oxidoreductase, putative [Campylobacter upsallensis RM3195]			1.1.99.1 6
10615, 10616	56459896	37	2.00E-15	Idiomarina lolihensis L2TR	DSBH domain containing protein [Idiomarina lolihensis L2TR] gb AAV81628.1 DSBH domain containing protein [Idiomarina lolihensis L2TR]			
10617, 10618	42526240	26	2.00E-25	Treponema denticola ATCC 35405	aldehyde oxidase and xanthine dehydrogenase family protein [Treponema denticola ATCC 35405] gb AAS11219.1 aldehyde oxidase and xanthine dehydrogenase family protein [Treponema denticola ATCC 35405]			1.1.1.20 4
10619, 10620	32262126	66	1.00E-84	Helicobacter hepaticus ATCC 51449	UTP-glucose-1-phosphate uridylyltransferase [Helicobacter hepaticus ATCC 51449] ref NP_860109.1 UTP-glucose-1-phosphate uridylyltransferase [Helicobacter hepaticus ATCC 51449]			2.7.7.9
10621, 10622	34556541	42	6.00E-30	Wolinella succinogenes DSM 1740	ANTHRANILATE SYNTHASE COMPONENT I [Wolinella succinogenes DSM 1740] emb CAE09256.1 ANTHRANILATE SYNTHASE COMPONENT I [Wolinella succinogenes]			
10623, 10624	54302166	27	8.00E-14	Photobacterium profundum SS9	hypothetical protein PBPRB0486 [Photobacterium profundum SS9] emb CAG22359.1 hypothetical protein [Photobacterium profundum]			
10625, 10626	45358586	30	1.00E-16	Methanococcus maripaludis S2	Transcriptional regulator, TetR Family Member [Methanococcus maripaludis S2] emb CAF30579.1 Transcriptional regulator, TetR Family Member [Methanococcus maripaludis S2]			
10627, 10628	23130537	45	4.00E-17	Nostoc punctiforme PCC 73102	COG0778: Nitroreductase [Nostoc punctiforme PCC 73102]			

1063,	21674172	32	6.00E-19	Chlorobium tepidum TLS	ABC transporter efflux protein [Chlorobium tepidum TLS] gb AAM72579.1			
1064	AAG8272			Chlorobium TLS	ABC transporter efflux protein [Chlorobium tepidum TLS]			
10633,					Desc:S. epidermidis open reading frame protein sequence SEQ ID NO:2538.			
10634	2	23	2.00E-07	Treponema denticola ATCC 35405	Org:Staphylococcus epidermidis			
10635,					cytidylate kinase/ribosomal protein S1 [Treponema denticola ATCC 35405]			2.7.7.8
10636	42527583	52	1.00E-38	Treponema denticola ATCC 35405	gb AAS12592.1 cytidylate kinase/ribosomal protein S1 [Treponema denticola ATCC 35405]			
10637,					conserved hypothetical protein [Helicobacter hepaticus ATCC 51449]			
10638	32262573	45	1.00E-31	Helicobacter hepaticus ATCC 51449	ref NP_860554.1 hypothetical protein HH1023 [Helicobacter hepaticus ATCC 51449]			
10639,					conserved hypothetical protein [Campylobacter lari RM2100]			
10640	57241759	38	2.00E-48	Campylobacter lari RM2100	gb EAL54429.1 conserved hypothetical protein [Campylobacter lari RM2100]			
10641,					aspartate carbamoyltransferase regulatory chain [Bacteroides fragilis YCH46] db BAD48954.1 aspartate carbamoyltransferase regulatory chain			2.1.3.2
10642	53713496	53	2.00E-30	Bacteroides fragilis YCH46	[Bacteroides fragilis YCH46]			
10643,					aspartate carbamoyltransferase regulatory chain [Bacteroides fragilis YCH46] db BAD48954.1 aspartate carbamoyltransferase regulatory chain			2.1.3.2
10644	53713496	53	3.00E-29	Bacteroides fragilis YCH46	[Bacteroides fragilis YCH46]			
1065,					two-component system, regulatory protein [Nostoc sp. PCC 7120]			
1066	17230650	40	4.00E-11	Nostoc sp. PCC 7120	db BAB74857.1 two-component system, regulatory protein [Nostoc sp. PCC 7120] pir AG2200 two-component system, regulatory protein alr3158 [Imported] - Nostoc sp. (strain PCC 7120)			2.7.3.-
10651,					hypothetical protein Meth02004168 [Methanosarcina barkeri str. fusaro]			
10652	48837993	46	2.00E-39	Methanosarcina barkeri str. fusaro				
10653,					COG0277: FAD/FMN-containing dehydrogenases [Cytophaga hutchinsonii]			1.1.99.5
10654	48853549	52	8.00E-42	Cytophaga hutchinsonii	putative sulfatase yidJ [Bacteroides thetaiotaomicron VPI-5482]			
10655,					gb AAO78904.1 putative sulfatase yidJ [Bacteroides thetaiotaomicron VPI-5482]			3.1.6.-
10656	29349207	39	9.00E-37	Bacteroides thetaiotaomicron VPI-5482				
10659,					COG1053: Succinate dehydrogenase/fumarate reductase, flavoprotein subunit [Geobacter metallireducens GS-15]			1.3.99.1
10660	48845483	41	2.00E-31	Geobacter metallireducens GS-15	putative transport protein [Bacteroides fragilis YCH46] db BAD49430.1			
10661,					putative transport protein [Bacteroides fragilis YCH46]			
10662	53713972	37	7.00E-36	Bacteroides fragilis YCH46	hypothetical protein MM0206 [Methanosarcina mazel Go1] gb AAM29902.1			
10663,					conserved protein [Methanosarcina mazel Goe1]			
10664	21226308	47	1.00E-17	Methanosarcina mazel Go1	exonuclease ABC subunit A [Bacteroides thetaiotaomicron VPI-5482]			
10665,					gb AAO75685.1 exonuclease ABC subunit A [Bacteroides thetaiotaomicron VPI-5482]			
10666	29345988	51	1.00E-69	Bacteroides thetaiotaomicron VPI-5482				

10667, 10668	53713904	75	9.00E-98	Bacteroides fragilis YCH46	excinuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46]	Haemophilus Influenzae excinuclease ABC subunit A (uvrA) gene, complete cds	82	3.00E-08	
10669, 10670	15605819	41	8.00E-20	Aquifex aeolicus VF5	endonuclease III [Aquifex aeolicus VF5] gb AAC06594.1 endonuclease III [Aquifex aeolicus VF5] pir H70325 endonuclease III - Aquifex aeolicus			4.2.99.1 8	
1067, 1068	28211966	65	1.00E-111	Clostridium tetani E88	ATP-dependent clp protease ATP-binding subunit clpX [Clostridium tetani E88] gb AAO36847.1 ATP-dependent clp protease ATP-binding subunit clpX [Clostridium tetani E88] sp Q891.8 CLPX_CLOTE ATP-dependent Clp protease ATP-binding subunit clpX	Caulobacter crescentus CB15 section 195 of 359 of the complete genome	85	1.00E-17	3.4.24.-
10671, 10672	57241904	79	1.00E-117	Campylobacter upsaliensis RM3195	transcription termination factor Rho [Campylobacter upsaliensis RM3195] gb EAL53877.1 transcription termination factor Rho [Campylobacter upsaliensis RM3195]	Campylobacter jejuni HS:19 lipooligosaccharide biosynthesis locus, partial sequence	80	1.00E-26	3.6.3.14
10677, 10678	29376809	40	8.00E-38	Enterococcus faecalis V583	hypothetical protein EF2307 [Enterococcus faecalis V583] gb AAO82033.1 conserved hypothetical protein [Enterococcus faecalis V583]				
10679, 10680	23099116	40	1.00E-23	Oceanobacillus lheyensis HTE831	adenylylsulfate kinase [Oceanobacillus lheyensis HTE831] dbj BAC13617.1 adenylylsulfate kinase [Oceanobacillus lheyensis HTE831]				2.7.1.25
10681, 10682	29346299	40	9.00E-40	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0889 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75996.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
10687, 10688	48854843	49	3.00E-34	Cytophaga hutchinsonii	COG0196: FAD synthase [Cytophaga hutchinsonii]				2.7.1.26
10689, 10690	57241016	35	3.00E-27	Campylobacter lari RM2100	methyl-accepting chemotaxis protein (tipB), putative [Campylobacter lari RM2100] gb EAL54712.1 methyl-accepting chemotaxis protein (tipB), putative [Campylobacter lari RM2100]				
1069, 1070	31194577	43	9.00E-67	Anopheles gambiae	ENSANGP00000000035 [Anopheles gambiae]				1.10.3.3
10691, 10692	32476967	29	4.00E-16	Rhodopirellula baltica SH 1	type I restriction enzyme EcoAI R protein [Rhodopirellula baltica SH 1] emb CAD79104.1 type I restriction enzyme EcoAI R protein [Pirellula sp.]				3.1.21.3

10697, 10698	15669884	39	1.00E-45	Methanocaldococcus jannaschii DSM 2661	Heterodisulfide reductase, subunit A [Methanocaldococcus jannaschii DSM 2661]			1.6.4.-
10699, 10700	32262118	57	2.00E-26	Helicobacter hepaticus ATCC 51449	competence protein ComM [Helicobacter hepaticus ATCC 51449] ref[NP_860101.1] competence protein ComM [Helicobacter hepaticus ATCC 51449]			
107, 108	48855577	48	3.00E-26	Cytophaga hutchinsonii	COG0858: Ribosome-binding factor A [Cytophaga hutchinsonii]			
10701, 10702	19704078	46	8.00E-29	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	ATP-dependent helicase, DinG family [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gblAAL94939.1] ATP-dependent helicase, DinG family [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			3.6.1.-
10703, 10704	48894830	41	9.00E-28	Trichodesmium erythraeum IMS101	COG0235: Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases [Trichodesmium erythraeum IMS101]			
10705, 10706	14518311	39	6.00E-24	Microscilla sp. PRE1	putative outer membrane protein [Microscilla sp. PRE1] gblAAK62828.1] IMS106, putative outer membrane protein [Microscilla sp. PRE1]			
10709, 10710	57240752	43	2.00E-25	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gblEAL55145.1] conserved hypothetical protein [Campylobacter lari RM2100]			
10711, 10712	24372039	40	3.00E-13	Shewanella oneidensis MR-1	hypothetical protein SO0444 [Shewanella oneidensis MR-1] gblAAN53526.1] hypothetical protein [Shewanella oneidensis MR-1]			
10713, 10714	34558169	32	2.00E-17	Wollinella succinogenes DSM 1740	conserved hypothetical protein-DNA polymerase III delta subunit [Wollinella succinogenes DSM 1740] emb CAE10884.1] conserved hypothetical protein-DNA polymerase III delta subunit [Wollinella succinogenes]			
10715, 10716	52007843	48	5.00E-32	Thiobacillus denitrificans ATCC 25259	COG0607: Rhodanese-related sulfurtransferase [Thiobacillus denitrificans ATCC 25259]			
10721, 10722	29346070	26	1.00E-11	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0660 [Bacteroides thetaiotaomicron VPI-5482] gblAAO75767.1] conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
10723, 10724	19704806	31	2.00E-13	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	N-acetylmannosamine kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gblAAL95667.1] N-acetylmannosamine kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			2.7.1.60
10725, 10726	51246738	68	6.00E-33	Desulfotalea psychrophila LSv54	probable pyruvate-flavodoxin oxidoreductase [Desulfotalea psychrophila LSv54] emb CAG37615.1] probable pyruvate-flavodoxin oxidoreductase [Desulfotalea psychrophila LSv54]			1.2.7.1

10727, 10728	20089049	29	5.00E-12	Methanosarcina acetivorans C2A	hypothetical protein MA0151 [Methanosarcina acetivorans C2A] gb AAM03604.1 predicted protein [Methanosarcina acetivorans str. C2A] tRNA pseudouridine synthase A [Campylobacter lari RM2100] gb EAL55500.1 tRNA pseudouridine synthase A [Campylobacter lari RM2100]				4.2.1.70
10729, 10730	57240386	37	1.00E-42	Campylobacter lari RM2100					
1073, 1074	31194811	42	2.00E-32	Anopheles gambiae	ENSANGP00000002016 [Anopheles gambiae] related to 27kDa outer membrane protein [Desulfotalea psychrophila LSV54] emb CAG36336.1 related to 27kDa outer membrane protein [Desulfotalea psychrophila LSV54]				3.1.-.-
10731, 10732	51245459	25	2.00E-07	Desulfotalea psychrophila LSV54	putative integrase/recombinase [Staphylococcus aureus subsp. aureus MRS252] emb CAG40230.1 putative integrase/recombinase [Staphylococcus aureus subsp. aureus MRS252]				
10733, 10734	49483415	32	6.00E-22	Staphylococcus aureus subsp. aureus MRS252	glucose inhibited division protein A [Campylobacter lari RM2100] gb EAL55623.1 glucose inhibited division protein A [Campylobacter lari RM2100]				
10735, 10736	57240509	56	3.00E-26	Campylobacter lari RM2100	COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Psychrobacter sp. 273-4]				2.3.1.51
10739, 10740	46141178	80	2.00E-98	Psychrobacter sp. 273-4	Desc:Herbicidally active polypeptide SEQ ID NO 1547. Org:Arabidopsis thaliana				
10741, 10742	ABB9233	6	7.00E-10						
10743, 10744	15896258	34	5.00E-43	Clostridium acetobutylicum ATCC 824	Zn-dependent peptidase, Insulinase family [Clostridium acetobutylicum ATCC 824] gb AAK80947.1 Zn-dependent peptidase, insulinase family [Clostridium acetobutylicum ATCC 824] pir H97269 Zn-dependent peptidase, insulinase family [imported] - Clostridium acetobutylicum				
10745, 10746	53712196	46	7.00E-63	Bacteroides fragilis YCH46	tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides fragilis YCH46] db BAD47654.1 tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides fragilis YCH46]				2.5.1.8
10747, 10748	13358424	30	2.00E-07	Lymphocystis disease virus 1	unknown [Lymphocystis disease virus 1]				
10749, 10750	23114483	45	6.00E-27	Desulfotobacterium hafniense DCB-2	COG2931: RTX toxins and related Ca2+-binding proteins [Desulfotobacterium hafniense DCB-2]				
1075, 1076	48853390	34	3.00E-31	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] co-chaperone-curved DNA binding protein A (CbpA) [Campylobacter upsaliensis RM3195] gb EAL53788.1 co-chaperone-curved DNA binding protein A (CbpA) [Campylobacter upsaliensis RM3195]				2.7.3.-
10751, 10752	57242326	28	2.00E-11	Campylobacter upsaliensis RM3195					

10755, 10756	34557593	49	3.00E-54	Wollinella succinogenes DSM 1740	hypothetical protein WS1227 [Wollinella succinogenes DSM 1740] emb CAE10308.1 hypothetical protein [Wollinella succinogenes] sp P59893 TRUD_WOLSU tRNA pseudouridine synthase D (Pseudouridyate synthase) [Uracil hydrolyase]				
10759, 10760	32469350	53	4.00E-25	Francisella tularensis subsp. novicida	unknown [Francisella tularensis subsp. novicida] TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wollinella succinogenes DSM 1740] emb CAE10442.1 TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wollinella succinogenes]			88	2.00E-07
10761, 10762	34557727	42	5.00E-18	Wollinella succinogenes DSM 1740					2.7.3.-
10763, 10764	34558250	67	1.00E-112	Wollinella succinogenes DSM 1740	EXINUCLEASE ABC SUBUNIT B [Wollinella succinogenes DSM 1740] emb CAE10965.1 EXINUCLEASE ABC SUBUNIT B [Wollinella succinogenes]			87	3.00E-12
10765, 10766	34557419	40	5.00E-21	Wollinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes]				2.7.3.-
10767, 10768	29347815	40	8.00E-39	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT2405 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77512.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
1077, 1078	48853455	28	2.00E-13	Cytophaga hutchinsonii	COG0806: RimM protein, required for 16S rRNA processing [Cytophaga hutchinsonii]				
10773, 10774	53711380	28	2.00E-07	Bacteroides fragilis YCH46	two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD46838.1 two-component system response regulator [Bacteroides fragilis YCH46]				
10775, 10776	29347827	28	8.00E-19	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT2417 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77524.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
10779, 10780	48834423	35	3.00E-27	Magnetococcus sp. MC-1	COG0535: Predicted Fe-S oxidoreductases [Magnetococcus sp. MC-1] dimethyladenosine transferase [Campylobacter jejuni RM1221] gb AAW34480.1 dimethyladenosine transferase [Campylobacter jejuni RM1221]				
10781, 10782	57236897	50	7.00E-44	Campylobacter jejuni RM1221					2.1.1.-
10783, 10784	53711848	32	3.00E-29	Bacteroides fragilis YCH46	putative outer membrane efflux protein [Bacteroides fragilis YCH46] dbj BAD47306.1 putative outer membrane efflux protein [Bacteroides fragilis YCH46]				

10787, 10788	53795029	29	1.00E-17	Chloroflexus aurantiacus	COG2202: FOG: PAS/PAC domain [Chloroflexus aurantiacus]			2.7.3.-
10789, 10790	34557494	69	4.00E-61	Wolinella succinogenes DSM 1740	PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes DSM 1740] emb CAE10209.1 PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes]	84	3.00E-08	6.3.5.-
10791, 10792	39996989	31	5.00E-29	Geobacter sulfurreducens PCA	response regulator [Geobacter sulfurreducens PCA] gb AAR35267.1 response regulator [Geobacter sulfurreducens PCA]			2.7.3.-
10793, 10794	48853942	37	1.00E-18	Cytophaga hutchinsonii	COG4206: Outer membrane cobalamin receptor protein [Cytophaga hutchinsonii]			
10795, 10796	48853942	35	9.00E-30	Cytophaga hutchinsonii	COG4206: Outer membrane cobalamin receptor protein [Cytophaga hutchinsonii]			
10797, 10798	34557362	27	7.00E-19	Wolinella succinogenes DSM 1740	TWO-COMPONENT HYBRID PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10077.1 TWO-COMPONENT HYBRID PROTEIN [Wolinella succinogenes]			
10799, 10800	47568045	48	1.00E-21	Bacillus cereus G9241	glycogen synthase [Bacillus cereus G9241] gb EAL13693.1 glycogen synthase [Bacillus cereus G9241]			2.4.1.21
10801, 10802	20807518	43	9.00E-58	Thermoanaerobact er tengcongensis MB4	Chemotaxis protein histidine kinase and related kinases [Thermoanaerobacter tengcongensis MB4] gb AAM24293.1 Chemotaxis protein histidine kinase and related kinases [Thermoanaerobacter tengcongensis MB4]			2.7.3.-
10803, 10804	1197006	55	8.00E-32	Bacteroides fragilis	unknown protein [Bacteroides fragilis] gb AAA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for insertion sequence element IS4351 (Transposon TN4551)	85	1.00E-09	
10805, 10806	34398065	28	8.00E-08	Porphyromonas gingivalis W83	ISPg2, transposase [Porphyromonas gingivalis W83] gb AAQ66749.1 ISPg2, transposase [Porphyromonas gingivalis W83] gb AAQ66414.1 ISPg2, transposase [Porphyromonas gingivalis W83] gb AAQ66012.1 ISPg2, transposase [Porphyromonas gingivalis W83] gb AAQ65497.1 ISPg2, transposase [Porphyromonas gingivalis W83] ref NP_906226.1 ISPg2, transposase [Porphyromonas gingivalis W83] ref NP_905850.1 ISPg2, transposase [Porphyromonas gingivalis W83] ref NP_905515.1 ISPg2, transposase [Porphyromonas gingivalis W83] ref NP_905113.1 ISPg2, transposase [Porphyromonas gingivalis W83] ref NP_904598.1 ISPg2, transposase [Porphyromonas gingivalis W83] gb AAC45368.1 putative transposase [Porphyromonas gingivalis]			

10809, 10810	34558040	45	1.00E-43	Wolinella succinogenes DSM 1740	hypothetical protein WS1730 [Wolinella succinogenes DSM 1740] emb CAE10755.1 conserved hypothetical protein [Wolinella succinogenes]					3.1.1.61
1081, 1082	48860907	37	4.00E-40	Microbulbifer degradans 2-40	COG3279: Response regulator of the LyfR/AIgR family [Microbulbifer degradans 2-40]					
10811, 10812	42561229	48	8.00E-22	Mycoplasma mycoides subsp. mycoides SC str. PG1	omithine carbamoyltransferase [Mycoplasma mycoides subsp. mycoides SC str. PG1] emb CAE77322.1 omithine carbamoyltransferase [Mycoplasma mycoides subsp. mycoides SC]					2.1.3.3
10815, 10816	ABG9157 1	36	4.00E-33		Desc:Purine/pyrimidine triphosphate type nucleotidyltransferase #156. Org:Aquifex aeolicus					2.7.7.13
10817, 10818	54298940	37	3.00E-33	Legionella pneumophila str. Paris	hypothetical protein lpp3007 [Legionella pneumophila str. Paris] emb CAH14160.1 hypothetical protein [Legionella pneumophila str. Paris]					
10819, 10820	39996002	42	2.00E-29	Geobacter sulfurreducens PCA	hypothetical protein GSU0897 [Geobacter sulfurreducens PCA] gb AAR34226.1 conserved hypothetical protein [Geobacter sulfurreducens PCA]					
10821, 10822	48838054	25	8.00E-10	Methanosarcina barkeri str. fusaro	COG0542: ATPases with chaperone activity, ATP-binding subunit [Methanosarcina barkeri str. fusaro]					
10823, 10824	48839054	29	2.00E-20	Methanosarcina barkeri str. fusaro	COG0542: ATPases with chaperone activity, ATP-binding subunit [Methanosarcina barkeri str. fusaro]					2.7.3.-
10827, 10828	34558244	35	2.00E-32	Wolinella succinogenes DSM 1740	SIGNAL TRANSDUCTION REGULATORY PROTEIN-CheY like receiver domain [Wolinella succinogenes DSM 1740] emb CAE10959.1 SIGNAL TRANSDUCTION REGULATORY PROTEIN-CheY like receiver domain [Wolinella succinogenes]					
10829, 10830	34557313	51	7.00E-31	Wolinella succinogenes DSM 1740	ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10028.1 ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes]					1.8.-
1083, 1084	48855328	79	1.00E-126	Cytophaga hutchinsonii	COG0085: DNA-directed RNA polymerase, beta subunit/140 kD subunit [Cytophaga hutchinsonii]	Bacteroides thetataomicron VPI-5482, section 12 of 21 of the complete genome	90	2.00E-13	2.7.7.6	
10831, 10832	34557317	35	3.00E-08	Wolinella succinogenes DSM 1740	hypothetical protein WS0928 [Wolinella succinogenes DSM 1740] emb CAE10032.1 hypothetical protein [Wolinella succinogenes]					
10833, 10834	34557316	35	8.00E-21	Wolinella succinogenes DSM 1740	hypothetical protein WS0927 [Wolinella succinogenes DSM 1740] emb CAE10031.1 hypothetical protein [Wolinella succinogenes]					

10837, 10838	32263347	48	1.00E-60	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861326.1 hypothetical protein HH1795 [Helicobacter hepaticus ATCC 51449]				
10841, 10842	34556857	48	2.00E-63	Wolinella succinogenes DSM 1740	DNA POLYMERASE I [Wolinella succinogenes DSM 1740] emb CAE09572.1 DNA POLYMERASE I [Wolinella succinogenes]				2.7.7.7
10843, 10844	34556857	60	4.00E-73	Wolinella succinogenes DSM 1740	DNA POLYMERASE I [Wolinella succinogenes DSM 1740] emb CAE09572.1 DNA POLYMERASE I [Wolinella succinogenes]				2.7.7.7
10845, 10846	29654150	46	2.00E-21	Coxiella burnetii RSA 493	hypothetical protein CBU0822 [Coxiella burnetii RSA 493] gb AAO90356.1 conserved hypothetical protein [Coxiella burnetii RSA 493]				
10847, 10848	48853408	46	2.00E-77	Cytophaga hutchinsonii	COG0567: 2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, and related enzymes [Cytophaga hutchinsonii]				1.2.4.2
10849, 10850	34556786	37	2.00E-42	Wolinella succinogenes DSM 1740	PUTATIVE PROCESSING PROTEASE [Wolinella succinogenes DSM 1740] emb CAE09501.1 PUTATIVE PROCESSING PROTEASE [Wolinella succinogenes]				3.4.-.-
1085, 1086	2281663	59	2.00E-76	Flavobacterium johnsoniae	gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding motility protein [imported] - Flavobacterium johnsoniae				1.8.-.-
10851, 10852	46580033	44	3.00E-47	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	phosphoribosylformylglycinamide synthase I [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96100.1 phosphoribosylformylglycinamide synthase I [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]				6.3.5.3
10857, 10858	29347851	35	7.00E-22	Bacteroides thetaiotaomicron VPI-5482	putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77548.1 putative 5'-nucleotidase/2',3'- cyclic phosphodiesterase [Bacteroides thetaiotaomicron VPI-5482]				3.1.4.16
10861, 10862	32262861	24	9.00E-10	Helicobacter hepaticus ATCC 51449	methyl-accepting chemotaxis protein [Helicobacter hepaticus ATCC 51449] ref NP_860841.1 methyl-accepting chemotaxis protein [Helicobacter hepaticus ATCC 51449]				
10863, 10864	ABP6590 6	61	1.00E-75		Desc:Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:650. Org:Bifidobacterium longum			86	1.00E-10 6.3.5.3
10865, 10866	29346742	52	2.00E-64	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT1332 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76439.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-

10867, 10868 10869, 10870	23002396 32473409	33 43	1.00E-31 4.00E-23	Lactobacillus gasseri Rhodopirellula baltica SH 1	COG2344: AT-rich DNA-binding protein [Lactobacillus gasseri] ref NP_964480.1 hypothetical protein LJO455 [Lactobacillus johnsonii NCC 533] gb AAS08446.1 hypothetical protein LJO455 [Lactobacillus johnsonii NCC 533] probable aminopeptidase [Rhodopirellula baltica SH 1] emb CAD78184.1 probable aminopeptidase [Pirellula sp.]			3.4.17.2 1	
10873, 10874	32261675	44	5.00E-56	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_859659.1 hypothetical protein HH0128 [Helicobacter hepaticus ATCC 51449]	Alvinella pompejana epibiont 6C8 fosmid clone 6C8, complete sequence	87	2.00E-09	6.3.2.15
10875, 10876	32477370	31	5.00E-19	Rhodopirellula baltica SH 1	phosphoribosylaminimidazole-succinocarboxamide synthase [Rhodopirellula baltica SH 1] emb CAD77441.1 phosphoribosylaminimidazole-succinocarboxamide synthase [Pirellula sp.]				6.3.2.6
10877, 10878	20806994	32	2.00E-27	Thermoanaerobact er tengcongensis MB4	ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member [Thermoanaerobacter tengcongensis MB4] gb AAM23769.1 ATP-dependent exoDNAse (exonuclease V), alpha subunit helicase superfamily I member [Thermoanaerobacter tengcongensis MB4]				3.1.11.5
10879, 10880	32263354	37	2.00E-24	Helicobacter hepaticus ATCC 51449	chemotaxis signal transduction protein CheV [Helicobacter hepaticus ATCC 51449] ref NP_861333.1 chemotaxis signal transduction protein CheV [Helicobacter hepaticus ATCC 51449]				2.7.3.-
10881, 10882	57241192	38	2.00E-48	Campylobacter lari RM2100	fructose-1,6-bisphosphatase [Campylobacter lari RM2100] gb EAL54888.1 fructose-1,6-bisphosphatase [Campylobacter lari RM2100]				3.1.3.11
10883, 10884	53712231	38	2.00E-20	Bacteroides fragilis YCH46	transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD47689.1 transcriptional regulator [Bacteroides fragilis YCH46]				
10885, 10886	15643941	57	3.00E-45	Thermotoga maritima MSB8	methylglyoxal synthase [Thermotoga maritima MSB8] gb AAD36260.1 methylglyoxal synthase [Thermotoga maritima MSB8] pir G72284				4.2.3.3
10889, 10890	48856411	56	4.00E-21	Cytophaga hutchinsonii	methylglyoxal synthase - Thermotoga maritima (strain MSB8) COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii]				1.8.-.-
10891, 10892	54031326	37	8.00E-46	Polaromonas sp. JS666	COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Polaromonas sp. JS666]				
10895, 10896	48856297	63	5.00E-42	Cytophaga hutchinsonii	COG0735: Fe2+/Zn2+ uptake regulation proteins [Cytophaga hutchinsonii]				
10897, 10898	48833126	35	1.00E-26	Magnetococcus sp. MC-1	COG1355: Predicted dioxygenase [Magnetococcus sp. MC-1]				

10899, 10900	32262440	21	4.00E-07	51449	Helicobacter hepaticus ATCC	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860422.1 hypothetical protein HH0891 [Helicobacter hepaticus ATCC 51449]			
109, 110	48854911	41	5.00E-35		Cytophaga hutchinsonii	COG0845: Membrane-fusion protein [Cytophaga hutchinsonii]			
10901, 10902	AAU4054	34	7.00E-34			Desc:Propionibacterium acnes immunogenic protein #1445. Org:Propionibacterium acnes			
10903, 10904	48855091	40	4.00E-31		Cytophaga hutchinsonii	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii]			2.7.3.-
10907, 10908	558266	68	1.00E-29		Wolinella succinogenes	orf [Wolinella succinogenes] pil[S50154 hypothetical protein 2 - Wolinella succinogenes]			
1091, 1092	21229419	43	2.00E-30		Methanosarcina mazel Go1	hypothetical protein MM3317 [Methanosarcina mazel Go1] gb AAM33013.1 hypothetical protein [Methanosarcina mazel Go1]			
10913, 10914	48866340	28	6.00E-19		Oenococcus oeni PSU-1	COG1252: NADH dehydrogenase, FAD-containing subunit [Oenococcus oeni PSU-1]			1.6.99.3
10915, 10916	45516527	47	6.00E-37		Ralstonia eutropha JMP134	COG0796: Glutamate racemase [Ralstonia eutropha JMP134]			5.1.1.3
10917, 10918	34398066	50	3.00E-74		Porphyromonas gingivalis W83	NADH:ubiquinone oxidoreductase, Na translocating, F subunit [Porphyromonas gingivalis W83] ref NP_906227.1 NADH:ubiquinone oxidoreductase, Na translocating, F subunit [Porphyromonas gingivalis W83]			1.6.5.-
10919, 10920	56418633	44	2.00E-52		Geobacillus kaustophilus HTA426	DNA-directed RNA polymerase beta subunit [Geobacillus kaustophilus HTA426] dbj BAD74383.1 DNA-directed RNA polymerase beta subunit [Geobacillus kaustophilus HTA426]	Bosea sp. 7F RNA polymerase beta subunit (poB) gene, complete cds	91	6.00E-07 2.7.7.6
10921, 10922	34558157	29	1.00E-16		Wolinella succinogenes DSM 1740	SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes DSM 1740] emb CAE10872.1 SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes]			2.7.3.-
10923, 10924	34557665	39	7.00E-46		Wolinella succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes]			2.7.3.-
10927, 10928	18653301	35	1.00E-08		Vibrio cholerae	putative Kdo transferase [Vibrio cholerae]			2.4.99.-
1093, 1094	15646208	39	3.00E-45		Helicobacter pylori 26695	Adenine-specific DNA methylase [Helicobacter pylori 26695]			2.1.1.72
10931, 10932	50085130	32	8.00E-16		Acinetobacter sp. ADP1	hypothetical protein ACIAD1995 [Acinetobacter sp. ADP1] emb CAG68818.1 hypothetical protein [Acinetobacter sp. ADP1]			
10933, 10934	57167696	50	2.00E-82		Campylobacter coli RM2228	primosomal protein N' [Campylobacter coli RM2228] gb EAL57482.1 primosomal protein N' [Campylobacter coli RM2228]			3.6.1.-

10935, 10936	51244082	49	3.00E-28	Desulfotalea psychrophila Lsv54	hypothetical protein DP0230 [Desulfotalea psychrophila Lsv54] emb[CAG34959.1] hypothetical protein [Desulfotalea psychrophila Lsv54]			2.7.3.-
10937, 10938	56461220	30	3.00E-31	Idiomarina loihiensis L2TR	Signal transduction histidine kinase [Idiomarina loihiensis L2TR] gb AAV82952.1 Signal transduction histidine kinase [Idiomarina loihiensis L2TR]			
10939, 10940	10567402	34	1.00E-07	Agrobacterium rhizogenes	hypothetical protein [Agrobacterium rhizogenes] ref NP_066673.1 hypothetical protein [Agrobacterium rhizogenes] db BAA97803.1			
10943, 10944	15606018	40	2.00E-28	Aquifex aeolicus VF5	hypothetical protein aq_563 [Aquifex aeolicus VF5] gb AAC06808.1			2.7.3.-
10945, 10946	48834077	46	2.00E-21	Magnetococcus sp. MC-1	hypothetical protein aq_563 - Aquifex aeolicus			2.7.3.-
10949, 10950	33596250	41	2.00E-24	Bordetella parapertussis 12822	COG0840: Methyl-accepting chemotaxis protein [Magnetococcus sp. MC-1]			2.7.3.-
10953, 10954	34556480	49	4.00E-42	Wolinella succinogenes DSM 1740	putative membrane protein [Bordetella parapertussis 12822] emb CAE36915.1 putative membrane protein [Bordetella parapertussis] GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes DSM 1740] emb CAE09195.1 GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes]			2.6.1.16
10955, 10956	15643834	34	3.00E-08	Thermotoga maritima MSB8	hypothetical protein TM1076 [Thermotoga maritima MSB8] gb AAD36153.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir D72296 VPS29-like phosphoesterase-related protein TM1076 [similarity] - Thermotoga maritima (strain MSB8)			
10957, 10958	42528087	26	2.00E-14	Treponema denticola ATCC 35405	endonuclease/exonuclease/phosphatase family protein [Treponema denticola ATCC 35405] gb AAS13104.1			
10959, 10960	48832245	49	7.00E-41	Magnetococcus sp. MC-1	endonuclease/exonuclease/phosphatase family protein [Treponema denticola ATCC 35405]			
10963, 10964	57241714	36	4.00E-38	Campylobacter lari RM2100	COG0379: Quinolinate synthase [Magnetococcus sp. MC-1] fibronectin/fibrinogen-binding protein, putative [Campylobacter lari RM2100] gb EAL54384.1 fibronectin/fibrinogen-binding protein, putative [Campylobacter lari RM2100]			
10965, 10966	39936981	50	5.00E-67	Rhodopseudomonas palustris CGA009	possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009] emb CAE29361.1 possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009]			2.7.-
10969, 10970	48853984	52	4.00E-74	Cytophaga hutchinsonii	COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii]			3.6.1.-

10971, 10972	15606287	34	5.00E-16	Aquifex aeolicus VF5	beta lactamase precursor [Aquifex aeolicus VF5] gb AAC07059.1 beta lactamase precursor [Aquifex aeolicus VF5] pir D70384 beta lactamase precursor - Aquifex aeolicus				
10973, 10974	24374636	33	4.00E-22	Shewanella oneidensis MR-1	thioredoxin, putative [Shewanella oneidensis MR-1] gb AAN56123.1 thioredoxin, putative [Shewanella oneidensis MR-1]				1.8.4.6
10975, 10976	53692808	33	6.00E-19	Haemophilus sommus 129PT	hypothetical protein Hsom02000323 [Haemophilus sommus 129PT]				
10977, 10978	34557339	39	2.00E-41	Wolinella succinogenes DSM 1740	SENSORY TRANSDUCTION REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10054.1 SENSORY TRANSDUCTION REGULATOR [Wolinella succinogenes]				2.7.3.-
10979, 10980	9947383	29	1.00E-17	Pseudomonas aeruginosa PAO1	conserved hypothetical protein [Pseudomonas aeruginosa PAO1] pir G83465 conserved hypothetical protein PA1433 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_250124.1 hypothetical protein PA1433 [Pseudomonas aeruginosa PAO1]				2.7.3.-
10981, 10982	34558459	42	3.00E-50	Wolinella succinogenes DSM 1740	hypothetical protein WS2183 [Wolinella succinogenes DSM 1740] emb CAE11174.1 hypothetical protein [Wolinella succinogenes]				2.1.1.-
10983, 10984	24373682	42	1.00E-18	Shewanella oneidensis MR-1	purine-binding chemotaxis protein CheW [Shewanella oneidensis MR-1] gb AAN55169.1 purine-binding chemotaxis protein CheW [Shewanella oneidensis MR-1]				2.7.3.-
10985, 10986	48859986	40	2.00E-10	Cytophaga hutchinsonii	COG4753: Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain [Cytophaga hutchinsonii]				
10987, 10988	48845271	53	3.00E-17	Geobacter metallireducens GS 15	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]				2.7.3.-
10989, 10990	34557204	44	3.00E-28	Wolinella succinogenes DSM 1740	hypothetical protein WS0806 [Wolinella succinogenes DSM 1740] emb CAE09919.1 conserved hypothetical protein [Wolinella succinogenes] UDP-N-acetylenolpyruvoylglucosamine reductase (murB) [Clostridium acetobutylicum ATCC 824] gb AAK78490.1 UDP-N- acetylenolpyruvoylglucosamine reductase (murB) [Clostridium acetobutylicum ATCC 824] pir G96962 UDP-N- acetylenolpyruvoylglucosamine reductase (murB) [Imported] - Clostridium acetobutylicum sp Q97LP4 MURB_CLOAB UDP-N- acetylenolpyruvoylglucosamine reductase (UDP-N-acetylmuramate dehydrogenase)				1.1.1.15 8
10991, 10992	48833775	35	2.00E-21	Magnetococcus sp. MC-1	COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Magnetococcus sp. MC-1]				2.7.3.-
10993, 10994	6460223	22	5.00E-12	Deinococcus radiodurans	cobW protein, putative [Deinococcus radiodurans] pir A75278 probable cobW protein - Deinococcus radiodurans (strain R1) ref NP_296129.1 cobW protein, putative [Deinococcus radiodurans R1]				

10997, 10998	48864458	60	2.00E-39	Microbubifer degradans 2-40	COG2824: Uncharacterized Zn-ribbon-containing protein involved in phosphonate metabolism [Microbubifer degradans 2-40]			
11, 12	29347043	42	4.00E-23	Bacteroides thetaiotaomicron VPI-5482	mannose-1-phosphate guanylyltransferase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO76740.1 mannose-1-phosphate guanylyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.7.7.13
11001, 11002	15606171	35	2.00E-25	Aquifex aeolicus VF5	hydrogenase small subunit [Aquifex aeolicus VF5] gb AAC06946.1 hydrogenase small subunit [Aquifex aeolicus VF5] pir H70369 hydrogenase small subunit - Aquifex aeolicus			1.18.99. 1
11003, 11004	ABG1373	45	4.00E-21		Desc:Novel human diagnostic protein #13722. Org:Homo sapiens			
11007, 11008	48856129	39	2.00E-43	Cytophaga hutchinsonii	COG1011: Predicted hydrolase (HAD superfamily) [Cytophaga hutchinsonii]			3.8.1.2
11009, 11010	23099302	34	7.00E-25	Oceanobacillus ihayensis HTE831	integrase: recombinase [Oceanobacillus ihayensis HTE831] dbj BAC13803.1 integrase : recombinase [Oceanobacillus ihayensis HTE831] sp Q7ZAM3 XERD_OCEIH Tyrosine recombinase xerD			
1101, 1102	48856112	35	1.00E-19	Cytophaga hutchinsonii	COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
11011, 11012	48854182	33	2.00E-20	Cytophaga hutchinsonii	COG1472: Beta-glucosidase-related glycosidases [Cytophaga hutchinsonii]			3.2.1.52
11013, 11014	18309655	38	4.00E-50	Clostridium perfringens str. 13	biotin-protein ligase [Clostridium perfringens str. 13] dbj BAB80379.1 biotin- protein ligase [Clostridium perfringens str. 13]			6.3.4.15
11015, 11016	57236927	67	4.00E-80	Campylobacter jejuni RM1221	hypothetical protein CJE0015 [Campylobacter jejuni RM1221] gb AAW34510.1 conserved hypothetical protein [Campylobacter jejuni RM1221]			
11017, 11018	57241729	49	9.00E-25	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54399.1 conserved hypothetical protein [Campylobacter lari RM2100]			
11019, 11020	21226543	27	4.00E-17	Methanosarcina mazei Go1	Methylenetetrahydrofolate cyclohydrolase; Methylenetetrahydrofolate dehydrogenase (NADP+) [Methanosarcina mazei Go1] gb AAM30137.1 Methylenetetrahydrofolate dehydrogenase (NADP+); Methylenetetrahydrofolate cyclohydrolase [Methanosarcina mazei Go1]			1.5.1.5
11021, 11022	56315983	48	2.00E-44	Azoarcus sp. EbN1	transposase [Azoarcus sp. EbN1] emb CAI10611.1 transposase [Azoarcus sp. EbN1]			
11025, 11026					Oryza sativa chromosome 11 BAC clone OSJNB0018N12, complete sequence		## 6.00E-10	
11027, 11028	18957982	50	2.00E-39	Xenorhabdus nematophila	putative transposase [Xenorhabdus nematophila]			

11029, 11030	57238615	31	6.00E-07	Campylobacter jejuni RM1221	HrgA protein [Campylobacter jejuni RM1221] gb AAW36198.1 HrgA protein [Campylobacter jejuni RM1221]				
1103, 1104	53714652	40	6.00E-25	Bacteroides fragilis YCH46	putative two-component system sensor protein [Bacteroides fragilis YCH46] dbj BAD50110.1 putative two-component system sensor protein [Bacteroides fragilis YCH46]				2.7.3.-
11031, 11032	52007199	26	8.00E-15	Thiobacillus denitrificans ATCC 25259	COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Thiobacillus denitrificans ATCC 25259]				
11033, 11034	29349224	48	6.00E-80	Bacteroides thetaiotaomicron VPI-5482	penicillin-binding protein 2 (PBP-2) [Bacteroides thetaiotaomicron VPI-5482] gb AAO78921.1 penicillin-binding protein 2 (PBP-2) [Bacteroides thetaiotaomicron VPI-5482]				
11035, 11036	50122190	47	3.00E-51	Erwinia carotovora subsp. atroseptica SCRI1043	putative toxin secretion ATP-binding protein [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG76166.1 putative toxin secretion ATP- binding protein [Erwinia carotovora subsp. atroseptica SCRI1043]				3.4.21.-
11037, 11038	21674374	39	4.00E-22	Chlorobium tepidum TLS	hypothetical protein CT1556 [Chlorobium tepidum TLS] gb AAM72781.1 conserved hypothetical protein [Chlorobium tepidum TLS]				3.4.21.-
11039, 11040	34557740	39	2.00E-55	Wolinella succinogenes DSM 1740	NIFEN2 [Wolinella succinogenes DSM 1740] emb CAE10455.1 NIFEN2 [Wolinella succinogenes]				1.18.6.1
11041, 11042	34556892	72	1.00E-114	Wolinella succinogenes DSM 1740	DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wolinella succinogenes DSM 1740] emb CAE09607.1 DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wolinella succinogenes] sp Q7MA56 RPBC_WOLSU Bifunctional DNA-directed RNA polymerase, beta and beta' chain [includes: DNA-directed RNA polymerase beta chain (Transcriptase beta chain) (RNA polymerase beta subunit); DNA-directed RNA polymerase beta' chain (Transcriptase beta' chain) (RNA polymerase beta' subunit)]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6	82	4.00E-36	2.7.7.6
11043, 11044	28899070	32	2.00E-13	Vibrio parahaemolyticus RIMD 2210633	membrane-bound lytic murein transglycosylase D [Vibrio parahaemolyticus RIMD 2210633] dbj BAC60559.1 membrane-bound lytic murein transglycosylase D [Vibrio parahaemolyticus]				3.2.1.-
11045, 11046	53715699	55	1.00E-75	Bacteroides fragilis YCH46	DNA topoisomerase I [Bacteroides fragilis YCH46] dbj BAD51157.1 DNA topoisomerase I [Bacteroides fragilis YCH46]				5.99.1.2
11047, 11048	46193085	30	2.00E-22	Rhodobacter sphaeroides 2.4.1	hypothetical protein RspH0300134.1 [Rhodobacter sphaeroides 2.4.1]				
11049, 11050	28897010	78	7.00E-83	Vibrio parahaemolyticus RIMD 2210633	nucleotide sugar dehydrogenase [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58499.1 nucleotide sugar dehydrogenase [Vibrio parahaemolyticus]	Vibrio vulnificus YJ016 DNA, chromosome I, complete sequence	86	1.00E-13	1.1.1.22

1105, 1106	56750395	34	4.00E-07	Synechococcus elongatus PCC 6301	hypothetical protein syc0386_c [Synechococcus elongatus PCC 6301] dbj BAD78576.1 unknown protein [Synechococcus elongatus PCC 6301]				
11051, 11052	53765426	33	3.00E-26	Anabaena variabilis ATCC 29413	COG0642: Signal transduction histidine kinase [Anabaena variabilis ATCC 29413]				2.7.3.-
11053, 11054	28900037	29	7.00E-19	Vibrio parahaemolyticus RIMD 2210633	putative C4-dicarboxylate transport sensor protein [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61525.1 putative C4-dicarboxylate transport sensor protein [Vibrio parahaemolyticus]				2.7.3.-
11057, 11058	32469831	37	5.00E-21	Campylobacter jejuni	VirD4 [Campylobacter jejuni] gb AA46901.1 VirD4 [Campylobacter jejuni]				
11059, 11060	53713904	73	1.00E-73	Bacteroides fragilis YCH46	excinuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46]	Haemophilus influenzae excinuclease ABC subunit A (uvrA) gene, complete cds	82	3.00E-08	
11061, 11062	34557850	62	1.00E-84	Wolinella succinogenes DSM 1740	3-DEHYDROQUINATE SYNTHASE [Wolinella succinogenes DSM 1740] emb CAE10565.1 3-DEHYDROQUINATE SYNTHASE [Wolinella succinogenes] sp Q7M8N9 AROB_WOLSU 3-dehydroquinase synthase				4.2.3.4
11065, 11066	48855885	61	5.00E-73	Cytophaga hutchinsonii	COG0209: Ribonucleotide reductase, alpha subunit [Cytophaga hutchinsonii]	Onyza sativa (japonica cultivar- group), mRNA	88	3.00E-08	1.17.4.1
11067, 11068	48860260	28	3.00E-26	Clostridium thermocellum ATCC 27405	COG0489: ATPases involved in chromosome partitioning [Clostridium thermocellum ATCC 27405]				2.7.1.11 2
11069, 11070	48857909	25	6.00E-08	Clostridium thermocellum ATCC 27405	COG1316: Transcriptional regulator [Clostridium thermocellum ATCC 27405]				
1107, 1108	42557777	53	2.00E-14	uncultured crenarchaeote	hypothetical protein [uncultured crenarchaeote]				
11071, 11072	34557590	31	6.00E-20	Wolinella succinogenes DSM 1740	PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10305.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes]				
11073, 11074	53684488	25	3.00E-07	Desulfitobacterium hafniense DCB-2	COG0840: Methyl-accepting chemotaxis protein [Desulfitobacterium hafniense DCB-2]				
11075, 11076	48855450	60	6.00E-35	Cytophaga hutchinsonii	COG0817: Holliday junction resolvase, endonuclease subunit [Cytophaga hutchinsonii]				3.1.22.4
11077, 11078	46425373	38	3.00E-32	Xanthomonas albilineans	McbG-like protein [Xanthomonas albilineans]				

11079, 11080	53714706	60	9.00E-83	Bacteroides fragilis YCH46	adenylosuccinate synthetase [Bacteroides fragilis YCH46] dbj BAD50164.1 adenylosuccinate synthetase [Bacteroides fragilis YCH46]			6.3.4.4
11081, 11082	29349257	37	1.00E-47	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3849 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78954.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
11083, 11084	23125110	28	3.00E-24	Nostoc punctiforme PCC 73102	COG0784: FOG: CheY-like receiver [Nostoc punctiforme PCC 73102]			2.7.3.-
11085, 11086	15605874	32	1.00E-33	Aquifex aeolicus VF5	hypothetical protein aq_367 [Aquifex aeolicus VF5] gb AAC06656.1 hypothetical protein [Aquifex aeolicus VF5] pir G70332 conserved hypothetical protein aq_367 - Aquifex aeolicus			
11087, 11088	54302389	56	2.00E-69	Photobacterium profundum SS9	hypothetical protein PBPRB0710 [Photobacterium profundum SS9] emb CAG22582.1 hypothetical protein [Photobacterium profundum]			6.3.2.3
11089, 11090	34557665	51	2.00E-24	Wolinella succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes]			2.7.3.-
11091, 11092	34556560	30	2.00E-27	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]			2.7.3.-
11093, 11094	48858102	46	1.00E-36	Clostridium thermocellum ATCC 27405	COG1905: NADH:ubiquinone oxidoreductase 24 kD subunit [Clostridium thermocellum ATCC 27405]			1.6.5.3
11095, 11096	53688150	26	9.00E-13	Nostoc punctiforme PCC 73102	COG0500: SAM-dependent methyltransferases [Nostoc punctiforme PCC 73102]			
11099, 11100	53713110	56	5.00E-32	Bacteroides fragilis YCH46	putative long-chain-fatty-acid-CoA ligase [Bacteroides fragilis YCH46] dbj BAD48568.1 putative long-chain-fatty-acid-CoA ligase [Bacteroides fragilis YCH46]			6.2.1.3
111, 112	29349624	54	5.00E-45	Bacteroides thetaiotaomicron VPI-5482	ubiquinone/menaquinone biosynthesis methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79321.1 ubiquinone/menaquinone biosynthesis methyltransferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A005 UBIE_BACTN Menaquinone biosynthesis methyltransferase ubiE			2.1.1.-
11103, 11104	57241252	41	2.00E-36	Campylobacter lari RM2100	signal-transducing protein, histidine kinase [Campylobacter lari RM2100] gb EAL54948.1 signal-transducing protein, histidine kinase [Campylobacter lari RM2100]			2.7.3.-
11105, 11106	51243987	26	2.00E-11	Desulfotalea psychrophila LSV54	hypothetical protein DP0135 [Desulfotalea psychrophila LSV54] emb CAG34864.1 hypothetical protein [Desulfotalea psychrophila LSV54]			2.7.3.-

11109, 11110	45507729	33	2.00E-47	Anabaena variabilis ATCC 29413	COG0479: Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit [Anabaena variabilis ATCC 29413]			1.3.99.1
11111, 11112	53715477	81	1.00E-116	Bacteroides fragilis YCH46	DNA-directed RNA polymerase beta chain [Bacteroides fragilis YCH46] dbj BAD50935.1 DNA-directed RNA polymerase beta chain [Bacteroides fragilis YCH46]			
11113, 11114	34557844	34	1.00E-22	Wolinella succinogenes DSM 1740	MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10559.1 MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes]		78 3.00E-15	2.7.7.6
11119, 11120	34558325	53	2.00E-69	Wolinella succinogenes DSM 1740	PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE11040.1 PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes] sp Q7M7W8 ENGA_WOLSU GTP-binding protein engA putative UROPORPHYRINOGEN-III SYNTHASE [Helicobacter pylori J99] gb AAD06731.1 putative UROPORPHYRINOGEN-III SYNTHASE [Helicobacter pylori J99] pir C71843 probable uroporphyrinogen-III synthase - Helicobacter pylori (strain J99)			
11121, 11122	15612210	33	9.00E-11	Helicobacter pylori J99				4.2.1.75
11123, 11124	46134647	29	4.00E-10	Anabaena variabilis ATCC 29413	COG0659: Sulfate permease and related transporters (MFS superfamily) [Anabaena variabilis ATCC 29413]			
11125, 11126	53712001	62	6.00E-86	Bacteroides fragilis YCH46	DNA polymerase III alpha subunit [Bacteroides fragilis YCH46] dbj BAD47459.1 DNA polymerase III alpha subunit [Bacteroides fragilis YCH46]			2.7.7.7
11129, 11130	17938569	39	2.00E-08	Agrobacterium tumefaciens str. C58	transcriptional regulator, AraC family [Agrobacterium tumefaciens str. C58] gb AAL45674.1 transcriptional regulator, AraC family [Agrobacterium tumefaciens str. C58] pir AD3157 transcription regulator, AraC family Atu4880 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)			
1113, 1114	48854348	55	4.00E-91	Cytophaga hutchinsonii	COG1530: Ribonucleases G and E [Cytophaga hutchinsonii]			3.1.4.-
11131, 11132	48853591	55	2.00E-65	Cytophaga hutchinsonii	COG1021: Peptide arylation enzymes [Cytophaga hutchinsonii]			
11133, 11134	53691920	22	5.00E-07	Desulfovibrio desulfuricans G20	COG0463: Glycosyltransferases involved in cell wall biogenesis [Desulfovibrio desulfuricans G20]			
11135, 11136	29347205	34	1.00E-30	Bacteroides thetaiotaomicron VPI-5482	putative two-component system sensor protein, no kinase domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76902.1 putative two- component system sensor protein, no kinase domain [Bacteroides thetaiotaomicron VPI-5482]			2.7.3.-

111143, 111144	48862944	32	4.00E-25	Microbulifer degradans 2-40	COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Microbulifer degradans 2-40]		
111145, 111146	48890454	35	1.00E-38	Trichodesmium erythraeum IMS101	COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] probable formate dehydrogenase [Clostridium perfringens str. 13] dbj BAB81254.1 probable formate dehydrogenase [Clostridium perfringens str. 13]	1.2.7.-	
111147, 111148	18310530	31	2.00E-27	Clostridium perfringens str. 13	probable formate dehydrogenase [Clostridium perfringens str. 13] dbj BAB81254.1 probable formate dehydrogenase [Clostridium perfringens str. 13]	1.7.99.4	
111149, 111150	18310530	29	8.00E-32	Clostridium perfringens str. 13	hypothetical protein-signal peptide and transmembrane prediction [Rhodopirellula baltica SH 1] emb CAD71383.1 hypothetical protein-signal peptide and transmembrane prediction [Pirellula sp.]		
111151, 111152	48833189	31	9.00E-19	Magnetococcus sp. MC-1	COG2143: Thioresdoxin-related protein [Magnetococcus sp. MC-1] hypothetical protein RS01112 [Raietonia solanacearum GM1000] emb CAD16190.1 CONSERVED HYPOTHETICAL PROTEIN [Raietonia solanacearum]		
111153, 111154	17547202	27	6.00E-09	Magnetococcus sp. MC-1	COG2200: FOG: EAL domain [Magnetococcus sp. MC-1]		
111155, 111156	48834030	37	1.00E-28	Magnetococcus sp. MC-1	Desc:Orthosomycin biosynthetic polypeptide SEQ ID NO 197. Org:Micromonospora carbonacea africana		
111159, 111160	ABP9930 5	24	4.00E-07	Campylobacter upsaliensis	aminoacyl-histidine dipeptidase [Campylobacter upsaliensis RM3195] gbl EAL53077.1 aminoacyl-histidine dipeptidase [Campylobacter upsaliensis RM3195]	3.4.13.3	
111161, 111162	57505466	39	2.00E-49	Bacteroides fragilis YCH46	DNA topoisomerase I [Bacteroides fragilis YCH46] dbj BAD51157.1 DNA topoisomerase I [Bacteroides fragilis YCH46]	5.99.1.2	
111163, 111164	53715699	45	2.00E-48	Trichodesmium erythraeum IMS101	COG1087: UDP-glucose 4-epimerase [Trichodesmium erythraeum IMS101]	5.1.3.2	
111165, 111166	48891975	54	1.00E-44	Geobacter sulfurreducens PCA	hypothetical protein GSU0680 [Geobacter sulfurreducens PCA] gbl AAR34010.1 conserved hypothetical protein [Geobacter sulfurreducens PCA]		
111167, 111168	39995786	32	4.00E-18	Bacteroides fragilis YCH46	putative glycosyltransferase [Bacteroides fragilis YCH46]		
11117, 11118	29349972	66	1.00E-89	Bacteroides fragilis YCH46	putative glycosyltransferase [Bacteroides fragilis YCH46]		
					Bacteroides fragilis YCH46 section 20 of 21 of the complete genome	85	2.00E-07 2.4.1.83

11173, 11174	51246493	35	1.00E-23	Desulfotalea psychrophila LSV54	related to peptidyl-prolyl cis-trans isomerase (FKBP-type) [Desulfotalea psychrophila LSV54] emb CAG37370.1 related to peptidyl-prolyl cis-trans isomerase (FKBP-type) [Desulfotalea psychrophila LSV54]			5.2.1.8
11175, 11176	53712042	45	5.00E-13	Bacteroides fragilis YCH46	hypothetical protein BF0749 [Bacteroides fragilis YCH46] dbj BAD47500.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
11177, 11178	48856222	33	9.00E-31	Cytophaga hutchinsonii	COG0438: Glycosyltransferase [Cytophaga hutchinsonii]			2.4.1.21
11179, 11180	57242490	57	1.00E-74	Campylobacter upsaliensis RM3195	Mg chelatase-related protein [Campylobacter upsaliensis RM3195] gb EAL53558.1 Mg chelatase-related protein [Campylobacter upsaliensis RM3195]			
11181, 11182	6967663	51	4.00E-38	Campylobacter jejuni subsp. jejuni NCTC.11168	hypothetical protein Cj0190c [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281400.1 hypothetical protein Cj0190c [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81437 hypothetical protein Cj0190c [imported] - Campylobacter jejuni (strain NCTC 11168)			
11183, 11184	48892769	26	4.00E-22	Trichodesmium erythraeum IMS101	COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101]			
11185, 11186	53729414	33	1.00E-36	Dechloromonas aromatica RCB	COG0515: Serine/threonine protein kinase [Dechloromonas aromatica RCB]			2.7.1.37
11187, 11188	39996253	30	4.00E-11	Geobacter sulfurreducens PCA	hypothetical protein GSU1151 [Geobacter sulfurreducens PCA] gb AAR34527.1 conserved hypothetical protein [Geobacter sulfurreducens PCA]			
11189, 11190	53713588	45	5.00E-22	Bacteroides fragilis YCH46	ATP-dependent RNA helicase [Bacteroides fragilis YCH46] dbj BAD49046.1 ATP-dependent RNA helicase [Bacteroides fragilis YCH46]			2.7.7.-
11191, 11192	48854956	38	2.00E-16	Cytophaga hutchinsonii	COG0513: Superfamily II DNA and RNA helicases [Cytophaga hutchinsonii]			2.7.7.-
11195, 11196	50085810	28	8.00E-13	Acinetobacter sp. ADP1	hypothetical protein ACIAD2753 [Acinetobacter sp. ADP1] emb CAG69498.1 hypothetical protein [Acinetobacter sp. ADP1]			
11199, 11200	23130207	34	7.00E-18	Nostoc punctiforme PCC 73102	COG0732: Restriction endonuclease S subunits [Nostoc punctiforme PCC 73102]			3.1.21.3
11205, 11206	11499361	39	5.00E-27	Archaeoglobus fulgidus DSM 4304	long-chain-fatty-acid-CoA ligase (fadD-7) [Archaeoglobus fulgidus DSM 4304] gb AAB89478.1 long-chain-fatty-acid-CoA ligase (fadD-7) [Archaeoglobus fulgidus DSM 4304] pir C69471 probable fatty-acid-CoA ligase (EC 6.2.1.-) fadD7 - Archaeoglobus fulgidus			6.2.1.3
11207, 11208	31195627	54	2.00E-70	Anopheles gambiae	ENSANGP00000000430 [Anopheles gambiae]			6.3.2.1

1121, 1122	45441661	24	1.00E-06	Yersinia pestis biovar Medievalis str. 91001	Transposase [Yersinia pestis biovar Medievalis str. 91001] gb AAS62077.1 Transposase [Yersinia pestis biovar Medievalis str. 91001]			
11211, 11212	53690630	28	1.00E-16	Desulfovibrio desulfuricans G20	COG1309: Transcriptional regulator [Desulfovibrio desulfuricans G20]			
11213, 11214	19705384	25	7.00E-12	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	General secretion pathway protein F [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94178.1 General secretion pathway protein F [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			
11217, 11218	54302389	49	4.00E-57	Photobacterium profundum SS9	hypothetical protein PBPR80710 [Photobacterium profundum SS9] emb CAG22582.1 hypothetical protein [Photobacterium profundum]			
11221, 11222	24374072	40	3.00E-46	Shewanella oneidensis MR-1	hypothetical protein SO2529 [Shewanella oneidensis MR-1] gb AAN55559.1 hypothetical protein [Shewanella oneidensis MR-1] conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54746.1 conserved hypothetical protein [Campylobacter lari RM2100]			
11223, 11224	57241050	26	6.00E-13	Campylobacter lari RM2100	putative two-component system sensor protein [Bacteroides fragilis YCH46] dbj BAD51256.1 putative two-component system sensor protein [Bacteroides fragilis YCH46]			2.7.3.-
11229, 11230	53715798	44	5.00E-34	Bacteroides fragilis YCH46	COG0857: BioD-like N-terminal domain of phosphotransacetylase			2.3.1.8
11231, 11232	23473597	33	5.00E-27	Desulfovibrio desulfuricans G20	[Desulfovibrio desulfuricans G20]			1.4.1.2
11233, 11234	48833808	41	6.00E-53	Magnetococcus sp. MC-1	COG2902: NAD-specific glutamate dehydrogenase [Magnetococcus sp. MC- 1]			2.7.2.11
11235, 11236	32261967	51	6.00E-51	Helicobacter hepaticus ATCC 51449	glutamate 5-kinase [Helicobacter hepaticus ATCC 51449] ref NP_859950.1 glutamate 5-kinase [Helicobacter hepaticus ATCC 51449] sp Q7VJ31 PROB_HELHP Glutamate 5-kinase (Gamma-glutamyl kinase) (GK)			
11237, 11238	48853332	35	1.00E-23	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]			
11239, 11240	32262492	41	2.00E-21	Helicobacter hepaticus ATCC 51449	transcriptional regulator [Helicobacter hepaticus ATCC 51449] ref NP_860473.1 transcriptional regulator [Helicobacter hepaticus ATCC 51449]			
11241, 11242	52007358	40	2.00E-48	Thiobacillus denitrificans ATCC 25259	COG5000: Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation [Thiobacillus denitrificans ATCC 25259] PUTATIVE TWO-COMPONENT SENSOR [Wolonia succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolonia succinogenes]			2.7.3.-
11243, 11244	34557419	34	4.00E-27	Wolonia succinogenes DSM 1740			88	4.00E-11 2.7.3.-

11245, 11246	53715283	35	1.00E-08	Bacteroides fragilis YCH46	putative exodeoxyribonuclease VII large subunit [Bacteroides fragilis YCH46] dbj BAD50741.1 putative exodeoxyribonuclease VII large subunit [Bacteroides fragilis YCH46]			3.1.11.6
11247, 11248	15643770	28	1.00E-10	Thermotoga maritima MSB8	hypothetical protein TM1012 [Thermotoga maritima MSB8] gb AAD36089.1 hypothetical protein TM1012 [Thermotoga maritima MSB8] pir D72305 hypothetical protein - Thermotoga maritima (strain MSB8)			
11249, 11250	27364626	43	2.00E-14	Vibrio vulnificus CMCP6	Hemolysin [Vibrio vulnificus CMCP6] ref NP_935939.1 hemolysin [Vibrio vulnificus YJ016] gb AAO09681.1 Hemolysin [Vibrio vulnificus CMCP6] dbj BAC95910.1 hemolysin [Vibrio vulnificus YJ016]			
11251, 11252	46201018	39	5.00E-55	Magnetospirillum magnetotacticum MS-1	COG2200: FOG: EAL domain [Magnetospirillum magnetotacticum MS-1] hypothetical protein aq_645 [Aquifex aeolicus VF5] gb AAC06850.1 putative protein [Aquifex aeolicus VF5] pir B70357 hypothetical protein aq_645 - Aquifex aeolicus			
11255, 11256	15608069	23	5.00E-12	Aquifex aeolicus VF5	COG1131: ABC-type multidrug transport system, ATPase component [Chloroflexus aurantiacus]			1.8.-
11257, 11258	53795187	41	2.00E-26	Chloroflexus aurantiacus				
11261, 11262	15965924	45	3.00E-25	Sinorhizobium melloti 1021	PROBABLE D-ALANINE-D-ALANINE LIGASE B PROTEIN [Sinorhizobium melloti 1021] emb CAC46750.1 PROBABLE D-ALANINE-D-ALANINE LIGASE B PROTEIN [Sinorhizobium melloti] sp Q92NM4 DDL_RHIME D- alanine-D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase)			6.3.2.4
11263, 11264	48858155	25	1.00E-07	Clostridium thermocellum ATCC 27405	COG0707: UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase [Clostridium thermocellum ATCC 27405]			2.4.1.-
11265, 11266	28854714	28	4.00E-19	Pseudomonas syringae pv. tomato str. DC3000	conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794082.1 hypothetical protein PSPT04326 [Pseudomonas syringae pv. tomato str. DC3000]			
11269, 11270	34558188	63	4.00E-44	Wolinella succinogenes DSM 1740	HOMOSERINE O-ACETYLTRANSFERASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10903.1 HOMOSERINE O- ACETYLTRANSFERASE PROTEIN [Wolinella succinogenes]			2.3.1.31
11271, 11272	32263208	35	4.00E-23	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861187.1 hypothetical protein HH1656 [Helicobacter hepaticus ATCC 51449]			2.7.-
11273, 11274	AAW2085 7	44	1.00E-37		Desc:H. pylori outer membrane protein, 12ap11614orf8. Org:Helicobacter pylori			2.7.1.13 0

11275, 11276	15896496	54	2.00E-55	Clostridium acetobutylicum ATCC 824	Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] gb AAK81185.1 Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] pir F97299 sensory transduction protein containing HD_GYP domain [Imported] - Clostridium acetobutylicum	Clostridium acetobutylicum ATCC 824 section 309 of 356 of the complete genome	93	1.00E-07	
11279, 11280	53765610	29	1.00E-11	Anabaena variabilis ATCC 29413	COG2319: FOG: WD40 repeat [Anabaena variabilis ATCC 29413]				
11281, 11282	557887	40	1.00E-17		Integrase prf 2115270D Integrase				
11285, 11286	53735965	41	2.00E-12	Crocospaera watsonii WH 8501	hypothetical protein Cwat03001093 [Crocospaera watsonii WH 8501] conserved hypothetical protein-Uncharacterized ATPase [Wolinella succinogenes DSM 1740] emb CAE10743.1 conserved hypothetical protein- Uncharacterized ATPase [Wolinella succinogenes]				
11289, 11290	34558028	35	6.00E-48	Wolinella succinogenes DSM 1740	RIBONUCLEASE HII RNASE HII [Wolinella succinogenes DSM 1740] emb CAE10744.1 RIBONUCLEASE HII RNASE HII [Wolinella succinogenes]				3.1.26.4
11291, 11292	34558029	53	9.00E-49	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09963.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes]				
11293, 11294	34557248	35	2.00E-23	Wolinella succinogenes DSM 1740	sensory box sensor histidine kinase/response regulator [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_230993.1 sensory box sensor histidine kinase/response regulator [Vibrio cholerae O1 biovar eltor str. N16961] pir H82211 sensory box sensor histidine kinase/response regulator VC1349 [Imported] - Vibrio cholerae (strain N16961 serogroup O1)				2.7.3.-
11295, 11296	9655841	47	4.00E-40	Vibrio cholerae O1 biovar eltor str. N16961	Nitroreductase family protein [Clostridium acetobutylicum ATCC 824] gb AAK79386.1 Nitroreductase family protein [Clostridium acetobutylicum ATCC 824] pir G97074 nitroreductase family protein [Imported] - Clostridium acetobutylicum				1.6.-
11299, 11300	15894697	36	3.00E-26	Clostridium acetobutylicum ATCC 824	EXCINUCLEASE ABC SUBUNIT A [Wolinella succinogenes DSM 1740] emb CAE10659.1 EXCINUCLEASE ABC SUBUNIT A [Wolinella succinogenes]	Helicobacter hepaticus ATCC 51449 section 1 of 6 of the complete genome	89	1.00E-13	
11301, 11302	34557944	78	1.00E-106	Wolinella succinogenes DSM 1740	COG2010: Cytochrome c, mono- and diheme variants [Magnetospirillum magnetotacticum MS-1]				1.9.3.2
11303, 11304	46202056	53	6.00E-59	Magnetospirillum magnetotacticum MS-1					

11305, 11306	48853436	65	3.00E-85	Cytophaga hutchinsonii	COG0677: UDP-N-acetyl-D-mannosaminuronate dehydrogenase [Cytophaga hutchinsonii]	Staphylococcus aureus M type 1 capsular polysaccharide biosynthesis gene cluster, complete sequence and unknown genes	88	5.00E-10	1.1.1.-
11307, 11308	34556660	49	4.00E-60	Wolinella succinogenes DSM 1740	METHIONYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE09375.1 METHIONYL-TRNA SYNTHETASE [Wolinella succinogenes]				6.1.1.10
11311, 11312	34557573	52	4.00E-28	Wolinella succinogenes DSM 1740	SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes]				2.7.3.-
11313, 11314	56460323	36	7.00E-16	Idiomarina lohiensis L2TR	hypothetical protein IL1215 [Idiomarina lohiensis L2TR] gb AAV82055.1 Hypothetical protein IL1215 [Idiomarina lohiensis L2TR]				
11317, 11318	57241658	69	1.00E-123	Campylobacter lari RM2100	ribonucleoside reductase, alpha subunit [Campylobacter lari RM2100] gb EAL54328.1 ribonucleoside reductase, alpha subunit [Campylobacter lari RM2100]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 1/6	81	7.00E-07	1.17.4.1
11321, 11322	48862680	61	3.00E-51	Microbulbifer degradans 2-40	COG2077: Peroxiredoxin [Microbulbifer degradans 2-40] RNB-like protein [Campylobacter jejuni RM1221] gb AAW34527.1 RNB-like protein [Campylobacter jejuni RM1221]				1.11.1.-
11325, 11326	57236944	38	7.00E-43	Campylobacter jejuni RM1221	archaeal ATPase [Thermococcus kodakaraensis] ref YP_182872.1 archaeal ATPase [Thermococcus kodakaraensis]				3.1.-.-
11327, 11328	57158718	29	1.00E-12	Thermococcus kodakaraensis	conserved protein found in conjugate transposon [Bacteroides thetaiotaomicron VPI-5482] gb AAO75200.1 conserved protein found in conjugate transposon [Bacteroides thetaiotaomicron VPI-5482]				
1133, 1134	29345503	66	1.00E-90	Bacteroides thetaiotaomicron VPI-5482	PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR [Wolinella succinogenes DSM 1740] emb CAE09950.1 PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR [Wolinella succinogenes]				
11331, 11332	34557235	46	4.00E-65	Wolinella succinogenes DSM 1740	COG2815: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
11333, 11334	48854867	30	5.00E-18	Cytophaga hutchinsonii	Desc:Purine/pyrimidine triphosphate type nucleotidyltransferase #156. Org:Aquifex aeolicus				2.7.1.37
11335, 11336	ABG9157 1	36	2.00E-33						2.7.7.13

11337, 11338	15643658	36	1.00E-16	Thermotoga maritima MSB8	galactose-1-phosphate uridylyltransferase, putative [Thermotoga maritima MSB8] gb AAD35977.1 galactose-1-phosphate uridylyltransferase, putative [Thermotoga maritima MSB8] pir J72322 hypothetical protein TM0896 - Thermotoga maritima (strain MSB8)				2.7.7.10
11339, 11340	57168791	27	2.00E-08	Campylobacter coli RM2228	probable lipoprotein Cj1649 [Campylobacter coli RM2228] gb EAL56521.1 probable lipoprotein Cj1649 [Campylobacter coli RM2228]				
11341, 11342	23129382	36	2.00E-21	Nostoc punctiforme PCC 73102	COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102]				2.7.3.-
11343, 11344	21227244	35	4.00E-20	Methanosarcina mazei Go1	glycosyltransferase [Methanosarcina mazei Go1] gb AAM30838.1 glycosyltransferase [Methanosarcina mazei Go1]				2.4.1.-
11347, 11348	12580885	23	2.00E-07	Guillardia theta	IAP100 protein [Guillardia theta] ref NP_113434.1 IAP100 protein [Guillardia theta] pir F90106 IAP100 protein [imported] - Guillardia theta nucleomorph				
1135, 1136	24214122	30	4.00E-26	Leptospira interrogans serovar Lai str. 56601	Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601]				
11351, 11352	42528087	26	2.00E-14	Treponema denticola ATCC 35405	endonuclease/exonuclease/phosphatase family protein [Treponema denticola ATCC 35405] gb AAS13104.1 endonuclease/exonuclease/phosphatase family protein [Treponema denticola ATCC 35405]				
11353, 11354	29840673	47	1.00E-39	Chlamydomonas caviae GPIC	helicase, Snf2 family [Chlamydomonas caviae GPIC] gb AAP05657.1 helicase, Snf2 family [Chlamydomonas caviae GPIC]				3.6.1.3
11357, 11358	23102242	33	8.00E-15	Azotobacter vinelandii	COG1345: Flagellar capping protein [Azotobacter vinelandii]				
11359, 11360	34556741	50	5.00E-52	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09456.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]				2.7.3.-
11361, 11362	32262499	49	3.00E-13	Helicobacter hepaticus ATCC 51449	hypothetical protein HH0949 [Helicobacter hepaticus ATCC 51449] ref NP_860480.1 hypothetical protein HH0949 [Helicobacter hepaticus ATCC 51449]				
11363, 11364	34556768	72	1.00E-84	Wolinella succinogenes DSM 1740	DIAMINOPIMELATE DECARBOXYLASE DAP DECARBOXYLASE [Wolinella succinogenes DSM 1740] emb CAE09483.1 DIAMINOPIMELATE DECARBOXYLASE DAP DECARBOXYLASE [Wolinella succinogenes]				4.1.1.20
11365, 11366	19704720	23	7.00E-09	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	hypothetical protein FN1385 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95581.1 Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]				

11369, 11370	57167845	55	2.00E-94	Campylobacter coli RM2228	glutamyl-tRNA synthetase [Campylobacter coli RM2228] gb EAL57631.1 glutamyl-tRNA synthetase [Campylobacter coli RM2228]			6.1.1.17
11371, 11372	48839710	28	1.00E-10	Methanosarcina barkeri str. fusaro	COG0286: Type I restriction-modification system methyltransferase subunit [Methanosarcina barkeri str. fusaro]			2.1.1.72
11375, 11376	34556741	51	8.00E-63	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09456.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]			2.7.3.-
11377, 11378	31241779	42	5.00E-24	Anopheles gambiae	ENSANGP0000012858 [Anopheles gambiae]	Wolinella succinogenes, complete genome; segment 4/7		6.2.1.-
11379, 11380	37678997	67	1.00E-107	Vibrio vulnificus YJ016	type I site-specific restriction-modification system, R (restriction) subunit [Vibrio vulnificus YJ016] dbj BAC93577.1 type I site-specific restriction-modification system, R (restriction) subunit [Vibrio vulnificus YJ016]		88	7.00E-10 3.1.21.3
11381, 11382	45524550	30	5.00E-09	Crocospaera watsonii WH 8501	hypothetical protein Cwat03005121 [Crocospaera watsonii WH 8501]			
11383, 11384	39995311	40	1.00E-48	Geobacter sulfurreducens PCA	isoquinoline 1-oxidoreductase, beta subunit [Geobacter sulfurreducens PCA] gb AAR33535.1 isoquinoline 1-oxidoreductase, beta subunit [Geobacter sulfurreducens PCA]			1.3.99.1 6
11385, 11386	48868595	50	6.00E-50	Haemophilus influenzae 86-028NP	COG0749: DNA polymerase I - 3'-5' exonuclease and polymerase domains [Haemophilus influenzae 86-028NP]			2.7.7.7
11387, 11388	34557172	32	2.00E-23	Wolinella succinogenes DSM 1740	SENSORY PROTEIN, CONTAINING EAL-DOMAIN [Wolinella succinogenes DSM 1740] emb CAE09887.1 SENSORY PROTEIN, CONTAINING EAL-DOMAIN [Wolinella succinogenes]			
11389, 11390	48856112	29	2.00E-19	Cytophaga hutchinsonii	COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
11391, 11392	48855575	42	2.00E-45	Cytophaga hutchinsonii	COG0553: Superfamily II DNA/RNA helicases, SNF2 family [Cytophaga hutchinsonii]			3.6.1.3
11393, 11394	48853532	42	5.00E-36	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]			
11395, 11396	53798771	59	4.00E-26	Chloroflexus aurantiacus	COG0305: Replicative DNA helicase [Chloroflexus aurantiacus]			3.6.1.-
11397, 11398	34556836	56	4.00E-42	Wolinella succinogenes DSM 1740	ABC TRANSPORTER [Wolinella succinogenes DSM 1740] emb CAE09551.1 ABC TRANSPORTER [Wolinella succinogenes]			
11401, 11402	46120825	27	9.00E-12	Methylobacillus flagellatus KT	COG1629: Outer membrane receptor proteins, mostly Fe transport [Methylobacillus flagellatus KT]			
11403, 11404	18311192	43	2.00E-33	Clostridium perfringens str. 13	hypothetical protein CPE2210 [Clostridium perfringens str. 13] dbj BAB81916.1 conserved hypothetical protein [Clostridium perfringens str. 13]			2.1.1.61

11405, 11406	46140543	32	5.00E-20	Dechloromonas aromatica RCB	COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Dechloromonas aromatica RCB]	2.7.3.-
11407, 11408	34556556	32	8.00E-25	Wollinella succinogenes DSM 1740	POSSIBLE PHOSPHATASE [Wollinella succinogenes DSM 1740] emb CAE09271.1 POSSIBLE PHOSPHATASE [Wollinella succinogenes]	3.6.1.11
11409, 11410	21673803	57	2.00E-45	Chlorobium tepidum TLS	sodium:solute symporter family protein [Chlorobium tepidum TLS] gb AAM72210.1 sodium:solute symporter family protein [Chlorobium tepidum TLS]	
1141, 1142	29346795	27	8.00E-12	Bacteroides thetaiotaomicron VPI-5482	transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO76492.1 transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482]	
11411, 11412	53714574	65	9.00E-46	Bacteroides fragilis YCH46	lactoylglutathione lyase and related protein [Bacteroides fragilis YCH46] dbj BAD50032.1 lactoylglutathione lyase and related protein [Bacteroides fragilis YCH46]	4.4.1.5
11413, 11414	34558230	38	8.00E-33	Wollinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT REGULATOR-CheY like receiver domain [Wollinella succinogenes] succinogenes]	
11415, 11416	29346070	27	4.00E-14	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0660 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75767.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]	
11417, 11418	50085130	32	1.00E-15	Acinetobacter sp. ADP1	hypothetical protein ACIAD1995 [Acinetobacter sp. ADP1] emb CAG68818.1 hypothetical protein [Acinetobacter sp. ADP1]	
11419, 11420	34556534	45	7.00E-28	Wollinella succinogenes DSM 1740	APOLIPOPROTEIN N-ACYLTRANSFERASE [Wollinella succinogenes DSM 1740] emb CAE09249.1 APOLIPOPROTEIN N-ACYLTRANSFERASE [Wollinella succinogenes] sp Q7MAR3 LNT_WOLSU Apolipoprotein N-acyltransferase (ALP N-acyltransferase)	2.3.1.-
11421, 11422	48855199	42	5.00E-07	Cytophaga hutchinsonii	hypothetical protein Chut02002271 [Cytophaga hutchinsonii]	
11425, 11426	50927567	29	7.00E-08	Oryza sativa (japonica cultivar-group)	OSJNBa0079A21.19 [Oryza sativa (japonica cultivar-group)] emb CAD41475.2 OSJNBa0079A21.19 [Oryza sativa (japonica cultivar-group)]	
11427, 11428	56478386	33	7.00E-10	Azoarcus sp. EbN1	cytochrome c family protein [Azoarcus sp. EbN1] emb CAI09074.1 Cytochrome c family protein [Azoarcus sp. EbN1]	
11429, 11430	4585802	41	7.00E-39	Pseudomonas stutzeri	DnrS protein [Pseudomonas stutzeri]	
1143, 1144	53712369	31	4.00E-27	Bacteroides fragilis YCH46	peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46] dbj BAD47827.1 peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46]	

11431, 11432	15643585	42	6.00E-55	Thermotoga maritima MSB8	phenylalanyl-tRNA synthetase, beta subunit [Thermotoga maritima MSB8] gb AAD35904.1 phenylalanyl-tRNA synthetase, beta subunit [Thermotoga maritima MSB8] pir A72330 phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Thermotoga maritima (strain MSB8) sp Q9WZS9 SYFB_THEMEA Phenylalanyl-tRNA synthetase beta chain (Phenylalanine-tRNA ligase beta chain) (PheRS)	6.1.1.20
11433, 11434	15643585	37	1.00E-38	Thermotoga maritima MSB8	phenylalanyl-tRNA synthetase, beta subunit [Thermotoga maritima MSB8] gb AAD35904.1 phenylalanyl-tRNA synthetase, beta subunit [Thermotoga maritima MSB8] pir A72330 phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Thermotoga maritima (strain MSB8) sp Q9WZS9 SYFB_THEMEA Phenylalanyl-tRNA synthetase beta chain (Phenylalanine-tRNA ligase beta chain) (PheRS)	6.1.1.20
11435, 11436	34557308	50	2.00E-35	Wolinella succinogenes DSM 1740	Nitrous oxidase accessory protein [Wolinella succinogenes DSM 1740] emb CAE10023.1 Nitrous oxidase accessory protein [Wolinella succinogenes]	
11437, 11438	15614433	29	6.00E-27	Bacillus halodurans C-125	hypothetical protein BH1870 [Bacillus halodurans C-125] dbj BAB05589.1 BH1870 [Bacillus halodurans C-125] pir F83883 hypothetical protein BH1870 [imported] - Bacillus halodurans (strain C-125)	3.2.1.22
11439, 11440	79388	42	2.00E-26		hypothetical protein - Bacteroides fragilis insertion sequence IS492 gb AAA22911.1 putative	
11441, 11442	15894773	32	5.00E-15	Clostridium acetobutylicum ATCC 824	Hypothetical protein, CF-32 family [Clostridium acetobutylicum ATCC 824] gb AAK79462.1 Hypothetical protein, CF-32 family [Clostridium acetobutylicum ATCC 824] pir C97084 hypothetical protein CAC1494 [Imported] - Clostridium acetobutylicum	
11445, 11446	57241158	29	1.00E-19	Campylobacter lari RM2100	ATP-dependent DNA helicase [Campylobacter lari RM2100] gb EAL54854.1 ATP-dependent DNA helicase [Campylobacter lari RM2100]	3.6.1.-
11447, 11448	29348169	51	4.00E-49	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein B72760 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77866.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]	4.2.1.28
11449, 11450	48855525	39	2.00E-30	Cytophaga hutchinsonii	hypothetical protein Chut02001868 [Cytophaga hutchinsonii]	
1145, 1146	28211915	43	4.00E-53	Clostridium tetani E88	imidazolonepropionase [Clostridium tetani E88] gb AAO36796.1 imidazolonepropionase [Clostridium tetani E88]	3.5.2.7
11451, 11452	46140552	39	2.00E-18	Dechloromonas aromatica RCB	COG0607: Rhodanese-related sulfurtransferase [Dechloromonas aromatica RCB]	
11455, 11456	48855525	43	4.00E-11	Cytophaga hutchinsonii	hypothetical protein Chut02001868 [Cytophaga hutchinsonii]	

11459, 11460	16125567	23	7.00E-10	Caulobacter crescentus CB15	outer membrane protein TolC, putative [Caulobacter crescentus CB15] gb AAK23299.1 outer membrane protein TolC, putative [Caulobacter crescentus CB15] pir G87412 outer membrane protein TolC, probable CC1318 [imported] - Caulobacter crescentus				
11461, 11462	57505540	43	6.00E-58	Campylobacter upsaliensis RM3195	conserved hypothetical protein [Campylobacter upsaliensis RM3195] gb EAL52874.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195]				
11465, 11466	23014415	49	3.00E-25	Magnetospirillum magnetotacticum MS-1	COG0784: FOG: CheY-like receiver [Magnetospirillum magnetotacticum MS- 1]				2.7.3.-
11467, 11468	38482512	44	1.00E-27	Photobacterium luminescens	putative toxin transporter [Photobacterium luminescens]				
11469, 11470	29348726	40	3.00E-23	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3317 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78423.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
11471, 11472	34557096	74	1.00E-132	Wolinella succinogenes DSM 1740	hypothetical protein WS0684 [Wolinella succinogenes DSM 1740] emb CAE09811.1 conserved hypothetical protein [Wolinella succinogenes]				1.17.4.2
11477, 11478	54639980	72	2.00E-71	Campylobacter jejuni	putative adenylsulfate kinase [Campylobacter jejuni]				2.7.1.25
11479, 11480	56469773	24	4.00E-07	Entamoeba histolytica HM- 1:IMSS	DNA repair protein Rad50, putative [Entamoeba histolytica HM-1:IMSS]				
11481, 11482	34558493	49	4.00E-62	Wolinella succinogenes DSM 1740	PUTATIVE ZINC PROTEASE [Wolinella succinogenes DSM 1740] emb CAE11208.1 PUTATIVE ZINC PROTEASE [Wolinella succinogenes]				3.4.-.-
11483, 11484	48833487	58	4.00E-34	Magnetococcus sp. MC-1	COG2326: Uncharacterized conserved protein [Magnetococcus sp. MC-1] glucose-6-phosphate isomerase [Helicobacter hepaticus ATCC 51449] ref NP_860022.1 glucose-6-phosphate isomerase [Helicobacter hepaticus ATCC 51449]				2.-.-.-
11485, 11486	32262039	41	5.00E-45	Helicobacter hepaticus ATCC 51449	COG0859: ADP-heptose:LPS heptosyltransferase [Geobacter metallireducens GS-15]				5.3.1.9
11489, 11490	48844440	22	2.00E-08	Geobacter metallireducens GS- 15	COG1843: Flagellar hook capping protein [Cytophaga hutchinsonii]				
1149, 1150	48853904	51	5.00E-43	Cytophaga hutchinsonii	COG0535: Predicted Fe-S oxidoreductases [Magnetococcus sp. MC-1]				
11491, 11492	48834423	33	1.00E-20	Magnetococcus sp. MC-1	transketolase, N-terminal subunit [Thermotoga maritima MSB8]				2.2.1.1
11493, 11494	15644626	42	2.00E-55	Thermotoga maritima MSB8					

11495, 11496	32261558	33	9.00E-19	51449	Helicobacter hepaticus ATCC	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_859542.1 hypothetical protein HH0011 [Helicobacter hepaticus ATCC 51449]				
11499, 11500	48834077	50	6.00E-32	MC-1	Magnetococcus sp.	COG0840: Methyl-accepting chemotaxis protein [Magnetococcus sp. MC-1]				2.7.3.-
115, 116						Eremothecium gossypii ATCC 10895 chromosome VI, complete sequence	## 5.00E-30			
11503, 11504	57504660	30	5.00E-12	RM2228	Campylobacter coli	hypothetical protein CCO1785 [Campylobacter coli RM2228] gb EAL56124.1 hypothetical protein CCO1785 [Campylobacter coli RM2228]				
11505, 11506	57240928	57	6.00E-67	RM2100	Campylobacter lari	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55321.1 conserved hypothetical protein [Campylobacter lari RM2100]				
11507, 11508	41724578	30	2.00E-24	Dechloromonas aromatica RCB	COG0842: ABC-type multidrug transport system, permease component [Dechloromonas aromatica RCB]					
11509, 11510	48839711	46	9.00E-25	Methanosarcina barkeri str. fusaro	COG0732: Restriction endonuclease S subunits [Methanosarcina barkeri str. fusaro]				3.1.21.3	
1151, 1152	53711702	83	8.00E-58	YCH46	Bacteroides fragilis	topoisomerase IV subunit A [Bacteroides fragilis YCH46] dbj BAD47160.1 topoisomerase IV subunit A [Bacteroides fragilis YCH46] SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]	Bacteroides fragilis YCH46 DNA, complete genome	82	6.00E-15	5.99.1.-
11511, 11512	34557246	27	6.00E-12	1740	Wolinella succinogenes DSM	hypothetical protein Mdeg02000469 [Microbulbifer degradans 2-40] aconitase [Aquifex aeolicus VF5] gb AAC07617.1 aconitase [Aquifex aeolicus VF5] pir F70453 aconitase - Aquifex aeolicus				4.2.1.3
11517, 11518	48864098	35	3.00E-12	degradans 2-40	Microbulbifer	COG0500: SAM-dependent methyltransferases [Nostoc punctiforme PCC 73102]				
11521, 11522	15606842	46	2.00E-35	VF5	Aquifex aeolicus	2-isopropylmalate synthase [Chlorobium tepidum TLS] gb AAM73323.1 2-isopropylmalate synthase [Chlorobium tepidum TLS] COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii]				4.1.3.12
11525, 11526	23129257	43	6.00E-30	PCC 73102	Nostoc punctiforme	COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii]				3.1.1.24
11527, 11528	21674916	60	4.00E-28	tepidum TLS	Chlorobium	ENSANGP00000016331 [Anopheles gambiae]				2.7.7.-
11529, 11530	48854159	38	4.00E-37	hutchinsonii	Cytophaga					
11531, 11532	31195987	58	1.00E-38	gambiae	Anopheles					

11533, 11534	38045894	29	2.00E-09	Homo sapiens	RAB6-interacting protein 2 isoform gamma [Homo sapiens] dbj BAC54108.1 ELKS gamma [Homo sapiens]				
11537, 11538	47525234	70	1.00E-113	Geobacter sulfurreducens PCA	chromosomal replication initiator protein DnaA [Geobacter sulfurreducens PCA] gb AAR99581.1 chromosomal replication initiator protein DnaA [Geobacter sulfurreducens PCA]			90	5.00E-17
11539, 11540	47525234	60	6.00E-47	Geobacter sulfurreducens PCA	chromosomal replication initiator protein DnaA [Geobacter sulfurreducens PCA] gb AAR99581.1 chromosomal replication initiator protein DnaA [Geobacter sulfurreducens PCA]				
11545, 11546	57505258	43	1.00E-30	Campylobacter upsaliensis RM3195	conserved hypothetical protein [Campylobacter upsaliensis RM3195] gb EAL53179.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195]				
11549, 11550	46446323	37	6.00E-18	Parachlamydia sp. UWE25	putative exodeoxyribonuclease V [Parachlamydia sp. UWE25] emb CAF23413.1 putative exodeoxyribonuclease V [Parachlamydia sp. UWE25]				3.1.11.5
11553, 11554	34557295	23	1.00E-09	Wolinella succinogenes DSM 1740	hypothetical protein WS0905 [Wolinella succinogenes DSM 1740] emb CAE10010.1 hypothetical protein [Wolinella succinogenes]				
11555, 11556	34557291	37	1.00E-46	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]				2.7.3.-
11557, 11558	53729414	30	9.00E-27	Dechloromonas aromatica RCB	COG0515: Serine/threonine protein kinase [Dechloromonas aromatica RCB]				3.1.3.16
11559, 11560	23121691	50	5.00E-17	Desulfotobacterium hafnense DCB-2	COG0784: FOG: CheY-like receiver [Desulfotobacterium hafnense DCB-2] hypothetical protein CPE1705 [Clostridium perfringens str. 13] sp Q8XJQ1 YH05_CLOPE Hypothetical UPF0102 protein CPE1705 dbj BAB81411.1 conserved hypothetical protein [Clostridium perfringens str. 13]				3.1.1.61
11561, 11562	18310687	35	7.00E-13	Clostridium perfringens str. 13	ABC transporter, ATP-binding protein, MsbA family [Porphyromonas gingivalis W83] ref NP_905827.1 ABC transporter, ATP-binding protein, MsbA family [Porphyromonas gingivalis W83]				
11565, 11566	34397664	39	6.00E-42	Porphyromonas gingivalis W83	COG0642: Signal transduction histidine kinase [Thiobacillus denitrificans ATCC 25259]				2.7.3.-
11567, 11568	52007424	36	1.00E-13	Thiobacillus denitrificans ATCC 25259	cGMP-dependent protein kinase 1, beta isozyme, putative [Plasmodium falciparum 3D7] gb AAN36959.1 cGMP-dependent protein kinase 1, beta isozyme, putative [Plasmodium falciparum 3D7] gb AAM22644.1 cGMP- dependent protein kinase [Plasmodium falciparum]				2.7.1.37
11569, 11570	23509568	31	2.00E-08	Plasmodium falciparum 3D7					

11571, 11572	31195951	55	2.00E-53	Anopheles gambiae	ENSANGP00000000471 [Anopheles gambiae] NAD dependent epimerase/dehydratase, UDP-glucose-4-epimerase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_123157.1 hypothetical protein lpp0827 [Legionella pneumophila str. Paris] gb AAU26850.1 NAD dependent epimerase/dehydratase, UDP- glucose-4-epimerase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAB65203.1 hypothetical protein [Legionella pneumophila] emb CAH11975.1 hypothetical protein [Legionella pneumophila str. Paris]			1.1.1.95
11573, 11574	52840998	34	5.00E-17	Legionella pneumophila subsp. pneumophila str. Philadelphia 1				5.1.3.-

11577, 11578, 11583, 11584	13491146 46934822	56 71	8.00E-41 1.00E-130	Aneurinibacillus thermoaerophilus Wolinella succinogenes	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [Aneurinibacillus thermoaerophilus] sp Q9AGY5 GMHB_ANETH D,D- heptose 1,7-bisphosphate phosphatase (D-glycero-D-manno-heptose 1,7- bisphosphate phosphatase)	Campylobacter jejuni putative ABC- type transport protein, putative UDP-glucose-4- epimerase, hypothetical protein, putative heptosyltransferase I, putative lipid A biosynthesis acyltransferase, putative two-domain glycosyltransferase, putative glycosyltransferase, putative beta-1,4-N- acetyl galactosamin yltransferase, putative beta-1,3- galactosyltransferas e, putative alpha- 2,3- sialyltransferase, putative sialic acid synthase, putative UDP-N- acetylglucosamine 2-epimerase/N- acetylmannosamine synthase, putative>	88 7.00E-09 3.1.3.15	1.7.99.6
11585, 11586	34556608	27	9.00E-27	Wolinella succinogenes DSM 1740	nitrous oxide reductase [Wolinella succinogenes]			
11587, 11588	34556616	43	4.00E-35	Wolinella succinogenes DSM 1740	hypothetical protein WS0160 [Wolinella succinogenes DSM 1740] emb CAE09323.1 conserved hypothetical protein [Wolinella succinogenes] CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes]			

11589, 11590	57240404	61	4.00E-52	Campylobacter lari RM2100	tRNA (guanine-N1)-methyltransferase [Campylobacter lari RM2100] gb EAL55518.1 tRNA (guanine-N1)-methyltransferase [Campylobacter lari RM2100]			2.1.1.31
1159, 1160	42520151	70	3.00E-68	Wolbachia endosymbiont of Drosophila melanogaster	hypothetical protein WD0259 [Wolbachia endosymbiont of Drosophila melanogaster] gb AAS14000.1 conserved hypothetical protein [Wolbachia endosymbiont of Drosophila melanogaster]			
11593, 11594	53714478	44	4.00E-39	Bacteroides fragilis YCH46	hypothetical protein BF3191 [Bacteroides fragilis YCH46] db BAD4936.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
11595, 11596	53713148	38	1.00E-53	Bacteroides fragilis YCH46	hypothetical protein BF1858 [Bacteroides fragilis YCH46] db BAD48606.1 hypothetical protein [Bacteroides fragilis YCH46]			
11597, 11598	1197006	47	5.00E-33	Bacteroides fragilis	unknown protein [Bacteroides fragilis] gb AAA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for insertion sequence element IS4351 (Transposon TN4551)			
11599, 11600	57241290	61	1.00E-40	Campylobacter lari RM2100	Uncharacterized BCR, YoeG family COG1559 [Campylobacter lari RM2100] gb EAL54986.1 Uncharacterized BCR, YoeG family COG1559 [Campylobacter lari RM2100]		97 3.00E-11	4.---
11601, 11602	3493599	24	3.00E-07	Proteus mirabilis	ZapD [Proteus mirabilis]			
11605, 11606	27117224	31	2.00E-23	Bacillus megaterium	uroporphyrinogen III synthase [Bacillus megaterium]			4.2.1.75
11607, 11608	48862680	63	4.00E-52	Microbulbifer degradans 2-40	COG2077: Peroxiredoxin [Microbulbifer degradans 2-40] proline-tRNA synthetase [Aquifex aeolicus VF5] gb AAC06648.1 proline- tRNA synthetase [Aquifex aeolicus VF5] pir F70332 proline-tRNA synthetase - Aquifex aeolicus			1.11.1.-
11609, 11610	15605873	44	1.00E-10	Aquifex aeolicus VF5	BpmI endonuclease-methyltransferase fusion protein type IIG [uncultured archaeon GZfos9D8]			6.1.1.15
1161, 1162	52550522	32	2.00E-09	uncultured archaeon GZfos9D8	putative putative two-component sensor C0035 [Campylobacter fetus]			2.7.3.-
11613, 11614	28974235	33	2.00E-27	Campylobacter fetus	hypothetical protein WS1227 [Wolbachia succinogenes DSM 1740] emb CAE10308.1 hypothetical protein [Wolbachia succinogenes] sp P59893 TRUD_WOLSU tRNA pseudouridine synthase D (Pseudouridylyl synthase) (Uracil hydrolyase)			
11615, 11616	34557593	42	1.00E-39	Wolbachia succinogenes DSM 1740	COG0849: Actin-like ATPase involved in cell division [Cytophaga hutchinsonii]			
11617, 11618	48854568	50	2.00E-35	Cytophaga hutchinsonii				

11619, 11620	27365538	31	2.00E-15	Vibrio vulnificus CMCP6	hypothetical protein VV12211 [Vibrio vulnificus CMCP6] gb AAO10593.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6]			2.7.3.-
11621, 11622	29349774	48	4.00E-33	Bacteroides thetataoamicron VPI-5482	putative transcription regulator [Bacteroides thetataoamicron VPI-5482] gb AAO79471.1 putative transcription regulator [Bacteroides thetataoamicron VPI-5482]			6.3.4.15
11625, 11626	48855427	30	1.00E-10	Cytophaga hutchinsonii	COG1521: Putative transcriptional regulator, homolog of Bvg accessory factor [Cytophaga hutchinsonii]			
1163, 1164	48856612	44	1.00E-32	Cytophaga hutchinsonii	COG1331: Highly conserved protein containing a thioredoxin domain [Cytophaga hutchinsonii]			
11631, 11632	46447193	60	1.00E-81	Parachlamydia sp. UWE25	putative ATP-dependent RNA helicase [Parachlamydia sp. UWE25] emb CAF24283.1 putative ATP-dependent RNA helicase [Parachlamydia sp. UWE25]	Lactobacillus johnsonii NCC 533, section 2 of 7 of the complete genome	97	4.00E-08 2.7.7.-
11633, 11634	34558815	75	1.00E-59	Alvinella pompejana epibiont 7G3	citrate lyase subunit 2 [Alvinella pompejana epibiont 7G3]	Alvinella pompejana epibiont 7G3 fosmid clone 7G3, complete sequence	90	2.00E-11 4.1.3.8
11635, 11636	34557183	47	3.00E-36	Wolinella succinogenes DSM 1740	PUTATIVE AMINOTRANSFERASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09898.1 PUTATIVE AMINOTRANSFERASE PROTEIN [Wolinella succinogenes]			2.6.1.-
11639, 11640	27376072	60	4.00E-46	Bradyrhizobium japonicum USDA 110	putative translation initiation factor [Bradyrhizobium japonicum USDA 110] dbj BAC46226.1 br0961 [Bradyrhizobium japonicum USDA 110]			
11641, 11642	45528473	35	9.00E-32	Crocospaera watsonii WH 8501	COG0457: FOG: TPR repeat [Crocospaera watsonii WH 8501]			5.2.1.8
11649, 11650	732729	36	1.00E-15	Haemophilus parahaemolyticus Bacteroides thetataoamicron VPI-5482	site-specific DNA-methyltransferase (cytosine-specific) [Haemophilus parahaemolyticus] sp P50192 MTTHA_HAEPH Modification methylase HphIA (Cytosine-specific methyltransferase HphIA) (M.HphIA) (M.HphI(C)) pir S70707 site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) HphI - Haemophilus parahaemolyticus (ATCC 49700) hypothetical protein BT3711 [Bacteroides thetataoamicron VPI-5482] gb AAO78816.1 conserved hypothetical protein [Bacteroides thetataoamicron VPI-5482]			2.1.1.73
1165, 1166	29349119	35	2.00E-13	Helicobacter hepaticus ATCC 51449	acetylornithine aminotransferase [Helicobacter hepaticus ATCC 51449] ref NP_860500.1 acetylornithine aminotransferase [Helicobacter hepaticus ATCC 51449]			
11653, 11654	32262519	52	2.00E-61					2.6.1.11

11655, 11656	34558829	47	1.00E-56	7G3	Alvinella pompejana epibiont	succinylornithine transaminase [Alvinella pompejana epibiont 7G3]			2.6.1.-
11657, 11658	48859331	23	3.00E-10	ATCC 27405	Clostridium thermocellum	COG1670: Acetyltransferases, including N-acetylases of ribosomal proteins [Clostridium thermocellum ATCC 27405]			
11661, 11662	53736042	42	7.00E-20	Watsonii WH 8501	Crocospaera watsonii WH 8501	hypothetical protein Cwat03001257 [Crocospaera watsonii WH 8501]			
11665, 11666	57240902	48	5.00E-39	RM2100	Campylobacter lari	conserved hypothetical protein [Campylobacter lari RM2100]			
11667, 11668	32473317	43	7.00E-39	Rhodopirellula baltica SH 1	Rhodopirellula baltica SH 1	gb EAL55295.1 conserved hypothetical protein [Campylobacter lari RM2100]			
11671, 11672	34556560	50	4.00E-55	1740	Wolinella succinogenes DSM	N-acetylglucosamine-6-sulfatase [Rhodopirellula baltica SH 1]			3.1.6.-
11673, 11674	34556560	37	3.00E-38	1740	Wolinella succinogenes DSM	emb CAD78091.1 N-acetylglucosamine-6-sulfatase [Pirellula sp.]			
11675, 11676	34557033	59	3.00E-40	1740	Wolinella succinogenes DSM	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740]			
11677, 11678	34557161	58	7.00E-40	1740	Wolinella succinogenes DSM	emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]			
11685, 11686	56418878	62	2.00E-73	HTA426	Geobacillus kaustophilus	GLUTAMINE AMIDOTRANSFERASE [Wolinella succinogenes DSM 1740]			
11687, 11688	48853288	36	2.00E-28	acidarmanus	Ferroplasma acidarmanus	emb CAE09748.1 GLUTAMINE AMIDOTRANSFERASE [Wolinella succinogenes] sp Q7M9X0 HIS5_WOLSU [imidazole glycerol phosphate synthase subunit hisH (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (ImGP synthase subunit hisH) (IGP synthase subunit hisH)]			2.4.2.-
1169, 1170	148397	59	3.00E-35	agglomerans	Pantoea agglomerans	PUTATIVE ARSENATE REDUCTASE [Wolinella succinogenes DSM 1740]			1.97.1.5
11691, 11692	34558827	50	2.00E-63	7G3	Alvinella pompejana epibiont	emb CAE09876.1 PUTATIVE ARSENATE REDUCTASE [Wolinella succinogenes]			
						type I restriction modification system M subunit (site-specific DNA-methyltransferase subunit) [Geobacillus kaustophilus HTA426]			
						dbj BAD74628.1 type I restriction modification system M subunit (site-specific DNA-methyltransferase subunit) [Geobacillus kaustophilus HTA426]			2.1.1.72
						COG0732: Restriction endonuclease S subunits [Ferroplasma acidarmanus]			3.1.21.3
						phytoene dehydrogenase [Pantoea agglomerans] pti S52586 phytoene			1.3.3.4
						dehydrogenase (EC 1.3.-.-) - Erwinia herbicola			
						riboflavin biosynthesis protein [Alvinella pompejana epibiont 7G3]			3.5.4.26

11693, 11694	46143552	43	5.00E-21	Actinobacillus pleuropneumoniae serovar 1 str. 4074	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Actinobacillus pleuropneumoniae serovar 1 str. 4074]				
11697, 11698	57167857	37	9.00E-16	Campylobacter coli RM2228	ferric uptake regulation protein, putative [Campylobacter coli RM2228] gb EAL57643.1 ferric uptake regulation protein, putative [Campylobacter coli RM2228]				
11699, 11700	42523774	33	6.00E-24	Bdellovibrio bacteriovorus HD100	HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] emb CAE0147.1 HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100]				
117, 118						Eremothecium gossypii ATCC 10895 chromosome VI, complete sequence ## 5.00E-30			
11701, 11702	34557750	40	3.00E-25	Wolinella succinogenes DSM 1740	FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10465.1 FUMARATE REDUCTASE FLAVOPROTEIN SUBUNIT [Wolinella succinogenes]				1.3.99.1
11703, 11704	30249464	40	1.00E-21	Nitrosomonas europaea ATCC 19718	Cytochrome c, class IC: Cytochrome c, class I [Nitrosomonas europaea ATCC 19718] emb CAD85404.1 Cytochrome c, class IC: Cytochrome c, class I [Nitrosomonas europaea ATCC 19718]				
11705, 11706	34558322	50	9.00E-19	Wolinella succinogenes DSM 1740	UDP-N-ACETYL MURAMOYLALANINE-D-GLUTAMATE LIGASE [Wolinella succinogenes DSM 1740] emb CAE11037.1 UDP-N- ACETYL MURAMOYLALANINE-D-GLUTAMATE LIGASE [Wolinella succinogenes]				6.3.2.9
11707, 11708	51245977	54	8.00E-40	Desulfotalea psychrophila LSV54	related to DNA repair photolyase [Desulfotalea psychrophila LSV54] emb CAG36854.1 related to DNA repair photolyase [Desulfotalea psychrophila LSV54]				4.1.99.-
11709, 11710	15679599	28	8.00E-08	Methanothermobac ter thermautotrophicus str. Delta H	acetyl-CoA synthetase [Methanothermobacter thermotrophicus str. Delta H] gb AAB86077.1 acetyl-CoA synthetase [Methanothermobacter thermautotrophicus str. Delta H] pir C69081 acetyl-CoA synthetase - Methanobacterium thermotrophicum (strain Delta H)				6.2.1.1
11711, 11712	39995927	48	5.00E-49	Geobacter sulfurreducens PCA	hypothetical protein GSU0821 [Geobacter sulfurreducens PCA] gb AAR34151.1 conserved hypothetical protein [Geobacter sulfurreducens PCA]				
11713, 11714	48855392	33	1.00E-27	Cytophaga hutchinsonii	COG0823: Periplasmic component of the Tol biopolymer transport system [Cytophaga hutchinsonii]				
11719, 11720	48834051	48	9.00E-39	Magnetococcus sp. MC-1	COG2602: Beta-lactamase class D [Magnetococcus sp. MC-1]				3.5.2.6

11721, 11722	17229972	41	7.00E-26	Nostoc sp. PCC 7120	beta-lactamase [Nostoc sp. PCC 7120] dbj BAB74179.1 beta-lactamase [Nostoc sp. PCC 7120] pir A12115 beta-lactamase [imported] - Nostoc sp. (strain PCC 7120)			3.5.2.6
11725, 11726	17232265	36	5.00E-20	Nostoc sp. PCC 7120	alpha-glucosidase [Nostoc sp. PCC 7120] pir AE2402 alpha-glucosidase [imported] - Nostoc sp. (strain PCC 7120) dbj BAB78472.1 alpha-glucosidase [Nostoc sp. PCC 7120]			3.2.1.20
11727, 11728	52841063	24	6.00E-11	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	agglutination protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_123217.1 hypothetical protein lpp0889 [Legionella pneumophila str. Paris] gb AAU26915.1 agglutination protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH12040.1 hypothetical protein [Legionella pneumophila str. Paris]			
11729, 11730	33147750	50	6.00E-18	Haemophilus ducreyi 35000HP	possible type II DNA modification enzyme (methyltransferase) [Haemophilus ducreyi 35000HP] ref NP_872883.1 possible type II DNA modification enzyme (methyltransferase) [Haemophilus ducreyi 35000HP]			2.1.1.72
11731, 11732	34763071	31	1.00E-22	Fusobacterium nucleatum subsp. vincentii ATCC 49256	Restriction enzyme BcgI beta subunit [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24368.1 Restriction enzyme BcgI beta subunit [Fusobacterium nucleatum subsp. vincentii ATCC 49256]			
11735, 11736	57240635	46	4.00E-58	Campylobacter lari RM2100	peptidase, M23/M37 family [Campylobacter lari RM2100] gb EAL55749.1 peptidase, M23/M37 family [Campylobacter lari RM2100]			3.5.1.-
11737, 11738	57240636	46	6.00E-54	Campylobacter lari RM2100	magnesium transporter, putative [Campylobacter lari RM2100] gb EAL55750.1 magnesium transporter, putative [Campylobacter lari RM2100]			3.6.1.-
11739, 11740	56707454	35	5.00E-33	Francisella tularensis subsp. tularensis Schu 4	hypothetical protein FTT0301 [Francisella tularensis subsp. tularensis Schu 4] gb AAV29706.1 NT02F70891 [synthetic construct] emb CAG44934.1 hypothetical protein [Francisella tularensis subsp. tularensis]			
11741, 11742	40062476	39	8.00E-43	uncultured bacterium 105	hypothetical protein EBAC750-01A01.2 [uncultured bacterium 105]			2.7.9.2
11745, 11746	53713382	48	1.00E-40	Bacteroides fragilis YCH46	outer membrane efflux protein [Bacteroides fragilis YCH46] dbj BAD48840.1 outer membrane efflux protein [Bacteroides fragilis YCH46]			
11747, 11748	57237698	36	7.00E-23	Campylobacter jejuni RM1221	molybdopterin biosynthesis MoeA protein, putative [Campylobacter jejuni RM1221] gb AAW35281.1 molybdopterin biosynthesis MoeA protein, putative [Campylobacter jejuni RM1221]			
11749, 11750	30020150	26	2.00E-07	Bacillus cereus ATCC 14579	Alpha/beta hydrolase [Bacillus cereus ATCC 14579] gb AAP08982.1 Alpha/beta hydrolase [Bacillus cereus ATCC 14579]			

1175, 1176	AAE0569 8	32	2.00E-20			Desc: <i>Bacillus deramificans</i> pullulanase variant G794P. Org: <i>Bacillus deramificans</i> Synthetic			3.2.1.41
11751, 11752	7481995	26	1.00E-06			protein P120 - Mycoplasma hominis gb AAA67449.1 P120 ATPase involved in DNA replication [Vibrio vulnificus CMCP6] gb AAO10830.1 ATPase involved in DNA replication [Vibrio vulnificus CMCP6]			
11753, 11754	27365775	35	2.00E-36	Vibrio vulnificus CMCP6					
11757, 11758	34557346	55	3.00E-14	Wolinella succinogenes DSM 1740		hypothetical protein WS0958 [Wolinella succinogenes DSM 1740] emb CAE10061.1 hypothetical protein [Wolinella succinogenes]			
11759, 11760	29346738	42	1.00E-52	Bacteroides thetaiotaomicron VPI-5482		hypothetical protein BT1328 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76435.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
11765, 11766	AAB4639 9	33	4.00E-23			Desc: H. pylori HPC099 protein. Org: <i>Helicobacter pylori</i>			
11767, 11768	24373542	41	1.00E-38	Shewanella oneidensis MR-1		hypothetical protein SO1978 [Shewanella oneidensis MR-1] gb AAN55029.1 conserved hypothetical protein [Shewanella oneidensis MR-1]			
1177, 1178	39996034	35	5.00E-27	Geobacter sulfurreducens PCA		Rhodanese-like domain protein [Geobacter sulfurreducens PCA] gb AAR34258.1 Rhodanese-like domain protein [Geobacter sulfurreducens PCA]			
11771, 11772	14518364	44	1.00E-58	Microscilla sp. PRE1		putative transposase [Microscilla sp. PRE1] gb AAK62881.1 MS159, putative transposase [Microscilla sp. PRE1]			
11775, 11776	48833468	27	8.00E-24	Magnetococcus sp. MC-1		COG0715: ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components [Magnetococcus sp. MC-1]			
11779, 11780	56460818	32	2.00E-31	Idiomarina loliensis L2TR		Secreted enzyme, contains two amidohydrolase related domains [Idiomarina loliensis L2TR] gb AAV82550.1 Secreted enzyme, contains two amidohydrolase related domains [Idiomarina loliensis L2TR]			
11781, 11782	21674138	52	1.00E-65	Chlorobium tepidum TLS		hydrolase, haloacid dehalogenase-like family [Chlorobium tepidum TLS] gb AAM72545.1 hydrolase, haloacid dehalogenase-like family [Chlorobium tepidum TLS]			5.4.2.6
11783, 11784	34556697	36	8.00E-25	Wolinella succinogenes DSM 1740		PUTATIVE CHEMOTAXIS PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09412.1 PUTATIVE CHEMOTAXIS PROTEIN [Wolinella succinogenes]			2.7.3.-
11787, 11788	48862510	42	5.00E-17	Microbulbifer degradans 2-40		COG0778: Nitroreductase [Microbulbifer degradans 2-40]			
11789, 11790	23130537	37	6.00E-35	Nostoc punctiforme PCC 73102		COG0778: Nitroreductase [Nostoc punctiforme PCC 73102]			

11791, 11792, 11793, 11794, 11795, 11796	53763585 53711768 53711768 57167724	35 22 22 43	1.00E-18 3.00E-17 1.00E-26	Anabaena variabilis ATCC 29413 Bacteroides fragilis YCH46 Campylobacter coli RM2228	COG4938: Uncharacterized conserved protein [Anabaena variabilis ATCC 29413] hypothetical protein BF0477 [Bacteroides fragilis YCH46] dbj BAD47226.1 hypothetical protein [Bacteroides fragilis YCH46] 16S rRNA processing protein RimM, putative [Campylobacter coli RM2228] gb EAL57510.1 16S rRNA processing protein RimM, putative [Campylobacter coli RM2228]				
11797, 11798	1197006	56	8.00E-49	Bacteroides fragilis	unknown protein [Bacteroides fragilis] gb AAA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for Insertion sequence element IS4351 (Transposon TN4551)	Vibrio vulnificus CMCP6 chromosome I section 9 of 11 of the complete sequence	85	2.00E-09	
11799, 11800, 11801, 11802, 11805, 11806	23126261 34556591 38016672	49 57 41	6.00E-53 8.00E-77 4.00E-20	Nostoc punctiforme PCC 73102 Wolfinella succinogenes DSM 1740 Klebsiella pneumoniae	COG2755: Lysophospholipase L1 and related esterases [Nostoc punctiforme PCC 73102] PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolfinella succinogenes DSM 1740] emb CAE09306.1 PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolfinella succinogenes] YebB [Klebsiella pneumoniae] ref NP_943343.1 YebB [Klebsiella pneumoniae]				4.2.1.70
11809, 11810	57241075	51	2.00E-81	Campylobacter lari RM2100	glycyl-tRNA synthetase, beta subunit [Campylobacter lari RM2100] gb EAL54771.1 glycyl-tRNA synthetase, beta subunit [Campylobacter lari RM2100]				6.1.1.14
1181, 1182	48854372	76	5.00E-67	Cytophaga hutchinsonii	COG0114: Fumarase [Cytophaga hutchinsonii]	Coxiella burnetii strain RSA 493, section 4 of 7 of the complete genome	83	1.00E-16	4.2.1.2
11811, 11812	46143552	44	2.00E-35	Actinobacillus pleuropneumoniae serovar 1 str. 4074	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Actinobacillus pleuropneumoniae serovar 1 str. 4074]				2.7.3.-
11813, 11814	23127773	43	3.00E-35	Nostoc punctiforme PCC 73102	COG0337: 3-dehydroquinase synthetase [Nostoc punctiforme PCC 73102]				4.2.3.4

11815, 11816	45658172	41	8.00E-35	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70895.1 serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				
11817, 11818	51244491	30	8.00E-20	Desulfotalea psychrophila LSV54	hypothetical membrane protein (BatB) [Desulfotalea psychrophila LSV54] emb CAG35368.1 hypothetical membrane protein (BatB) [Desulfotalea psychrophila LSV54]				
11823, 11824	34556560	41	5.00E-56	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]				
11825, 11826	48855584	37	6.00E-42	Cytophaga hutchinsonii	COG0010: Arginase/agmatinase/formiminoglutamate hydrolase, arginase family [Cytophaga hutchinsonii]				3.5.3.1
11827, 11828	15607089	63	1.00E-43	Aquifex aolicus VF5	hypothetical protein aq_2146 [Aquifex aolicus VF5] gb AAC07873.1 hypothetical protein [Aquifex aolicus VF5] pir B70484 conserved hypothetical protein aq_2146 - Aquifex aolicus				2.7.4.9
11829, 11830	34396965	37	2.00E-11	Porphyromonas gingivalis W83	hypothetical protein PG0883 [Porphyromonas gingivalis W83] ref NP_905130.1 hypothetical protein PG0883 [Porphyromonas gingivalis W83]				
1183, 1184	15603823	34	7.00E-10	Pasteurella multocida subsp. multocida str. Pm70	hypothetical protein PM1958 [Pasteurella multocida subsp. multocida str. Pm70] gb AAK04042.1 unknown [Pasteurella multocida subsp. multocida str. Pm70] sp Q9CJN9 J58_PASMU Hypothetical UPF0306 protein PM1958				
11831, 11832	34556779	26	1.00E-17	Wolinella succinogenes DSM 1740	GGDEF DOMAIN PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09494.1 GGDEF DOMAIN PROTEIN [Wolinella succinogenes]				
11837, 11838	57237396	76	4.00E-38	Campylobacter jejuni RM1221	excinuclease ABC, A subunit [Campylobacter jejuni RM1221] gb AAW34979.1 excinuclease ABC, A subunit [Campylobacter jejuni RM1221]				
11839, 11840	48832174	25	6.00E-17	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]				
11841, 11842	48833886	54	4.00E-32	Magnetococcus sp. MC-1	COG2202: FOG: PAS/PAC domain [Magnetococcus sp. MC-1]				
11843, 11844	48786283	54	8.00E-66	Burkholderia fungorum LB400	COG0436: Aspartate/tyrosine/aromatic aminotransferase [Burkholderia fungorum LB400]				2.6.1.1
11845, 11846	32262039	41	2.00E-46	Helicobacter hepaticus ATCC 51449	glucose-6-phosphate isomerase [Helicobacter hepaticus ATCC 51449] ref NP_860022.1 glucose-6-phosphate isomerase [Helicobacter hepaticus ATCC 51449]				5.3.1.9
11851, 11852	53714985	33	1.00E-27	Bacteroides fragilis YCH46	putative membrane peptidase [Bacteroides fragilis YCH46] db BAD50443.1 putative membrane peptidase [Bacteroides fragilis YCH46]				

11857, 11858	34556460	56	2.00E-53	Wolnella succinogenes DSM 1740	DNA POLYMERASE III, BETA CHAIN [Wolnella succinogenes DSM 1740] embjCAE09175.1] DNA POLYMERASE III, BETA CHAIN [Wolnella succinogenes]			2.7.7.7
11859, 11860	34558792	31	4.00E-18	Alvinella pompejana epibiont 6C6	conserved hypothetical protein [Alvinella pompejana epibiont 6C6]			
11861, 11862	54302166	29	2.00E-10	Photobacterium profundum SS9	hypothetical protein PBRB0486 [Photobacterium profundum SS9] embjCAG23359.1] hypothetical protein [Photobacterium profundum]			
11863, 11864	34104262	33	1.00E-09	Chromobacterium violaceum ATCC 12472	conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] refjNP_902623.1] hypothetical protein CV2953 [Chromobacterium violaceum ATCC 12472]			2.7.3.-
11865, 11866	34557749	53	2.00E-34	Wolnella succinogenes DSM 1740	hypothetical protein WS1398 [Wolnella succinogenes DSM 1740] embjCAE10464.1] conserved hypothetical protein [Wolnella succinogenes]			
1187, 1188	48855923	46	9.00E-35	Cytophaga hutchinsonii	COG2812: DNA polymerase III, gamma/tau subunits [Cytophaga hutchinsonii]			2.7.7.7
11873, 11874	AAU3577 1	80	1.00E-123		Desc:Helicobacter pylori cellular proliferation protein #84. Org:Helicobacter pylori	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6	80	1.00E-11
11875, 11876	57168227	45	4.00E-40	Campylobacter coli RM2228	probable flagellar protein Cj1312 [Campylobacter coli RM2228] gbjEAL57270.1] probable flagellar protein Cj1312 [Campylobacter coli RM2228]			
11877, 11878	6968747	46	1.00E-24	Campylobacter jejuni subsp. jejuni NCTC 11168	possible flagellar protein [Campylobacter jejuni subsp. jejuni NCTC 11168] refjNP_282459.1] possible flagellar protein [Campylobacter jejuni subsp. jejuni NCTC 11168] pirjF81274 probable flagellar protein Cj1313 [imported] - Campylobacter jejuni (strain NCTC 11168)			
11879, 11880	26247620	24	5.00E-09	Escherichia coli CFT073	Hypothetical protein yciR [Escherichia coli CFT073] gbjAAN80222.1] Hypothetical protein yciR [Escherichia coli CFT073]			
11881, 11882	34556462	71	6.00E-49	Wolnella succinogenes DSM 1740	hypothetical protein WS0003 [Wolnella succinogenes DSM 1740] embjCAE09177.1] conserved hypothetical protein [Wolnella succinogenes]			
11883, 11884	34556772	61	1.00E-69	Wolnella succinogenes DSM 1740	ENDOPEPTIDASE CLP ATP-BINDING CHAIN A [Wolnella succinogenes DSM 1740] embjCAE09487.1] ENDOPEPTIDASE CLP ATP-BINDING CHAIN A [Wolnella succinogenes]	Desc:Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1142. Org:Staphylococcus epidermidis	87	3.00E-08

11885, 11886	57240902	49	8.00E-35	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55295.1 conserved hypothetical protein [Campylobacter lari RM2100]				
1189, 1190	19703759	29	9.00E-23	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Type III restriction-modification system restriction subunit [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94620.1 Type III restriction-modification system restriction subunit [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			3.1.21.5	
11891, 11892	34557016	52	3.00E-23	Wolinella succinogenes DSM 1740	hypothetical protein WS0599 [Wolinella succinogenes DSM 1740] emb CAE09731.1 conserved hypothetical protein [Wolinella succinogenes] COG0840: Methyl-accepting chemotaxis protein [Microbulifer degradans 2- 40]				
11893, 11894	48863731	30	9.00E-19	Microbulifer degradans 2-40					
11895, 11896	51891413	30	3.00E-07	Symbiobacterium thermophilum IAM 14863	transposase [Symbiobacterium thermophilum IAM 14863] dbj BAD39260.1 transposase [Symbiobacterium thermophilum IAM 14863]				
11897, 11898	34557509	48	7.00E-30	Wolinella succinogenes DSM 1740	hypothetical protein WS1135 [Wolinella succinogenes DSM 1740] emb CAE10224.1 hypothetical protein [Wolinella succinogenes]				
11899, 11900	53795617	36	1.00E-42	Chloroflexus aurantiacus	COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Chloroflexus aurantiacus]			2.7.3.-	
119, 120	48854510	57	5.00E-44	Cytophaga hutchinsonii	COG0622: Predicted phosphoesterase [Cytophaga hutchinsonii]				
11901, 11902	34557246	55	6.00E-74	Wolinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]			2.7.3.-	
11903, 11904	57236987	51	3.00E-85	Campylobacter jejuni RM1221	primosomal protein N' [Campylobacter jejuni RM1221] gb AAW34570.1 primosomal protein N' [Campylobacter jejuni RM1221]				
11905, 11906	34556865	56	3.00E-58	Wolinella succinogenes DSM 1740	PUTATIVE D-ALANINE-D-ALANINE LIGASE [Wolinella succinogenes DSM 1740] emb CAE09580.1 PUTATIVE D-ALANINE-D-ALANINE LIGASE [Wolinella succinogenes] sp Q7MA71 DDL_WOLSU D-alanine-D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase)			6.3.2.4	
11909, 11910	22651592	68	9.00E-98	Sulfurospirillum barnesii	periplasmic nitrate reductase [Sulfurospirillum barnesii]	Sulfurospirillum barnesii SES-3 periplasmic nitrate reductase (napA) gene, partial cds	86	4.00E-08	1.7.99.4
11913, 11914	52426060	41	2.00E-29	Mannheimia succiniciproducens MBEL 55E	hypothetical protein MS2005 [Mannheimia succiniciproducens MBEL55E] gb AAU38612.1 unknown [Mannheimia succiniciproducens MBEL55E]				

11915, 11916	34558488	61	2.00E-42	Wolinella succinogenes DSM 1740	PUTATIVE ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE11203.1 PUTATIVE ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes] hypothetical protein CPE1902 [Clostridium perfringens str. 13] dbj BAB81608.1 conserved hypothetical protein [Clostridium perfringens str. 13]			1.8.-:-
11917, 11918	18310884	28	8.00E-10	Clostridium perfringens str. 13				
11919, 11920	34556640	75	3.00E-57	Wolinella succinogenes DSM 1740	30S RIBOSOMAL PROTEIN S2 [Wolinella succinogenes DSM 1740] emb CAE09355.1 30S RIBOSOMAL PROTEIN S2 [Wolinella succinogenes] uracil phosphoribosyltransferase [Aquifex aeolicus VF-5] gb AAC07880.1 uracil phosphoribosyltransferase [Aquifex aeolicus VF5] pir F70485 uracil phosphoribosyltransferase (EC 2.4.2.9) upp-type - Aquifex aeolicus sp Q67914 UUP_AQUAE Uracil phosphoribosyltransferase (UMP pyrophosphorylase) (UPRTase)	Helicobacter hepaticus ATCC 51449 section 4 of 6 of the complete genome	82	1.00E-12
11921, 11922	15607101	41	1.00E-42	Aquifex aeolicus VF5				2.4.2.9
11923, 11924	15611181	58	6.00E-86	Helicobacter pylori J99	PHOSPHOENOLPYRUVATE SYNTHASE [Helicobacter pylori J99] gb AAD05690.1 PHOSPHOENOLPYRUVATE SYNTHASE [Helicobacter pylori J99] pir E71972 pyruvate, water dikinase (EC 2.7.9.2) - Helicobacter pylori (strain J99) sp Q9ZMV4 PPSA_HELPJ Phosphoenolpyruvate synthase (Pyruvate, water dikinase) (PEP synthase) dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis Schu 4] emb CAG46097.1 dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis] gb AAS60284.1 sugar dehydratase [Francisella tularensis subsp. tularensis]			2.7.9.2
11925, 11926	56708505	63	4.00E-50	Francisella tularensis subsp. tularensis Schu 4				4.2.1.-
11927, 11928	51245971	68	1.00E-105	Desulfotalea psychrophila LSV54	probable flavoprotein [Desulfotalea psychrophila LSV54] emb CAG36848.1 probable flavoprotein [Desulfotalea psychrophila LSV54] hypothetical protein GSU1360 [Geobacter sulfurreducens PCA] gb AAR34736.1 hypothetical protein GSU1360 [Geobacter sulfurreducens PCA] COG3735: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
11929, 11930	39996462	38	1.00E-25	Geobacter sulfurreducens PCA				
1193, 1194	48856757	38	5.00E-07	Cytophaga hutchinsonii				
11931, 11932	48764556	29	9.00E-13	Rhodospirillum rubrum	hypothetical protein Rub02001299 [Rhodospirillum rubrum]			
11935, 11936	48771616	29	2.00E-21	Ralstonia metallidurans CH34				
11937, 11938	48853332	31	2.00E-32	Cytophaga hutchinsonii	hypothetical protein Reut02000360 [Ralstonia metallidurans CH34] COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]			

11939, 11940	48853332	26	2.00E-13	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]				
11941, 11942	34557573	33	1.00E-30	Wolinella succinogenes DSM 1740	SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes]				2.7.3.-
11943, 11944	34557118	46	6.00E-23	Wolinella succinogenes DSM 1740	MOLYBDOPTERIN OXIDOREDUCTASE, IRON-SULFUR BINDING SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE09833.1 MOLYBDOPTERIN OXIDOREDUCTASE, IRON-SULFUR BINDING SUBUNIT [Wolinella succinogenes]				1.2.7.-
11945, 11946	28851369	59	4.00E-19	Pseudomonas syringae pv. tomato str. DC3000	methyl-accepting chemotaxis protein [Pseudomonas syringae pv. tomato str. DC3000] ref NP_790751.1 methyl-accepting chemotaxis protein [Pseudomonas syringae pv. tomato str. DC3000]				
11947, 11948	ABP3072 8	56	5.00E-34		Desc:Streptococcus polypeptide SEQ ID NO 10632. Org:Streptococcus agalactiae				
11949, 11950	ABP3072 8	47	4.00E-28		Desc:Streptococcus polypeptide SEQ ID NO 10632. Org:Streptococcus agalactiae				
11951, 11952	48855487	73	2.00E-37	Cytophaga hutchinsonii	COG1048: Aconitase A [Cytophaga hutchinsonii]				4.2.1.3
11953, 11954	42521967	43	7.00E-37	Bdellovibrio bacteriovorus HD100	hypothetical protein Bd0347 [Bdellovibrio bacteriovorus HD100] emb CAE78001.1 conserved hypothetical protein [Bdellovibrio bacteriovorus HD100]				
11955, 11956	34558795	50	9.00E-80	Alvinella pompejana epibiont 6C6	TonB-dependent receptor [Alvinella pompejana epibiont 6C6]				
11957, 11958	40063642	43	9.00E-12	uncultured bacterium 582	oxidoreductase, 2OG-Fe(II) oxygenase family [uncultured bacterium 582] PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR				
11959, 11960	34557235	47	4.00E-26	Wolinella succinogenes DSM 1740	[Wolinella succinogenes DSM 1740] emb CAE09950.1 PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR [Wolinella succinogenes]				
11963, 11964	34558815	57	5.00E-51	Alvinella pompejana epibiont 7G3	citrate lyase subunit 2 [Alvinella pompejana epibiont 7G3]				4.1.3.8
11965, 11966	42525634	34	4.00E-14	Treponema denticola ATCC 35405	hypothetical protein TDE0115 [Treponema denticola ATCC 35405] gb AA10613.1 conserved hypothetical protein [Treponema denticola ATCC 35405]				
11969, 11970	48854887	43	1.00E-41	Cytophaga hutchinsonii	COG0538: Isocitrate dehydrogenases [Cytophaga hutchinsonii]				

11971, 11972	34556565	30	4.00E-19	Wolnella succinogenes DSM 1740	PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolnella succinogenes DSM 1740] emb CAE09280.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolnella succinogenes] emb CAD23185.1 putative transcriptional regulator protein [Wolnella succinogenes]			
11973, 11974	23102480	42	6.00E-45	Azotobacter vinelandii	COG3649: Uncharacterized protein predicted to be involved in DNA repair [Azotobacter vinelandii]			
11978, 11980	23103021	31	1.00E-23	Azotobacter vinelandii	COG3321: Polyketide synthase modules and related proteins [Azotobacter vinelandii]			2.3.1.39
11981, 11982	19704257	29	4.00E-11	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Homoserine kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95118.1 Homoserine kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			2.7.1.39
11983, 11984	37787364	45	1.00E-33	Thiocapsa roseopersicina	HoxY [Thiocapsa roseopersicina]			1.12.-.-
11985, 11986	57237690	29	3.00E-16	Campylobacter jejuni RM1221	hypothetical protein CJE0936 [Campylobacter jejuni RM1221] gb AAW35273.1 hypothetical protein CJE0936 [Campylobacter jejuni RM1221]			
11987, 11988	57241378	56	5.00E-53	Campylobacter lari RM2100	molybdopterin cofactor biosynthesis protein A [Campylobacter lari RM2100] gb EAL54490.1 molybdopterin cofactor biosynthesis protein A [Campylobacter lari RM2100]			
11989, 11990	37528276	41	6.00E-54	Photobacterium luminescens subsp. laumondii TTO1	hypothetical protein plu4453 [Photobacterium luminescens subsp. laumondii TTO1] emb CAE16825.1 unnamed protein product [Photobacterium luminescens subsp. laumondii TTO1]			
11991, 11992	57241378	56	5.00E-49	Campylobacter lari RM2100	molybdopterin cofactor biosynthesis protein A [Campylobacter lari RM2100] gb EAL54490.1 molybdopterin cofactor biosynthesis protein A [Campylobacter lari RM2100]			
11993, 11994	34556682	61	3.00E-66	Wolnella succinogenes DSM 1740	TYROSYL-TRNA SYNTHETASE [Wolnella succinogenes DSM 1740] emb CAE09397.1 TYROSYL-TRNA SYNTHETASE [Wolnella succinogenes]			6.1.1.1
12001, 12002	23128981	32	1.00E-13	Nostoc punctiforme PCC 73102	COG2319: FOG: WD40 repeat [Nostoc punctiforme PCC 73102]			2.7.1.37
12003, 12004	48870994	32	2.00E-09	Pedococcus pentosaceus ATCC 25745	COG0679: Predicted permeases [Pedococcus pentosaceus ATCC 25745] Protein containing HTH-type DNA-binding domain and DOC/FIC domain involved in death-on-curing system [Idiomarina loihiensis L2TR] gb AAV82879.1 Protein containing HTH-type DNA-binding domain and DOC/FIC domain involved in death-on-curing system [Idiomarina loihiensis L2TR]			
12005, 12006	56461147	37	5.00E-44	Idiomarina loihiensis L2TR				

12007,	50122189	24	2.00E-13	Erwinia carotovora subsp. atroseptica SCRI1043	agglutination protein [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG76165.1 agglutination protein [Erwinia carotovora subsp. atroseptica SCRI1043]			
12008,	18858717	36	9.00E-10	Danio rerio	alpha(1,3)fucosyltransferase [Danio rerio]			2.4.1.-
12009,	32477759	39	5.00E-26	Rhodopirellula baltica SH 1	hypothetical protein RB12866 [Rhodopirellula baltica SH 1]			
1201,	32262039	36	1.00E-14	Helicobacter hepaticus ATCC 51449	emb CAD77830.1 conserved hypothetical protein [Pirellula sp.] glucose-6-phosphate isomerase [Helicobacter hepaticus ATCC 51449] ref NP_860022.1 glucose-6-phosphate isomerase [Helicobacter hepaticus ATCC 51449]			5.3.1.9
12013,	53756727	23	6.00E-12	Methylococcus capsulatus str. Bath	conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_115226.1 hypothetical protein MCA2832 [Methylococcus capsulatus str. Bath]			
12014,	56387326	38	6.00E-34	Clostridium saccharoperbutylacetonicum	uptake hydrogenase [Clostridium saccharoperbutylacetonicum]			1.6.5.3
12021,	53685438	37	5.00E-41	Desulfitobacterium hafniense DCB-2	COG2081: Predicted flavoproteins [Desulfitobacterium hafniense DCB-2]			
12022,	56707780	59	3.00E-84	Francisella tularensis subsp. tularensis Schu 4	DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis Schu 4] emb CAG45292.1 DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis]			
12023,	18310859	31	1.00E-11	Clostridium perfringens str. 13	probable glycerophosphodiester phosphodiesterase [Clostridium perfringens str. 13] dbj BAB81583.1 probable glycerophosphodiester phosphodiesterase [Clostridium perfringens str. 13]			3.1.4.46
12031,	48891084	30	1.00E-14	Trichodesmium erythraeum IMS101	COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101]			2.4.1.-
12032,	34397216	50	8.00E-23	Porphyromonas gingivalis W83	conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_905380.1 hypothetical protein PG1179 [Porphyromonas gingivalis W83]			
12035,	53713673	42	7.00E-30	Bacteroides fragilis YCH46	hypothetical protein BF2382 [Bacteroides fragilis YCH46] dbj BAD49131.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
12036,	34558322	46	4.00E-52	Wolinella succinogenes DSM 1740	UDP-N-ACETYLMURAMOYLALANINE-D-GLUTAMATE LIGASE [Wolinella succinogenes DSM 1740] emb CAE11037.1 UDP-N-ACETYLMURAMOYLALANINE-D-GLUTAMATE LIGASE [Wolinella succinogenes]			6.3.2.9
12037,	46118943	49	8.00E-19	Crocospaera watsonii WH 8501	COG0545: FKBP-type peptidyl-prolyl cis-trans isomerases 1 [Crocospaera watsonii WH 8501]			5.2.1.8

12049, 12050	48864040	22	1.00E-11	Microbulbifer degradans 2-40	hypothetical protein Mdeg02000406 [Microbulbifer degradans 2-40]			
1205, 1206	15602459	59	7.00E-16	Pasteurella multocida subsp. multocida str. Pm70	hypothetical protein PM0594 [Pasteurella multocida subsp. multocida str. Pm70] gb AAK02678.1 unknown [Pasteurella multocida subsp. multocida str. Pm70]			
12057, 12058	48846045	35	2.00E-21	Geobacter metallireducens GS-15	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]			2.7.3.-
12059, 12060	15639357	39	5.00E-11	Treponema pallidum subsp. pallidum str. Nichols	chemotaxis response regulator (cheY) [Treponema pallidum subsp. pallidum str. Nichols] gb AAC65351.1 chemotaxis response regulator (cheY) [Treponema pallidum subsp. pallidum str. Nichols] gb AAD45223.1 chemotaxis protein CheY [Treponema pallidum subsp. pertenue] gb AAC45558.1 chemotaxis protein CheY pir D71335 probable chemotaxis response regulator (cheY) - syphilis spirochete sp P96126 CHEY_TREPA Chemotaxis protein cheY			2.7.3.-
12061, 12062	34557846	43	1.00E-34	Wolinella succinogenes DSM 1740	hypothetical protein WS1513 [Wolinella succinogenes DSM 1740] emb CAE10561.1 conserved hypothetical protein [Wolinella succinogenes]			
12063, 12064	34557848	61	2.00E-72	Wolinella succinogenes DSM 1740	conserved hypothetical protein-2-methylthioadenine synthetase [Wolinella succinogenes DSM 1740] emb CAE10563.1 conserved hypothetical protein-2-methylthioadenine synthetase [Wolinella succinogenes]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6	89	5.00E-07 1.8.-
12065, 12066	37694419	41	6.00E-51	Flavobacterium columnare	membrane-associated zinc metalloprotease [Flavobacterium columnare]	Flavobacterium columnare strain G4 membrane- associated zinc metalloprotease gene, complete cds	81	4.00E-14 3.4.24.-
12067, 12068	29349509	45	8.00E-57	Bacteroides thetaiotaomicron VPI-5482	alanine racemase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79206.1 alanine racemase [Bacteroides thetaiotaomicron VPI-5482]			5.1.1.1
12069, 12070	53736047	43	2.00E-60	Crocospaera watsonii WH 8501	COG4889: Predicted helicase [Crocospaera watsonii WH 8501]			
1207, 1208	48854861	43	3.00E-35	Cytophaga hutchinsonii	COG0438: Glycosyltransferase [Cytophaga hutchinsonii]			2.4.1.-
12071, 12072	57241408	36	2.00E-25	Campylobacter lari RM2100	rod shape-determining protein (mreC), putative [Campylobacter lari RM2100] gb EAL54520.1 rod shape-determining protein (mreC), putative [Campylobacter lari RM2100]			

12073,	48853984	59	1.00E-104	Cytophaga hutchinsonii	COG1197: Transcription-repair coupling factor (superfamily II helicase)				3.6.1.-
12074					[Cytophaga hutchinsonii]				
12075,	48853984	41	1.00E-56	Cytophaga hutchinsonii	COG1197: Transcription-repair coupling factor (superfamily II helicase)				
12076					[Cytophaga hutchinsonii]				
12079,				Wollinella succinogenes DSM	PENICILLIN-BINDING PROTEIN 1A PBP-1A [Wollinella succinogenes DSM				2.4.2.-
12080	34558334	49	3.00E-44	1740	1740] emb CAE11049.1 PENICILLIN-BINDING PROTEIN 1A PBP-1A [Wollinella succinogenes]				
12081,				Microbulbifer degradans 2-40	COG3176: Putative hemolysin [Microbulbifer degradans 2-40]			Wollinella succinogenes, complete genome; segment 6/7	89 5.00E-10
12082	48861085	48	1.00E-56						
12083,				Magnetospirillum magnetotacticum	COG2200: FOG: EAL domain [Magnetospirillum magnetotacticum MS-1]				
12084	46201018	35	3.00E-37	MS-1					
12085,				Campylobacter lari	ParB family protein [Campylobacter lari RM2100]				
12086	57240722	33	2.00E-11	RM2100	family protein [Campylobacter lari RM2100]				
12089,				Synechocystis sp.	hypothetical protein sir2110 [Synechocystis sp. PCC 6803] dbj BAA18047.1				
12090	16330639	41	4.00E-18	PCC 6803	sir2110 [Synechocystis sp. PCC 6803] pir S75486 hypothetical protein sir2110 - Synechocystis sp. (strain PCC 6803)				
1209,				Bacteroides fragilis	tRNA nucleotidyltransferase [Bacteroides fragilis YCH46] dbj BAD50383.1				2.7.7.19
1210	53714925	62	6.00E-74	YCH46	tRNA nucleotidyltransferase [Bacteroides fragilis YCH46]				
12097,				Bacteroides thetaiotaomicron	hypothetical protein BT2505 [Bacteroides thetaiotaomicron VPI-5482]				
12098	29347915	36	3.00E-31	VPI-5482	gb AAO77612.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
12099,				Wollinella succinogenes DSM	hypothetical protein WS2211 [Wollinella succinogenes DSM 1740]				
12100	34558485	38	2.00E-40	1740	emb CAE11200.1 hypothetical protein [Wollinella succinogenes]				
12101,				Wollinella succinogenes DSM	PUTATIVE TWO-COMPONENT REGULATOR-CheY like receiver domain [Wollinella succinogenes DSM 1740] emb CAE10945.1 PUTATIVE TWO-COMPONENT REGULATOR-CheY like receiver domain [Wollinella succinogenes]				
12102	34558230	50	8.00E-25	1740					
12103,				Wollinella succinogenes DSM	hypothetical protein WS1588 [Wollinella succinogenes DSM 1740]				
12104	34557912	44	5.00E-26	1740	emb CAE10627.1 conserved hypothetical protein [Wollinella succinogenes]				
12105,				Vibrio vulnificus	type I restriction-modification system methyltransferase subunit [Vibrio vulnificus YJ016] dbj BAC93560.1 type I restriction-modification system methyltransferase subunit [Vibrio vulnificus YJ016]				2.1.1.72
12106	37679000	68	3.00E-69	YJ016	conserved hypothetical protein TIGR00486 [Campylobacter upsaliensis RM3195] gb EAL53410.1 conserved hypothetical protein TIGR00486 [Campylobacter upsaliensis RM3195]				
12107,				Campylobacter upsaliensis					
12108	57242697	47	1.00E-58	RM3195					

1211, 1212	21226234	63	2.00E-38	Methanosarcina mazel Go1	hypothetical protein MM0132 [Methanosarcina mazel Go1] gb AAM29828.1 conserved protein [Methanosarcina mazel Go1]			
					hypothetical protein c5144 [Escherichia coli CFT073] ref NP_755482.1			
					hypothetical protein c3607 [Escherichia coli CFT073] ref NP_753439.1			
					hypothetical protein c1530 [Escherichia coli CFT073] gb AAN83566.1			
12113, 12114	26250952	36	3.00E-23	Escherichia coli CFT073	Hypothetical protein [Escherichia coli CFT073] gb AAN82055.1 Hypothetical protein [Escherichia coli CFT073] gb AAN79999.1 Hypothetical protein [Escherichia coli CFT073]			
12115, 12116	48892683	28	2.00E-11	Trichodesmium erythraeum IMS101	COG0515: Serine/threonine protein kinase [Trichodesmium erythraeum IMS101]			2.7.1.37
12121, 12122	29347740	27	1.00E-24	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT2330 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77437.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
12123, 12124	45658174	39	1.00E-18	Leptospira interrogans serovar Copenhagen str. Flocruz L1-130	hypothetical protein LIC12326 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70897.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			
12125, 12126	51245405	41	2.00E-32	Desulfotalea psychrophila LSV54	hypothetical protein DP1553 [Desulfotalea psychrophila LSV54] emb CAG36282.1 unknown protein [Desulfotalea psychrophila LSV54]			
12127, 12128	34556927	60	9.00E-81	Wolinella succinogenes DSM 1740	PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09642.1 PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes]			
1213, 1214	31195995	54	1.00E-39	Anopheles gambiae	ENSANGP00000000470 [Anopheles gambiae]			2.3.1.-
12131, 12132	20559765	41	6.00E-52	Pseudomonas aeruginosa	ORF_15; similar to Glycosyl transferases group 1 [Pseudomonas aeruginosa] gb AAO17396.1 glycosyl transferases group 1-like protein [Pseudomonas aeruginosa]			2.4.1.-
12135, 12136	48855632	32	8.00E-25	Cytophaga hutchinsonii	COG0712: F0F1-type ATP synthase, delta subunit (mitochondrial oligomycin sensitivity protein) [Cytophaga hutchinsonii]			3.6.3.14
12137, 12138	48857000	35	3.00E-16	Cytophaga hutchinsonii	COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii]			
12139, 12140	57506236	65	1.00E-35	Campylobacter upsaliensis RM3195	malate:quinone oxidoreductase, putative [Campylobacter upsaliensis RM3195] gb EAL52259.1 malate:quinone oxidoreductase, putative [Campylobacter upsaliensis RM3195]			1.1.99.1 6
12141, 12142	34557578	41	2.00E-38	Wolinella succinogenes DSM 1740	CIAB PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10293.1 CIAB PROTEIN [Wolinella succinogenes]			

12143, 12144	24372513	31	1.00E-19	Shewanella oneidensis MR-1	acetyltransferase, GNAT family [Shewanella oneidensis MR-1] gb AAAN54000.1 acetyltransferase, GNAT family [Shewanella oneidensis MR-1]				
12145, 12146	17549647	60	5.00E-40	Ralstonia solanacearum GMI1000	hypothetical protein RS03114 [Ralstonia solanacearum GMI1000] emb CAD18579.1 CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum]				
12147, 12148	48854194	42	7.00E-23	Cytophaga hutchinsonii	COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii]				
12149, 12150	52007438	67	1.00E-72	Thiobacillus denitrificans ATCC 25259	COG0677: UDP-N-acetyl-D-mannosaminuronate dehydrogenase [Thiobacillus denitrificans ATCC 25259]	Shigella sonnei O antigen gene cluster, complete sequence; insertion sequences IS1 InsB (InsB), InsA (InsA), IS630 transposase, IS629 ORFA (orfA), IS91 transposase (InsB) and InsA (InsA), and IS911 InsB (InsB) genes, complete cds	91	2.00E-09	1.1.1.-
12151, 12152	53612047	51	1.00E-49	Azotobacter vinelandii	COG0419: ATPase involved in DNA repair [Azotobacter vinelandii] Lysyl-tRNA synthetase class II [Thermoanaerobacter tengcongensis MB4]	Prochlorococcus marinus MED4 complete genome; segment 5/5			
12153, 12154	20808736	48	2.00E-71	Thermoanaerobact er tengcongensis MB4	gb AAM2551.1 Lysyl-tRNA synthetase class II [Thermoanaerobacter tengcongensis MB4] sp Q8R7N1 SYK_THETN Lysyl-tRNA synthetase (Lysine-tRNA ligase) (LysRS) oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter jejuni RM1221] gb AAW35807.1 oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter jejuni RM1221] emb CAB75216.1 putative oxidoreductase [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281763.1 putative oxidoreductase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81405 probable oxidoreductase Cj0580c [imported] - Campylobacter jejuni (strain NCTC 11168)		86	1.00E-08	6.1.1.6
12155, 12156	57238224	44	3.00E-49	Campylobacter jejuni RM1221					1.-.-.-
12159, 12160	48846045	40	1.00E-27	Geobacter metallireducens GS-15	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]				2.7.3.-

12161, 12162	48825033	38	7.00E-20	Enterococcus faecium	COG0463: Glycosyltransferases involved in cell wall biogenesis [Enterococcus faecium]			2.4.-.-
12165, 12166	21673395	49	1.00E-60	Chlorobium tepidum TLS	NH(3)-dependent NAD+ synthetase [Chlorobium tepidum TLS] gb AAAM71802.1 NH(3)-dependent NAD+ synthetase [Chlorobium tepidum TLS] sp Q8KEX2 NADE_CHL TE NH(3)-dependent NAD(+) synthetase			6.3.5.1
12167, 12168	48861330	39	5.00E-21	Microbulbifer degradans 2-40	COG0457: FOG: TPR repeat [Microbulbifer degradans 2-40]			
12169, 12170	34557419	36	2.00E-36	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]			2.7.3.-
1217, 1218	5360168	33	6.00E-27	Flavobacterium johnsoniae	GldB [Flavobacterium johnsoniae]			
12171, 12172	34556479	41	4.00E-15	Wolinella succinogenes DSM 1740	POSSIBLE NUCLEOTIDYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09194.1 POSSIBLE NUCLEOTIDYLTRANSFERASE [Wolinella succinogenes]			
12173, 12174	34556480	66	1.00E-63	Wolinella succinogenes DSM 1740	GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes DSM 1740] emb CAE09195.1 GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes]			2.6.1.16
12175, 12176	57236944	46	2.00E-43	Campylobacter jejuni RM1221	RNB-like protein [Campylobacter jejuni RM1221] gb AAW34527.1 RNB-like protein [Campylobacter jejuni RM1221]			3.1.-.-
12177, 12178	34557504	71	1.00E-109	Wolinella succinogenes DSM 1740	HSDR PROTEIN PROBABLE TYPE I RESTRICTION ENZYME RESTRICTIONCHAIN [Wolinella succinogenes DSM 1740] emb CAE10219.1 HSDR PROTEIN PROBABLE TYPE I RESTRICTION ENZYME RESTRICTIONCHAIN [Wolinella succinogenes]			3.1.21.3
12185, 12186	48855392	28	8.00E-16	Cytophaga hutchinsonii	COG0823: Periplasmic component of the Tol biopolymer transport system [Cytophaga hutchinsonii]			
12189, 12190	21228324	28	4.00E-17	Methanosarcina mazel Go1	Galactosyltransferase [Methanosarcina mazel Go1] gb AAM31918.1 Galactosyltransferase [Methanosarcina mazel Goe1]			2.4.1.-
1219, 1220	30023200	42	4.00E-55	Bacillus cereus ATCC 14579	Excinuclease ABC subunit A [Bacillus cereus ATCC 14579] gb AAP12032.1 Excinuclease ABC subunit A [Bacillus cereus ATCC 14579]			
12191, 12192	24214122	34	1.00E-30	Leptospira interrogans serovar Lai str. 56601	Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601]			
12193, 12194	32262126	63	5.00E-75	Helicobacter hepaticus ATCC 51449	UTP-glucose-1-phosphate uridylyltransferase [Helicobacter hepaticus ATCC 51449] ref NP_860109.1 UTP-glucose-1-phosphate uridylyltransferase [Helicobacter hepaticus ATCC 51449]			2.7.7.9

12197, 12198	57242699	51	5.00E-39	Campylobacter upsallensis RM3195	conserved hypothetical protein [Campylobacter upsallensis RM3195] gb EAL53412.1 conserved hypothetical protein [Campylobacter upsallensis RM3195]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6	80	9.00E-11		
12199, 12200	48846029	36	1.00E-45	Geobacter metallireducens GS 15	COG0747: ABC-type dipeptide transport system, periplasmic component [Geobacter metallireducens GS-15]					
12201, 12202	57505780	44	2.00E-33	Campylobacter upsallensis RM3195	Phosphoglycolate phosphatase [Campylobacter upsallensis RM3195] gb EAL52841.1 Phosphoglycolate phosphatase [Campylobacter upsallensis RM3195]			3.1.3.18		
12203, 12204	34556865	58	3.00E-72	Wolinella succinogenes DSM 1740	PUTATIVE D-ALANINE--D-ALANINE LIGASE [Wolinella succinogenes DSM 1740] emb CAE09580.1 PUTATIVE D-ALANINE--D-ALANINE LIGASE [Wolinella succinogenes] sp Q7MA71 DDL_WOLSU D-alanine--D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase)			6.3.2.4		
12205, 12206	21241197	25	7.00E-08	Xanthomonas axonopodis pv. citri str. 306	hypothetical protein XAC0424 [Xanthomonas axonopodis pv. citri str. 306] gb AAM35315.1 conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306]					
12207, 12208	34556865	53	2.00E-46	Wolinella succinogenes DSM 1740	PUTATIVE D-ALANINE--D-ALANINE LIGASE [Wolinella succinogenes DSM 1740] emb CAE09580.1 PUTATIVE D-ALANINE--D-ALANINE LIGASE [Wolinella succinogenes] sp Q7MA71 DDL_WOLSU D-alanine--D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase)			6.3.2.4		
12209, 12210	21674916	59	4.00E-35	Chlorobium tepidum TLS	2-isopropylmalate synthase [Chlorobium tepidum TLS] gb AAM73323.1 2- isopropylmalate synthase [Chlorobium tepidum TLS]			4.1.3.12		
1221, 1222	29349121	46	1.00E-24	Bacteroides thetaiotaomicron VPI-5482	D-alanine--D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78818.1 D-alanine--D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A1F3 DDL_BACTN D-alanine--D-alanine ligase (D- alanylalanine synthetase) (D-Ala-D-Ala ligase)			6.3.2.4		
12211, 12212	48855427	42	6.00E-48	Cytophaga hutchinsonii	COG1521: Putative transcriptional regulator, homolog of Bvg accessory factor [Cytophaga hutchinsonii]					
12213, 12214	52840981	40	8.00E-15	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	GGDEF domain protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_123139.1 hypothetical protein lpp0809 [Legionella pneumophila str. Paris] gb AAU26833.1 GGDEF domain protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH11957.1 hypothetical protein [Legionella pneumophila str. Paris]			2.7.3.-		
12215, 12216	48890755	37	8.00E-29	Trichodesmium erythraeum IMS101	COG4121: Uncharacterized conserved protein [Trichodesmium erythraeum IMS101]					

12217, 12218, 12219, 12220, 12221, 12222	34557949 48832299 34557782	47 48 43	1.00E-64 4.00E-35 1.00E-16	Wolinella succinogenes DSM 1740 Magnetococcus sp. MC-1 Wolinella succinogenes DSM 1740	ADENYLATE CYCLASE [Wolinella succinogenes DSM 1740] emb CAE10864.1 ADENYLATE CYCLASE [Wolinella succinogenes] COG2206: HD-GYP domain [Magnetococcus sp. MC-1] PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]			4.6.1.1 3.1.4.17 2.7.3.-
12227, 12228	34558149	22	1.00E-10	Wolinella succinogenes DSM 1740	SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes DSM 1740] emb CAE10864.1 SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes]			
12229, 12230, 12231, 12232	53735717 48853873 46142567	54 65 35	8.00E-77 1.00E-92 1.00E-31	Crocospaera watsonii WH 8501 Cytophaga hutchinsonii Methanococcoides burtonii DSM 6242	COG1505: Serine proteases of the peptidase family S9A [Crocospaera watsonii WH 8501] COG0162: Tyrosyl-tRNA synthetase [Cytophaga hutchinsonii] COG0270: Site-specific DNA methylase [Methanococcoides burtonii DSM 6242]	Nostoc sp. PCC 7120 DNA, complete genome	86	3.4.21.2 6.00E-076 6.1.1.1
12235, 12236	6968709	35	2.00E-43	Campylobacter jejuni subsp. jejuni NCTC 11168	putative integral membrane protein [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282423.1 putative integral membrane protein [Campylobacter jejuni subsp. jejuni NCTC 11168] pir F81335 probable integral membrane protein Cj1276c [imported] - Campylobacter jejuni (strain NCTC 11168)			
12239, 12240	20808111	28	1.00E-10	Thermoanaerobact er tengcongensis MB4	MutS-like ATPases involved in mismatch repair, family 1 [Thermoanaerobacter tengcongensis MB4] gb AAM24886.1 MutS-like ATPases involved in mismatch repair, family 1 [Thermoanaerobacter tengcongensis MB4] sp Q8R9D0 MUS2_THETN MutS2 protein			
12241, 12242	37527394	29	6.00E-20	Photorhabdus luminescens subsp. laumondii TTO1	hypothetical protein plu3521 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15894.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1]			
12243, 12244	34556470	50	4.00E-47	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09185.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes]			2.7.-.-
12245, 12246	34396443	33	2.00E-21	Porphyrromonas gingivalis W83	hypothetical protein PG0290 [Porphyrromonas gingivalis W83] ref NP_904610.1 hypothetical protein PG0290 [Porphyrromonas gingivalis W83]			

12247,	57233639	38	3.00E-36	Dehalococcoides ethenogenes 195	DNA internalization-related competence protein ComEC/Rec2 [Dehalococcoides ethenogenes 195] gb AAW39144.1 DNA internalization-related competence protein ComEC/Rec2 [Dehalococcoides ethenogenes 195]				
12248,	46119473	48	9.00E-40	Crocospaera watsonii WH 8501	COG2200: FOG: EAL domain [Crocospaera watsonii WH 8501]				
12249,	48855955	45	6.00E-16	Cytophaga hutchinsonii	COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii]				1.11.1.5
12250,	29346292	50	1.00E-43	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0882 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75989.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
12251,	48832069	36	8.00E-31	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] putative outer membrane protein [Bacteroides fragilis YCH46]				2.7.3.-
12252,	53713571	29	4.00E-22	Bacteroides fragilis YCH46	COG1666: Uncharacterized protein conserved in bacteria [Desulfovibrio desulfuricans G20]				
12253,	23474131	50	1.00E-42	Desulfovibrio desulfuricans G20					
12254,									
12255,									
12256,									
12257,									
12258,									
12259,									
12260,									
12261,									
12262,	48855897	64	9.00E-99	Cytophaga hutchinsonii	COG1123: ATPase components of various ABC-type transport systems, contain duplicated ATPase [Cytophaga hutchinsonii]				
12263,	13542183	48	3.00E-46	Thermoplasma volcanium GSS1	Pyruvate-formate lyase-activating enzyme [Thermoplasma volcanium GSS1]				1.97.1.4
12264,				Wolinella succinogenes DSM 1740	hypothetical protein WS0005 [Wolinella succinogenes DSM 1740] emb CAE09179.1 hypothetical protein [Wolinella succinogenes]				4.1.2.25
12265,	34556464	30	5.00E-07	Thermoanaerobacter tengcongensis MB4	predicted Zn-dependent protease and their inactivated homologs [Thermoanaerobacter tengcongensis MB4] predicted Zn-dependent protease and their inactivated homologs [Thermoanaerobacter tengcongensis MB4]				
12266,									
12267,									
12268,									
12269,									
12270,	20809066	48	6.00E-67	Thermoanaerobacter tengcongensis MB4					3.4.24.-

12271, 12272	17934430	38	4.00E-29	Agrobacterium tumefaciens str. C58	chemotaxis methyltransferase [Agrobacterium tumefaciens str. C58] gb AAL41536.1 chemotaxis methyltransferase [Agrobacterium tumefaciens str. C58] gb AAK86332.1 AGR_C_914p [Agrobacterium tumefaciens str. C58] gb AAC25078.1 CheR homolog [Agrobacterium tumefaciens str. C58] ref NP_353547.1 hypothetical protein AGR_C_914 [Agrobacterium tumefaciens str. C58] pir AB2640 chemotaxis methyltransferase [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir C97422 cheR homolog (AF044495) [imported] - Agrobacterium tumefaciens (strain C58, Cereon) (AF044495) [imported]				2.1.1.80
12273, 12274	39935922	23	7.00E-10	Rhodopseudomonas s. palustris CGA009	hypothetical protein RPA2857 [Rhodopseudomonas palustris CGA009] emb CAE28298.1 unknown protein [Rhodopseudomonas palustris CGA009]				
12275, 12276	38482512	35	2.00E-38	Photobacterium luminescens	putative toxin transporter [Photobacterium luminescens] HlyD family secretion protein [Pseudomonas putida KT2440] gb AAN70493.1 HlyD family secretion protein [Pseudomonas putida KT2440]				
12277, 12278	26991604	35	5.00E-10	Pseudomonas putida KT2440	hypothetical protein PBPRB0708 [Photobacterium profundum SS9] emb CAG22580.1 hypothetical protein [Photobacterium profundum]				
12279, 12280	54302387	41	3.00E-59	Photobacterium profundum SS9	weak similarity to chloramphenicol phosphotransferase [Mesorhizobium loti MAFF303099] db BAB50605.1 ml3789 [Mesorhizobium loti MAFF303099]				
12281, 12282	13473252	34	2.00E-22	Mesorhizobium loti MAFF303099	COG0500: SAM-dependent methyltransferases [Nostoc punctiforme PCC 73102]				
12285, 12286	23129257	39	6.00E-23	Nostoc punctiforme PCC 73102	2-isopropylmalate synthase [Clostridium acetobutylicum ATCC 824] gb AAK78254.1 2-isopropylmalate synthase [Clostridium acetobutylicum ATCC 824] pir C96933 2-isopropylmalate synthase [imported] - Clostridium acetobutylicum sp Q97MC5 LEU1_CLOAB 2-isopropylmalate synthase (Alpha-isopropylmalate synthase) (Alpha-IPM synthetase) DIGUANYLATE CYCLASE (FRAGMENT) [Wolnella succinogenes DSM 1740] emb CAE10122.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolnella succinogenes]			4.1.3.12	
12287, 12288	15893565	50	2.00E-59	Clostridium acetobutylicum ATCC 824	GGDEF FAMILY PROTEIN [Wolnella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolnella succinogenes]				2.7.3.-
12289, 12290	34557407	31	3.00E-30	Wolnella succinogenes DSM 1740	ENSANGP00000000374 [Anopheles gambiae] putative endonuclease [Bacteroides fragilis YCH46] db BAD48444.1 putative endonuclease [Bacteroides fragilis YCH46]				3.4.21.-
12291, 12292	34556560	36	2.00E-38	Wolnella succinogenes DSM 1740					3.1.30.-
12293, 12294	31195611	57	4.00E-87	Anopheles gambiae					
12295, 12296	53712986	46	1.00E-12	Bacteroides fragilis YCH46					

12297,	48854967	55	4.00E-25	Cytophaga hutchinsonii	COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii]				
12298					hypothetical protein PA0172 [Pseudomonas aeruginosa PAO1] pir[E83623]				
12299,				Pseudomonas	hypothetical protein PA0172 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_248862.1 hypothetical protein PA0172 [Pseudomonas aeruginosa PAO1]				2.7.3.-
12300	9946005	33	2.00E-28	aeruginosa PAO1	pilus assembly protein [Bradyrhizobium japonicum USDA 110]				
12301,				Bradyrhizobium japonicum USDA 110	dbj BAC46701.1 pilus assembly protein [Bradyrhizobium japonicum USDA 110]				
12302	27376547	32	3.00E-28	110	hypothetical protein MMP1269 [Methanococcus maripaludis S2]				
12303,				Methanococcus maripaludis S2	emb CAF30825.1 unnamed protein product [Methanococcus maripaludis S2]				
12304	45358832	50	5.00E-23	maripaludis S2	lactoylglutathione lyase and related protein [Bacteroides fragilis YCH46]				4.4.1.5
12309,				Bacteroides fragilis YCH46	dbj BAD50032.1 lactoylglutathione lyase and related protein [Bacteroides fragilis YCH46]				
12310	53714574	65	9.00E-46	YCH46	fragilis YCH46]				
1231,				Bacteroides thetaiotaomicron VPI-5482	L-aspartate oxidase [Bacteroides thetaiotaomicron VPI-5482]				1.4.3.16
1232	29348593	50	1.00E-33	VPI-5482	gb AAO78290.1 L-aspartate oxidase [Bacteroides thetaiotaomicron VPI-5482]				
					histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_712713.1 two-component hybrid sensor and regulator [Leptospira interrogans serovar Lai str. 56601]				
12313,				Leptospira interrogans serovar Copenhageni str.	gb AAN49731.1 two-component hybrid sensor and regulator [Leptospira interrogans serovar lai str. 56601] gb AAS70039.1 histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				2.7.3.-
12314	45657316	34	6.00E-26	Flocruz L1-130					
12315,				Wolinella succinogenes DSM 1740	hypothetical protein WS2202 [Wolinella succinogenes DSM 1740]				
12316	34558477	36	8.00E-15	1740	emb CAE11192.1 hypothetical protein [Wolinella succinogenes]				
				Wolinella succinogenes DSM 1740	hypothetical protein WS1135 [Wolinella succinogenes DSM 1740]				
12317,				Wolinella succinogenes DSM 1740	emb CAE10224.1 hypothetical protein [Wolinella succinogenes]				
12318	34557509	53	8.00E-55	1740	hypothetical protein BF0900 [Bacteroides fragilis YCH46] dbj BAD47651.1			92 3.00E-11	
12321,				Bacteroides fragilis YCH46	hypothetical protein [Bacteroides fragilis YCH46]				2.7.3.-
12322	53712193	32	7.00E-14	YCH46					
				Leptospira interrogans serovar Lai str. 56601	Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601]				
12323,				Leptospira interrogans serovar Lai str. 56601					
12324	24214122	35	8.00E-32	Lai str. 56601					
12325,				Cytophaga hutchinsonii	COG4261: Predicted acyltransferase [Cytophaga hutchinsonii]				
12326	48856697	30	4.00E-22	hutchinsonii					

12329, 12330	34557169	37	9.00E-47	Wolinella succinogenes DSM 1740	ACRIFLAVIN RESISTANCE A PRECURSOR [Wolinella succinogenes DSM 1740] emb CAE09884.1 ACRIFLAVIN RESISTANCE A PRECURSOR [Wolinella succinogenes]				
1233, 1234	15606535	25	1.00E-09	Aquifex aeolicus VF5	hypothetical protein aq_1332 [Aquifex aeolicus VF5] gb AAC07320.1 hypothetical protein [Aquifex aeolicus VF5] pir D70415 conserved hypothetical protein aq_1332 - Aquifex aeolicus				
12331, 12332	34556919	27	8.00E-09	Wolinella succinogenes DSM 1740	hypothetical protein WS0496 [Wolinella succinogenes DSM 1740] emb CAE09634.1 hypothetical protein [Wolinella succinogenes]				
12333, 12334	34557848	59	2.00E-74	Wolinella succinogenes DSM 1740	conserved hypothetical protein-2-methylthioadenine synthetase [Wolinella succinogenes DSM 1740] emb CAE10563.1 conserved hypothetical protein- 2-methylthioadenine synthetase [Wolinella succinogenes]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6	89	5.00E-07	1.8--
12335, 12336	AAW9853 5	56	1.00E-36		Desc:H. pylori GHPO 1479 protein. Org:Helicobacter pylori dnaA, probable chromosomal replication initiator protein [Wolinella succinogenes DSM 1740] emb CAE09174.1 dnaA, probable chromosomal replication initiator protein [Wolinella succinogenes]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6	95	2.00E-08	1.8--
12337, 12338	34556459	64	4.00E-82	Wolinella succinogenes DSM 1740	hypothetical protein WS0806 [Wolinella succinogenes DSM 1740] emb CAE09919.1 conserved hypothetical protein [Wolinella succinogenes]				
12339, 12340	34557204	38	8.00E-40	Wolinella succinogenes DSM 1740	(MiaB-like tRNA modifying enzyme [Campylobacter coli RM2228] gb EAL56394.1 MiaB-like tRNA modifying enzyme [Campylobacter coli RM2228])	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6	89	4.00E-07	1.8--
12341, 12342	57168872	56	2.00E-54	Campylobacter coli RM2228	hypothetical protein WS1513 [Wolinella succinogenes DSM 1740] emb CAE10561.1 conserved hypothetical protein [Wolinella succinogenes]				
12345, 12346	34557846	43	9.00E-35	Wolinella succinogenes DSM 1740	COG0006: Xaa-Pro aminopeptidase [Crocospaera watsonii WH 8501]				3.4, 11.9
12347, 12348	45525497	37	2.00E-38	Crocospaera watsonii WH 8501	COG0195: Transcription elongation factor [Cytophaga hutchinsonii]				
1235, 1236	48853541	41	7.00E-29	Cytophaga hutchinsonii	phosphatase, YrbI family [Campylobacter jejuni RM1221] gb AAW34543.1 phosphatase, YrbI family [Campylobacter jejuni RM1221]				3.1, 3.29
12351, 12352	57236960	57	6.00E-29	Campylobacter jejuni RM1221					

12353, 12354, 12357, 12358	24374626 14600147 29654029	47 39 48	3.00E-35 4.00E-47 1.00E-26	Shewanella oneidensis MR-1 Coxiella burnetii Coxiella burnetii RSA 493	hypothetical protein SO3107 [Shewanella oneidensis MR-1] gb AAN56113.1 conserved hypothetical protein [Shewanella oneidensis MR-1] S-adenosyl-dependent methyl transferase [Coxiella burnetii] NDP-hexose 3-C-methyltransferase TyICIII [Coxiella burnetii RSA 493] gb AAO90235.1 NDP-hexose 3-C-methyltransferase TyICIII [Coxiella burnetii RSA 493] conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55403.1 conserved hypothetical protein [Campylobacter lari RM2100] alanine racemase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir A81364 alanine racemase (EC 5.1.1.1) Cj0905c [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282058.1 alanine racemase [Campylobacter jejuni subsp. jejuni NCTC 11168] sp Q9PP26 ALR_CAMJE Alanine racemase			2.1.1.- 2.1.1.-
12363, 12364	57240289	56	4.00E-35	Campylobacter lari RM2100	hypothetical protein Avar03006438 [Anabaena variabilis ATCC 29413]			
12369, 12370	6968343	42	2.00E-34	Campylobacter jejuni subsp. jejuni NCTC 11168	RNA POLYMERASE SIGMA FACTOR [Wolonia succinogenes DSM 1740] emb CAE10900.1 RNA POLYMERASE SIGMA FACTOR [Wolonia succinogenes]	83	7.00E-28	5.1.1.1
12371, 12372	48134374	46	9.00E-07	Anabaena variabilis ATCC 29413	COG0151: Phosphoribosylamine-glycine ligase [Cytophaga hutchinsonii] gb AAV81405.1 Dihydrofolate reductase [Bacillus cereus ATCC 14579] gb AAP09158.1 Dihydrofolate reductase [Bacillus cereus ATCC 14579]			6.3.4.13 1.5.1.3
12373, 12374	34558185	81	1.00E-103	Wolonia succinogenes DSM 1740	Nucleoside-diphosphate-sugar epimerase [Idiomarina loihiensis L2TR] gb AAV81405.1 Nucleoside-diphosphate-sugar epimerase [Idiomarina loihiensis L2TR]			
12375, 12376	48855741	62	1.00E-46	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]			
12377, 12378	30020326	50	8.00E-40	Bacillus cereus ATCC 14579	exch nuclease ABC subunit C [Bacteroides thetaiotaomicron VPI-5482] gb AAO78372.1 exch nuclease ABC subunit C [Bacteroides thetaiotaomicron VPI-5482]	90	5.00E-12	5.1.3.-
12379, 12380	56459673	65	7.00E-51	Idiomarina loihiensis L2TR				
12383, 12384	48855208	53	6.00E-52	Cytophaga hutchinsonii				
12385, 12386	29348675	58	6.00E-74	Bacteroides thetaitaomicron VPI-5482				

12387,	34556919	27	8.00E-09	Wolinella succinogenes DSM 1740	hypothetical protein WS0496 [Wolinella succinogenes DSM 1740] emb CAE09634.1 hypothetical protein [Wolinella succinogenes]				
12388					outer membrane assembly protein [Bacteroides fragilis YCH46]				
12389,	53712279	31	1.00E-37	Bacteroides fragilis YCH46	dbj BAD47737.1 outer membrane assembly protein [Bacteroides fragilis YCH46]				
12390									
1239,									
1240	48854815	64	2.00E-48	Cytophaga hutchinsonii	COG0719: ABC-type transport system involved in Fe-S cluster assembly, permease component [Cytophaga hutchinsonii]				
12391,									
12392	48845271	47	6.00E-54	Geobacter metallireducens GS-15	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]				2.7.3.-
12393,									
12394	34557715	26	4.00E-16	Wolinella succinogenes DSM 1740	hypothetical protein WS1362 [Wolinella succinogenes DSM 1740] emb CAE10430.1 hypothetical protein [Wolinella succinogenes]				
12395,									
12396	29349781	31	1.00E-16	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT4373 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79478.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482]				
12397,									
12398	48853591	57	1.00E-85	Cytophaga hutchinsonii	COG1021: Peptide arylation enzymes [Cytophaga hutchinsonii]				
12401,									
12402	53714372	28	6.00E-07	Bacteroides fragilis YCH46	hypothetical protein BF5085 [Bacteroides fragilis YCH46] dbj BAD49830.1 hypothetical protein [Bacteroides fragilis YCH46]				
12403,									
12404	23474406	25	3.00E-12	Desulfovibrio desulfuricans G20	COG1887: Putative glycosylglycerophosphate transferases involved in teichoic acid biosynthesis TagF/TagB/EpsJ/RodC [Desulfovibrio desulfuricans G20]				
12405,									
12406	29347060	39	1.00E-18	Bacteroides thetaiotaomicron VPI-5482	putative teichoic acid biosynthesis protein F [Bacteroides thetaiotaomicron VPI-5482] gb AAO76757.1 putative teichoic acid biosynthesis protein F [Bacteroides thetaiotaomicron VPI-5482]				
1241,									
1242	55163168	34	9.00E-25	Yersinia enterocolitica	putative NTP-binding protein [Yersinia enterocolitica]				
12411,									
12412	37682097	27	3.00E-08	Danilo rerio	KIAA1706-like protein [Danilo rerio] ref NP_991322.1 hypothetical protein zgc:77395 [Danilo rerio]				
12413,									
12414	53714342	51	8.00E-48	Bacteroides fragilis YCH46	phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide (ProFAR) isomerase [Bacteroides fragilis YCH46] dbj BAD49800.1 phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide (ProFAR) isomerase [Bacteroides fragilis YCH46]				5.3.1.16
12415,									
12416	3769356	40	2.00E-29	Helicobacter pylori	lcaA1 [Helicobacter pylori]				3.1.21.4
12417,									
12418	47095888	39	4.00E-21	Listeria monocytogenes str. 1/2a F6854	DNA helicase II, putative [Listeria monocytogenes str. 1/2a F6854] gb EAL06694.1 DNA helicase II, putative [Listeria monocytogenes str. 1/2a F6854]				

12419, 12420	45523887	26	1.00E-09	Crocospaera watsonii WH 8501	COG5433: Transposase [Crocospaera watsonii WH 8501]			
12425, 12426	29347740	28	9.00E-25	Bacteroides thetataomicron VPI-5482	hypothetical protein BT2330 [Bacteroides thetataomicron VPI-5482] gb AAO77437.1 hypothetical protein [Bacteroides thetataomicron VPI-5482]			
12427, 12428	51244378	32	7.00E-32	Desulfotalea psychrophila Lsv54	related to ATP-dependent dsDNA exonuclease (SBCC) [Desulfotalea psychrophila Lsv54] embjCAG35255.1 related to ATP-dependent dsDNA exonuclease (SBCC) [Desulfotalea psychrophila Lsv54]			3.1.11.-
12429, 12430	47778428	35	2.00E-22	Bacillus anthracis str. 'Ames 'Ancestor'	response regulator lytR [Bacillus anthracis str. 'Ames Ancestor'] ref YP_039431.1 response regulator [Bacillus thuringiensis serovar konkukian str. 97-27] ref YP_031532.1 response regulator LytR [Bacillus anthracis str. Sterne] ref NP_847837.1 response regulator LytR [Bacillus anthracis str. Ames] ref NP_653909.1 response_reg. Response regulator receiver domain [Bacillus anthracis str. A2012] gb AAP29323.1 response regulator LytR [Bacillus anthracis str. Ames] gb AAT62659.1 response regulator [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAT35470.1 response regulator LytR [Bacillus anthracis str. 'Ames Ancestor'] gb AAT57582.1 response regulator LytR [Bacillus anthracis str. Sterne] sp Q81JL3 LYT_BACAN Sensory transduction protein lytJ			3.1.1.61
12437, 12438	29346033	45	1.00E-18	Bacteroides thetataomicron VPI-5482	putative UDP-glucose 4-epimerase [Bacteroides thetataomicron VPI-5482] gb AAO75730.1 putative UDP-glucose 4-epimerase [Bacteroides thetataomicron VPI-5482]			5.1.3.2
12443, 12444	48862917	75	1.00E-121	Microbulbifer degradans 2-40	COG3459: Cellobiose phosphorylase [Microbulbifer degradans 2-40]	Clostridium thermocellum YM4 cellobiose phosphorylase (cbp) gene, complete cds	83	1.00E-11 2.4.1.20
12447, 12448	18977730	29	6.00E-12	Pyrococcus furfosus DSM 3638	glycosyl transferase [Pyrococcus furiosus DSM 3638] gb AAL81482.1 glycosyl transferase [Pyrococcus furiosus DSM 3638]			
12451, 12452	ABB6448 3	24	1.00E-07		Desc:Drosophila melanogaster polypeptide SEQ ID NO 20241. Org:Drosophila melanogaster			

12455, 12456	18977973	33	3.00E-07	Pyrococcus furius DSM 3638	transcriptional regulatory protein, asnC family [Pyrococcus furius DSM 3638] gblAAL81725.1] transcriptional regulatory protein, asnC family [Pyrococcus furius DSM 3638] gblAAD20389.1] transcriptional regulator LrpA [Pyrococcus furius] plj]T46972 transcription regulator lrpA [validated] - Pyrococcus furius pdb]111G]B Chain B, Crystal Structure Of The Lrp-Like Transcriptional Regulator From The Archaeon Pyrococcus Furius (pdb]111G]A Chain A, Crystal Structure Of The Lrp-Like Transcriptional Regulator From The Archaeon Pyrococcus Furius sp]P42180]REG7_PYRFU HTH-type transcriptional regulator lrpA				
12457, 12458	29348750	38	7.00E-30	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3341 [Bacteroides thetaiotaomicron VPI-5482] gblAAO78447.1] conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
12459, 12460	29347220	45	7.00E-15	Bacteroides thetaiotaomicron VPI-5482	GAF domain-containing protein, involved in signal transduction [Bacteroides thetaiotaomicron VPI-5482] gblAAO76917.1] GAF domain-containing protein, involved in signal transduction [Bacteroides thetaiotaomicron VPI-5482]				
12461, 12462	53715640	44	4.00E-52	Bacteroides fragilis YCH46	Xaa-Pro aminopeptidase [Bacteroides fragilis YCH46] dbj]BAD51098.1] Xaa-Pro aminopeptidase [Bacteroides fragilis YCH46]				3.4.13.9
12463, 12464	53685204	25	3.00E-12	Desulfotobacterium hafnense DCB-2	COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Desulfotobacterium hafnense DCB-2]				1.2.1.2
12465, 12466	45505347	41	8.00E-35	Anabaena variabilis ATCC 29413	COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Anabaena variabilis ATCC 29413]				1.1.1.10 0
12467, 12468	42522911	31	2.00E-21	Bdellovibrio bacteriovorus HD100	hypothetical protein Bd1393 [Bdellovibrio bacteriovorus HD100] emb]CAE79284.1] hypothetical protein predicted by Glimmer/Critica [Bdellovibrio bacteriovorus HD100]				
12469, 12470	34556972	51	3.00E-16	Wolinella succinogenes DSM 1740	SERINE ACETYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb]CAE09687.1] SERINE ACETYLTRANSFERASE [Wolinella succinogenes]				
1247, 1248	20807036	39	5.00E-23	Thermoanaerobacter tengcongensis MB4	predicted ATPase or kinase [Thermoanaerobacter tengcongensis MB4] gblAAM23811.1] predicted ATPase or kinase [Thermoanaerobacter tengcongensis MB4]				
12471, 12472	21673150	45	5.00E-53	Chlorobium tepidum TLS	isoleucyl-tRNA synthetase [Chlorobium tepidum TLS] gblAAM71557.1] isoleucyl-tRNA synthetase [Chlorobium tepidum TLS]				6.1.1.5
12473, 12474	48853745	32	6.00E-50	Cytophaga hutchinsonii	hypothetical protein Chut02003380 [Cytophaga hutchinsonii]				
12477, 12478	48833211	45	2.00E-31	Magnetococcus sp. MC-1	COG2114: Adenylate cyclase, family 3 (some proteins contain HAMP domain) [Magnetococcus sp. MC-1]				4.6.1.1

12479, 12480	53711472	40	1.00E-13	Bacteroides fragilis YCH46	signal peptidase I [Bacteroides fragilis YCH46] dbj BAD46930.1 signal peptidase I [Bacteroides fragilis YCH46]			
12485, 12486	34558058	64	1.00E-100	Wolinella succinogenes DSM 1740	OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE [Wolinella succinogenes DSM 1740] emb CAE10773.1 OXYGEN- INDEPENDENT COPROPORPHYRINOGEN III OXIDASE [Wolinella succinogenes]	Wolinella succinogenes, complete genome; segment 5/7	83	1.00E-08 1.-.-.-
12489, 12490	16648662	27	1.00E-11	Edwardsiella ictaluri	UDP-glucose 4-epimerase [Edwardsiella ictaluri]			5.1.3.-
12491, 12492	15643366	56	8.00E-77	Thermotoga maritima MSB8	hypothetical protein TM0600 [Thermotoga maritima MSB8] gb AAD35685.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir A72358 conserved hypothetical protein - Thermotoga maritima (strain MSB8)			
12493, 12494	48839007	27	8.00E-27	Methanosarcina barkeri str. fusaro	COG1721: Uncharacterized conserved protein (some members contain a von Willebrand factor type A (VWA) domain) [Methanosarcina barkeri str. fusaro]			
12495, 12496	34557573	38	9.00E-39	Wolinella succinogenes DSM 1740	SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes]			2.7.3.-
12497, 12498	46202456	42	7.00E-51	Magnetospirillum magnetotacticum MS-1	COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1]			2.7.3.-
12499, 12500	46202456	29	7.00E-12	Magnetospirillum magnetotacticum MS-1	COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1]			
12501, 12502	39937848	39	3.00E-25	Rhodopseudomonas palustris CGA009	response regulator receiver:histidine kinase [Rhodopseudomonas palustris CGA009] emb CAE30230.1 response regulator receiver:histidine kinase [Rhodopseudomonas palustris CGA009]			2.7.3.-
12505, 12506	20091276	47	2.00E-22	Methanosarcina acetivorans C2A	response regulator receiver [Methanosarcina acetivorans C2A] gb AAM05831.1 response regulator receiver [Methanosarcina acetivorans str. C2A]			2.7.3.-
12507, 12508	53735771	34	3.00E-18	Crocospaera watsonii WH 8501	hypothetical protein Cwat03001968 [Crocospaera watsonii WH 8501]			
12509, 12510	48853585	34	4.00E-31	Cytophaga hutchinsonii	COG0768: Cell division protein FtsI/penicillin-binding protein 2 [Cytophaga hutchinsonii]			
12511, 12512	48856170	29	3.00E-24	Cytophaga hutchinsonii	COG1452: Organic solvent tolerance protein OstA [Cytophaga hutchinsonii]			
12515, 12516	48853184	25	6.00E-09	Ferroplasma acidarmanus	COG3547: Transposase and inactivated derivatives [Ferroplasma acidarmanus]			
12517, 12518	53763644	28	4.00E-11	Anabaena variabilis ATCC 29413	COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Anabaena variabilis ATCC 29413]			

12519, 12520	14521387	24	8.00E-09	Pyrococcus abyssi GE5	hypothetical protein PAB0790 [Pyrococcus abyssi GE5] emb CAB50093.1 Hypothetical protein [Pyrococcus abyssi] pir H75098 hypothetical protein PAB0790 - Pyrococcus abyssi (strain Orsay)			3.6.1.-
12521, 12522	16077745	66	1.00E-116	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU06770 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12497.1 yeeB [Bacillus subtilis subsp. subtilis str. 168] gb AA066475.1 yeeB [Bacillus subtilis] pir F69792 hypothetical protein yeeB - Bacillus subtilis	97	2.00E-07	Bacillus subtilis complete genome (section 4 of 21): from 611631 to 813719
12525, 12526	48832594	29	2.00E-17	Magnetococcus sp. MC-1	COG0438: Glycosyltransferase [Magnetococcus sp. MC-1]			
12527, 12528	51891165	48	5.00E-30	Symbiobacterium thermophilum IAM 14863	hypothetical protein STH27 [Symbiobacterium thermophilum IAM 14863] dbj BAD39012.1 conserved hypothetical protein [Symbiobacterium thermophilum IAM 14863]			
12529, 12530	48844902	50	2.00E-37	Geobacter metallireducens GS 15	COG0582: Integrase [Geobacter metallireducens GS-15]			
1253, 1254	48895710	39	8.00E-18	Trichodesmium erythraeum IMS101	hypothetical protein Tery02000770 [Trichodesmium erythraeum IMS101]			
12531, 12532	53730726	28	5.00E-12	Dechloromonas aromatica RCB	COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB]			
12535, 12536	34397371	71	1.00E-105	Porphyrromonas gingivalis W83	lysyl-tRNA synthetase [Porphyrromonas gingivalis W83] ref NP_905535.1 lysyl-tRNA synthetase [Porphyrromonas gingivalis W83] sp Q7MUU7 SYK_PORGI Lysyl-tRNA synthetase (Lysine-tRNA ligase) (LysRS)	97	7.00E-10	Mesoplasma florum L1 complete genome
12537, 12538	45157173	41	3.00E-53	Escherichia coli	endonuclease [Escherichia coli] sp P25239 T257_ECOLI Type IIS restriction enzyme Eco57I (Endonuclease Eco57I) [Includes: Adenine-specific methyltransferase activity Eco57IA (M.Eco57IA)]			
12539, 12540	57238087	53	3.00E-23	Campylobacter jejuni RM1221	peptidase, M23/M37 family [Campylobacter jejuni RM1221] gb AAW35670.1 peptidase, M23/M37 family [Campylobacter jejuni RM1221]			3.5.1.-
12541, 12542	48892348	27	8.00E-23	Trichodesmium erythraeum IMS101	COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] fibronectin/fibrinogen-binding protein, putative [Campylobacter upsaliensis RM3195] gb EAL53665.1 fibronectin/fibrinogen-binding protein, putative [Campylobacter upsaliensis RM3195]			
12543, 12544	57242203	44	3.00E-18	Campylobacter upsaliensis RM3195				
12545, 12546	23126057	22	3.00E-07	Nostoc punctiforme PCC 73102	COG0457: FOG: TPR repeat [Nostoc punctiforme PCC 73102]			

12547, 12548	48853732	48	1.00E-28	Cytophaga hutchinsonii	COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Cytophaga hutchinsonii]			3.1.1.61
12549, 12550	48853733	31	3.00E-07	Cytophaga hutchinsonii	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii]			
12551, 12552	48853332	34	1.00E-35	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]			
12555, 12556	52840989	29	3.00E-20	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	N-acetylneuraminic acid synthetase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU26841.1 N-acetylneuraminic acid synthetase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] hypothetical protein sir2110 [Synecocystis sp. PCC 6803] dbj BAA18047.1 sir2110 [Synecocystis sp. PCC 6803] pir S75486 hypothetical protein sir2110 - Synecocystis sp. (strain PCC 6803)		4.1.3.19	
12557, 12558	16330639	44	1.00E-13	Synechocystis sp. PCC 6803	FERREDOXIN DOMAIN INTEGRAL MEMBRANE [Wolinella succinogenes DSM 1740] emb CAE09765.1 FERREDOXIN DOMAIN INTEGRAL MEMBRANE [Wolinella succinogenes]			
12561, 12562	34557050	50	6.00E-31	Wolinella succinogenes DSM 1740	ABC transporter, ATP-binding protein [Campylobacter jejuni RM1221] gb AAW35635.1 ABC transporter, ATP-binding protein [Campylobacter jejuni RM1221]			1.8.-
12567, 12568	57238052	58	4.00E-65	Campylobacter jejuni RM1221	hypothetical protein PH1688 [Pyrococcus horikoshii OT3] dbj BAA30800.1 352aa long hypothetical protein [Pyrococcus horikoshii OT3] pir JA71176 hypothetical protein PH1688 - Pyrococcus horikoshii			
1257, 1258	14591451	36	1.00E-15	Pyrococcus horikoshii OT3	hypothetical protein PH1688 [Pyrococcus horikoshii OT3] dbj BAD50833.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
1257, 1258	53715375	34	3.00E-24	Bacteroides fragilis YCH46	ABC-type iron(III) transport system, ATP binding protein [Methanococcus maripaludis S2] emb CAF29754.1 ABC-type iron(III) transport system, ATP binding protein [Methanococcus maripaludis S2]			3.4.21.-
12571, 12572	45357761	37	1.00E-33	Methanococcus maripaludis S2	iron compound ABC transporter, iron compound-binding protein, putative [Staphylococcus aureus subsp. aureus COL] ref YP_185549.1 iron compound ABC transporter, iron compound-binding protein, putative [Staphylococcus aureus subsp. aureus COL]			
12573, 12574	57284261	26	9.00E-07	Staphylococcus aureus subsp. aureus COL	ferrichrome transport ATP-binding protein [Pyrococcus horikoshii OT3] dbj BAA30335.1 250aa long hypothetical ferrichrome transport ATP-binding protein [Pyrococcus horikoshii OT3] pir E71067 probable ferrichrome transport ATP-binding protein - Pyrococcus horikoshii			
12575, 12576	14591054	35	7.00E-13	Pyrococcus horikoshii OT3				

12577, 12578	2314022	59	2.00E-71	26695	Helicobacter pylori	cysteinyI-tRNA synthetase (cysS) [Helicobacter pylori 26695] pir F64630 cysteine-tRNA ligase (EC 6.1.1.16) - Helicobacter pylori (strain 26695) ref NP_207679.1 cysteinyI-tRNA synthetase (cysS) [Helicobacter pylori 26695] sp P41259 SYC_HELPY CysteinyI-tRNA synthetase (Cysteine-tRNA ligase) (CysRS)	Fusobacterium nucleatum subsp. nucleatum ATCC 25586, section 8 of 197 of the complete genome	91	6.00E-10	6.1.1.16
12579, 12580	9654643	31	4.00E-27	N16961	Vibrio cholerae O1 biovar eltor str.	lipopolysaccharide biosynthesis protein, putative [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229892.1 lipopolysaccharide biosynthesis protein, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir E82349 probable lipopolysaccharide biosynthesis protein VC0235 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				
12581, 12582	AAV4378 0	22	6.00E-08			Desc:Amino acid sequence of the eps4 of Lactobacillus helveticus LH59. Org:Lactobacillus helveticus				
12585, 12586	52082595	56	2.00E-81	14580	Bacillus licheniformis ATCC	hypothetical protein BL02386 [Bacillus licheniformis ATCC 14580] gb AAU25748.1 hypothetical protein BL02386 [Bacillus licheniformis ATCC 14580]				
12587, 12588	20808081	38	3.00E-24	MB4	Thermoanaerobact er tengcongensis	hypothetical protein TTE1654 [Thermoanaerobacter tengcongensis MB4] gb AAM24856.1 conserved hypothetical protein [Thermoanaerobacter tengcongensis MB4] sp Q8R9F8 MRZ_THETN Protein mraZ				
12589, 12590	32472855	32	6.00E-17	ba1tica SH 1	Rhodopirellula	transposase [Rhodopirellula ba1tica SH 1] emb CAD73534.1 transposase [Pirellula sp.]				
1259, 1260	53715375	36	8.00E-19	YCH46	Bacteroides fragilis	hypothetical protein BF4091 [Bacteroides fragilis YCH46] db BAD50833.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
12591, 12592	34557638	66	3.00E-31	1740	Wolinella succinogenes DSM	QUINOLINATE SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10353.1 QUINOLINATE SYNTHETASE [Wolinella succinogenes]				
12593, 12594	53713904	74	1.00E-110	YCH46	Bacteroides fragilis	excinuclease ABC subunit A [Bacteroides fragilis YCH46] db BAD49362.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46]	Coxiella burnetii strain RSA 493, section 1 of 7 of the complete genome	93	6.00E-07	
12597, 12598	33861871	33	8.00E-13	CCMP1986	Prochlorococcus marinus subsp. pastoris str.	Ketol-acid reductoisomerase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19774.1 Ketol-acid reductoisomerase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] sp Q7V0F0 ILVC_PROMP Ketol-acid reductoisomerase (Acetohydroxy-acid isomeroreductase) (Alpha-keto-beta-hydroxyacid reductoisomerase)				1.1.1.86

12599, 12600	46578913	29	1.00E-17	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	iron-sulfur cluster-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94980.1 iron-sulfur cluster-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAM06751.1 glutamate-ammonia ligase [Methanosarcina acetivorans C2A] str. C2A]					6.3.1.2
12601, 12602	20092196	60	3.00E-48	Methanosarcina acetivorans C2A	hypothetical protein DP2996 [Desulfotalea psychrophila LSV54] emb CAG37725.1 unknown protein [Desulfotalea psychrophila LSV54]					
12603, 12604	51246848	22	3.00E-07	Desulfotalea psychrophila LSV54	thiamine monophosphate synthase [Helicobacter hepaticus ATCC 51449] ref NP_861359.1 thiamine monophosphate synthase [Helicobacter hepaticus ATCC 51449]					2.5.1.3
12605, 12606	32263380	51	3.00E-17	Helicobacter hepaticus ATCC 51449	hypothetical protein Chut02003091 [Cytophaga hutchinsonii]					
12613, 12614	48854003	30	1.00E-18	Cytophaga hutchinsonii	COG0726: Predicted xylanase/chitin deacetylase [Magnetospirillum magnetotacticum MS-1]					
12615, 12616	46201112	30	3.00E-22	Magnetospirillum magnetotacticum MS-1	flavocytochrome C sulfide dehydrogenase [Aquifex aeolicus VF5] gb AAC06555.1 flavocytochrome C sulfide dehydrogenase [Aquifex aeolicus VF5] pir B70321 flavocytochrome C sulfide dehydrogenase - Aquifex aeolicus					1.8.2.-
12617, 12618	15605781	42	1.00E-57	Aquifex aeolicus VF5	hypothetical iron-regulated protein [Photobacterium profundum SS9] emb CAG21164.1 hypothetical iron-regulated protein [Photobacterium profundum]					
12619, 12620	54309946	31	2.00E-21	Photobacterium profundum SS9	iron transport protein [Synechocystis sp. PCC 6803] dbj BAA16842.1 iron transport protein [Synechocystis sp. PCC 6803] pir S74691 iron transport protein - Synechocystis sp. (strain PCC 6803)					
12625, 12626	16329434	51	1.00E-72	Synechocystis sp. PCC 6803	Carbamoyltransferase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19705.1 Carbamoyltransferase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]					2.-.-.-
12629, 12630	33861802	41	2.00E-32	Prochlorococcus marinus subsp. pastoris str. CCMP1986	DNA POLYMERASE III SUBUNITS GAMMA AND TAU [Wolinnella succinogenes DSM 1740] emb CAE11094.1 DNA POLYMERASE III SUBUNITS GAMMA AND TAU [Wolinnella succinogenes]					2.7.7.7
12633, 12634	34558379	38	1.00E-45	Wolinnella succinogenes DSM 1740	Desc: Mouse protein kinase #5. Org: Mus sp					2.7.1.-
12635, 12636	AAY4394 1	41	1.00E-09	Wolinnella succinogenes DSM 1740	CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN [Wolinnella succinogenes DSM 1740] emb CAE11050.1 CARBAMOYL-PHOSPHATE SYNTHASE SMALL CHAIN [Wolinnella succinogenes]					6.3.5.5

12639, 12640	34558810	33	1.00E-27	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09525.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]			2.7.3.-
12641, 12642	45655762	29	8.00E-25	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	response regulator [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714779.1 probable protein contain EAL family signaling protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51794.1 probable protein contain EAL family signaling protein [Leptospira interrogans serovar lai str. 56601] gb AAS72208.1 response regulator [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			
12643, 12644	13474570	29	2.00E-26	Mesorhizobium loti MAFF303099	hypothetical protein mlf5479 [Mesorhizobium loti MAFF303099] db BAB51925.1 mlf5479 [Mesorhizobium loti MAFF303099]			
12649, 12650	57238220	50	3.00E-22	Campylobacter jejuni RM1221	DNA polymerase III, delta prime subunit, homolog [Campylobacter jejuni RM1221] gb AAW35803.1 DNA polymerase III, delta prime subunit, homolog [Campylobacter jejuni RM1221]			2.7.7.7
1265, 1266	53714275	44	7.00E-27	Bacteroides fragilis YCH46	UDP-N-acetylenolpyruvoylglucosamine reductase [Bacteroides fragilis YCH46] db BAD49733.1 UDP-N-acetylenolpyruvoylglucosamine reductase [Bacteroides fragilis YCH46]			1.1.1.15 8
12651, 12652	48857483	42	5.00E-18	Clostridium thermocellum ATCC 27405	COG2217: Cation transport ATPase [Clostridium thermocellum ATCC 27405]			3.6.3.4
12653, 12654	53612326	49	8.00E-53	Azotobacter vinelandii	COG1391: Glutamine synthetase adenylyltransferase [Azotobacter vinelandii]			2.7.7.42
12655, 12656	54311293	36	3.00E-35	Xenopus laevis	Unknown (protein for MGC:86416) [Xenopus laevis]			1.1.3.8
12657, 12658	34558426	59	6.00E-74	Wolinella succinogenes DSM 1740	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN [Wolinella succinogenes DSM 1740] emb CAE11141.1 CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN [Wolinella succinogenes]	Efflatouniella aegyptiaca CAD (r) gene, partial cds	87	4.00E-08 6.3.5.5
12659, 12660	34557622	75	4.00E-89	Wolinella succinogenes DSM 1740	PREPROTEIN TRANSLOCASE SECA SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10337.1 PREPROTEIN TRANSLOCASE SECA SUBUNIT [Wolinella succinogenes]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6	79	1.00E-32
12663, 12664	53766156	34	2.00E-17	Rubrobacter xylanophilus DSM 9941	COG1583: Uncharacterized protein predicted to be involved in DNA repair (RAMP superfamily) [Rubrobacter xylanophilus DSM 9941]			
12665, 12666	57237408	40	4.00E-19	Campylobacter jejuni RM1221	phosphatase, Ppx/GppA family [Campylobacter jejuni RM1221] gb AAW34991.1 phosphatase, Ppx/GppA family [Campylobacter jejuni RM1221]			3.6.1.40

12667, 12668	29346111	55	8.00E-58	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0701 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75808.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]	Bacteroides fragilis YCH46 DNA, complete genome	86	5.00E-07		
12669, 12670	34556867	54	1.00E-47	Wolinella succinogenes DSM 1740	PUTATIVE HOLLIDAY JUNCTION DNA HELICASE [Wolinella succinogenes DSM 1740] emb CAE09582.1 PUTATIVE HOLLIDAY JUNCTION DNA HELICASE [Wolinella succinogenes] sp Q7MA70 RUVA_WOLSU Holliday junction DNA helicase ruva conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55132.1 conserved hypothetical protein [Campylobacter lari RM2100]					
12671, 12672	57240739	51	4.00E-24	Campylobacter lari RM2100						
12673, 12674	34558426	73	4.00E-95	Wolinella succinogenes DSM 1740	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN [Wolinella succinogenes DSM 1740] emb CAE11141.1 CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN [Wolinella succinogenes] aspartate carbamoyltransferase [Campylobacter lari RM2100] gb EAL55577.1 aspartate carbamoyltransferase [Campylobacter lari RM2100]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 1/6	81	5.00E-41	6.3.5.5	
12675, 12676	57240463	54	3.00E-40	Campylobacter lari RM2100						2.1.3.2
12677, 12678	42628871	31	2.00E-10	Haemophilus influenzae R2846	COG0147: Anthranilate/para-aminobenzoate synthases component I [Haemophilus influenzae R2846]					4.1.3.-
12679, 12680	34557248	36	2.00E-25	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09963.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes]					
12681, 12682	34557101	40	2.00E-19	Wolinella succinogenes DSM 1740	hypothetical protein WS0690 [Wolinella succinogenes DSM 1740] emb CAE09816.1 conserved hypothetical protein [Wolinella succinogenes]					4.-.-.-
12683, 12684	34556480	65	5.00E-76	Wolinella succinogenes DSM 1740	GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes DSM 1740] emb CAE09195.1 GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes]					2.6.1.16
12685, 12686	15606338	64	2.00E-87	Aquifex aeolicus VF5	phosphate transport ATP binding protein [Aquifex aeolicus VF5] gb AAC07112.1 phosphate transport ATP binding protein [Aquifex aeolicus VF5] pir G70390 phosphate transport ATP binding protein - Aquifex aeolicus sp O67154 PSTB_AQUAE Phosphate import ATP-binding protein pstB (Phosphate-transporting ATPase) [ABC phosphate transporter] hypothetical protein aq_367 [Aquifex aeolicus VF5] gb AAC06656.1 hypothetical protein [Aquifex aeolicus VF5] pir G70332 conserved hypothetical protein aq_367 - Aquifex aeolicus					3.4.21.-
12687, 12688	15605874	29	6.00E-09	Aquifex aeolicus VF5						

12689, 12690	34556462	70	3.00E-48	Wolonia succinogenes DSM 1740	hypothetical protein WS0003 [Wolonia succinogenes DSM 1740] emb CAE09177.1 conserved hypothetical protein [Wolonia succinogenes]			
12691, 12692	15606018	42	1.00E-34	Aquifex aeolicus VF5	hypothetical protein aq_563 [Aquifex aeolicus VF5] gb AAC06808.1 hypothetical protein [Aquifex aeolicus VF5] pir G70350 conserved hypothetical protein aq_563 - Aquifex aeolicus			2.7.3.-
12693, 12694	52842284	57	9.00E-88	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	reverse transcriptase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28136.1 reverse transcriptase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			2.7.7.49
12695, 12696	34556575	60	5.00E-97	Wolonia succinogenes DSM 1740	PUTATIVE FORMATE DEHYDROGENASE, ALPHA SUBUNIT [Wolonia succinogenes DSM 1740] emb CAE09290.1 PUTATIVE FORMATE DEHYDROGENASE, ALPHA SUBUNIT [Wolonia succinogenes]			1.2.1.2
12697, 12698	53714874	38	3.00E-26	Bacteroides fragilis YCH46	putative outer membrane protein [Bacteroides fragilis YCH46] dbj BAD50332.1 putative outer membrane protein [Bacteroides fragilis YCH46]			
12701, 12702	24375806	25	1.00E-16	Shewanella oneidensis MR-1	GGDEF domain protein [Shewanella oneidensis MR-1] gb AAN57293.1 GGDEF domain protein [Shewanella oneidensis MR-1]			2.7.3.-
12703, 12704	6967929	65	1.00E-89	Campylobacter jejuni subsp. jejuni NCTC 11168	hypothetical protein Cj0458c [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281645.1 hypothetical protein Cj0458c [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81390 hypothetical protein Cj0458c [Imported] - Campylobacter jejuni (strain NCTC 11168)			1.8.-
12705, 12706	57240857	64	1.00E-60	Campylobacter lari RM2100	tRNA-(6)A37 thiotransferase enzyme MiaB [Campylobacter lari RM2100] gb EAL55250.1 tRNA-(6)A37 thiotransferase enzyme MiaB [Campylobacter lari RM2100]			1.8.-
12707, 12708	34558204	30	6.00E-12	Wolonia succinogenes DSM 1740	GUANOSINE PENTAPHOSPHATE PHOSPHOHYDROLASE GPPA [Wolonia succinogenes DSM 1740] emb CAE10919.1 GUANOSINE PENTAPHOSPHATE PHOSPHOHYDROLASE GPPA [Wolonia succinogenes]			3.6.1.11
12711, 12712	29348760	61	2.00E-94	Bacteroides thetaiotaomicron VPI-5482	cysteinyI-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78457.1 cysteinyI-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482]			6.1.1.16
12713, 12714	34397363	38	4.00E-25	Porphyromonas gingivalis W83	conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_905527.1 hypothetical protein PG1362 [Porphyromonas gingivalis W83]			2.1.1.-
12715, 12716	29348664	50	3.00E-37	Bacteroides thetaiotaomicron VPI-5482	putative N6-adenine-specific DNA methylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78361.1 putative N6-adenine-specific DNA methylase [Bacteroides thetaiotaomicron VPI-5482]			2.1.1.-

12719, 12720	29346657	29	2.00E-26	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT1247 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76354.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
12721, 12722	54302195	27	2.00E-10	Photobacterium profundum SS9	hypothetical protein PBPRB0515 [Photobacterium profundum SS9] emb CAG22388.1 hypothetical protein [Photobacterium profundum]				
12723, 12724	15896082	40	2.00E-15	Clostridium acetobutylicum ATCC 824	S-adenosylmethionine-dependent methyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK80771.1 S-adenosylmethionine- dependent methyltransferase [Clostridium acetobutylicum ATCC 824] pir H97247 S-adenosylmethionine-dependent methyltransferase [imported] - Clostridium acetobutylicum				
12727, 12728	48858098	54	2.00E-29	Clostridium thermocellum ATCC 27405	COG2172: Anti-sigma regulatory factor (Ser/Thr protein kinase) [Clostridium thermocellum ATCC 27405]				
12729, 12730	48854896	69	1.00E-104	Cytophaga hutchinsonii	COG0825: Acetyl-CoA carboxylase alpha subunit [Cytophaga hutchinsonii]				6.4.1.2
12731, 12732	51244185	23	6.00E-08	Desulfotalea psychrophila LSv54	hypothetical protein DP0333 [Desulfotalea psychrophila LSv54] emb CAG35062.1 unknown protein [Desulfotalea psychrophila LSv54]				
12733, 12734	42629381	48	1.00E-32	Haemophilus influenzae R2846	hypothetical protein HflU103001140 [Haemophilus influenzae R2846]				
12737, 12738	6969058	53	3.00E-65	Campylobacter jejuni subsp. jejuni NCTC 11168	UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diamide ligase [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282769.1 UDP-N- acetylmuramoylalanyl-D-glutamate-2,6-diamide ligase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir G81260 UDP-N-acetylmuramoylalanyl-D- glutamate-2,6-diamino-pimelate ligase (EC 6.3.2.13) C 1641 [imported] - Campylobacter jejuni (strain NCTC 11168) sp O69290 MURE_CAMJE UDP- N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase (UDP-N- acetylmuramyl-tripeptide synthetase) (Meso-diaminopimelate-adding enzyme) (UDP-MurNAc-tripeptide synthetase)				6.3.2.13
12739, 12740	34557608	26	2.00E-24	Wolinella succinogenes DSM 1740	hypothetical protein WS1243 [Wolinella succinogenes DSM 1740] emb CAE10323.1 conserved hypothetical protein [Wolinella succinogenes]				2.7.3.-
12743, 12744	34556884	47	4.00E-60	Wolinella succinogenes DSM 1740	hypothetical protein WS0457 [Wolinella succinogenes DSM 1740] emb CAE09599.1 conserved hypothetical protein [Wolinella succinogenes] protein of unknown function / conserved hypothetical protein TIGR00296 [Dehalococcoides ethenogenes 195] gb AAW39480.1 protein of unknown function / conserved hypothetical protein TIGR00296 [Dehalococcoides ethenogenes 195]				1.-.-.-
12745, 12746	57233975	29	2.00E-21	Dehalococcoides ethenogenes 195					

12747, 12748	28210824	44	5.00E-47	E88	Clostridium tetani	transcriptional regulatory protein [Clostridium tetani E88] gb AAO35705.1 transcriptional regulatory protein [Clostridium tetani E88]				2.7.3.-
12749, 12750	23097516	37	7.00E-28		Oceanobacillus lheyensis HTE831	stage V sporulation protein C [Oceanobacillus lheyensis HTE831] dbj BAC12017.1 stage V sporulation protein C (peptidyl-tRNA hydrolase (PTH)) [Oceanobacillus lheyensis HTE831] sp Q8CXP8 PTH_OCEIH Peptidyl-tRNA hydrolase (PTH)				3.1.1.29
1275, 1276	57169064	54	1.00E-22	RM2228	Campylobacter coli	conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228]				
12751, 12752	6968169	49	1.00E-37	NCTC 11168	Campylobacter jejuni subsp. jejuni	putative 16S rRNA processing protein [Campylobacter jejuni subsp. jejuni] NCTC 11168] pir C81342 probable 16S rRNA processing protein Cj0712 [Imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281884.1 putative 16S rRNA processing protein [Campylobacter jejuni subsp. jejuni] NCTC 11168] sp Q9PPJ5 RIMM_CAMJE Probable 16S rRNA processing protein rimM				
12753, 12754	33861802	44	1.00E-43	CCMP1986	Prochlorococcus marinus subsp. pastoris str.	Carbamoyltransferase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19705.1 Carbamoyltransferase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]				2.-.-
12757, 12758	33864985	39	2.00E-31	WH 8102	Synechococcus sp.	putative N-acetylglucosamine-6-phosphate 2-epimerase/N-acetyl... [Synechococcus sp. WH 8102] emb CAE06964.1 putative N- acetylglucosamine-6-phosphate 2-epimerase/N-acetylglucosamine-6- phosphatase [Synechococcus sp. WH 8102]				5.1.3.-
12763, 12764	38233578	47	9.00E-30	13129	Corynebacterium diphtheriae NCTC	hypothetical protein DIP0983 [Corynebacterium diphtheriae NCTC 13129] emb CAE49501.1 Conserved hypothetical protein [Corynebacterium diphtheriae]				1.1.1.85
12765, 12766	34557329	37	3.00E-45	1740	Wolinella succinogenes DSM	hypothetical protein WS0940 [Wolinella succinogenes DSM 1740] emb CAE10044.1 conserved hypothetical protein [Wolinella succinogenes]				2.7.3.-
12767, 12768	1769991	52	4.00E-19		Geobacillus stearothermophilus	site-specific DNA-methyltransferase [Geobacillus stearothermophilus]				2.1.1.72
12769, 12770	50083438	54	2.00E-50	ADP1	Acinetobacter sp.	hypothetical protein ACIAD0152 [Acinetobacter sp. ADP1] emb CAG67126.1 conserved hypothetical protein [Acinetobacter sp. ADP1] COG1166: Arginine decarboxylase (spermidine biosynthesis) [Cytophaga hutchinsonii]				
1277, 1278	48853912	48	2.00E-33		Cytophaga hutchinsonii					

12773,	27383072	40	1.00E-13	110	Bradyrhizobium japonicum USDA	probable HspC2 heat shock protein [Bradyrhizobium japonicum USDA 110] dbj BAC53226.1 bnr7961 [Bradyrhizobium japonicum USDA 110]				
12774						transposase [Methanosarcina acetivorans C2A] gb AAM07337.1				
12775,	20092782	51	1.00E-55		Methanosarcina acetivorans C2A	transposase [Methanosarcina acetivorans str. C2A]				
12776										
12777,	48854025	37	1.00E-16		Cytophaga hutchinsonii	hypothetical protein Chut02003116 [Cytophaga hutchinsonii]				
12778										
12779,	15793038	64	1.00E-58		Neisseria meningitidis Z2491	hypothetical protein NMA0004 [Neisseria meningitidis Z2491] emb CAB83324.1 hypothetical protein NMA0004 [Neisseria meningitidis Z2491] gb AAF40709.1 cell filamentation protein Fic-related protein Fic-related protein NMB0255 [imported] - Neisseria meningitidis (strain MC58 serogroup B, strain Z2491 serogroup A) ref NP_273311.1 cell filamentation protein Fic-related protein [Neisseria meningitidis MC58]				
12780										
12781,	48854252	26	6.00E-08		Cytophaga hutchinsonii	COG1125: ABC-type proline/glycine betaine transport systems, ATPase components [Cytophaga hutchinsonii]				
12782										
12783,	48854252	26	7.00E-08		Cytophaga hutchinsonii	COG1125: ABC-type proline/glycine betaine transport systems, ATPase components [Cytophaga hutchinsonii]				
12784										
12789,	56808559	30	6.00E-07		Streptococcus pyogenes M49 591	COG3754: Lipopolysaccharide biosynthesis protein [Streptococcus pyogenes M49 591]				
12790										
1279,					Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	precortin methylase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS72156.1 precortin methylase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				2.1.1.13
1280	45655710	34	3.00E-26		Fiocruz L1-130	conserved hypothetical protein [Neisseria meningitidis MC58] pir A81107				1
12791,					Neisseria meningitidis MC58	conserved hypothetical protein NMB1232 [imported] - Neisseria meningitidis (strain MC58 serogroup B) ref NP_274256.1 hypothetical protein NMB1232 [Neisseria meningitidis MC58]				
12792	7226471	41	2.00E-16		Rhodopirellula ballica SH 1	hypothetical protein RB711 [Rhodopirellula ballica SH 1] emb CAD71713.1				2.1.1.-
12795,	32471046	44	9.00E-30		Vibrio parahaemolyticus	conserved hypothetical protein [Pirellula sp.]				
12796										
12797,	22036085	37	1.00E-11		Bacteroides fragilis	hypothetical ATP-binding protein [Vibrio parahaemolyticus]				
12798										
12799,	53711926	38	1.00E-09		YCH46	hypothetical protein BF0635 [Bacteroides fragilis YCH46] db BAD47384.1				
12800						hypothetical protein [Bacteroides fragilis YCH46]				
12801,					Methanosarcina acetivorans C2A	hypothetical protein MA0188 [Methanosarcina acetivorans C2A] gb AAM03641.1 hypothetical protein (multi-domain) [Methanosarcina acetivorans str. C2A]				2.4.1.-
12802	20089086	40	5.00E-35							

12805, 12806 12807, 12808 1281, 1282	21674062 32417538 AAG8240 1	49 30 28	1.00E-54 2.00E-18 1.00E-07	Chlorobium tepidum TLS Neurospora crassa	preprotein translocase SecA subunit [Chlorobium tepidum TLS] gb AAM72469.1 preprotein translocase SecA subunit [Chlorobium tepidum TLS] hypothetical protein [Neurospora crassa] gb EAA34777.1 hypothetical protein [Neurospora crassa] Desc: S. epidermidis open reading frame protein sequence SEQ ID NO: 1896. Org: Staphylococcus epidermidis	Arabidopsis thaliana chromosome 1 BAC F8K7 sequence, complete sequence 95 2.00E-09			2.7.3.- 3.4.11.1 8
12813, 12814 12815, 12816 12817, 12818	57240977 34557665 46202294	62 41 41	5.00E-98 3.00E-41 5.00E-42	Campylobacter lari RM2100 Wolinella succinogenes DSM 1740 Magnetospirillum magnetotacticum MS-1	DNA-directed RNA polymerase, beta subunit [Campylobacter lari RM2100] gb EAL55370.1 DNA-directed RNA polymerase, beta subunit [Campylobacter lari RM2100] DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes] COG0840: Methyl-accepting chemotaxis protein [Magnetospirillum magnetotacticum MS-1]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6 84 6.00E-32 2.7.7.6			2.7.3.- 2.7.3.-
12819, 12820 12821, 12822 12823, 12824 12825, 12826 12827, 12828	24214445 24374136 28262612 15606018 34556481	24 56 52 30 44	9.00E-20 5.00E-84 2.00E-74 9.00E-16 1.00E-37	Leptospira interrogans serovar Lai str. 56601 Shewanella oneidensis MR-1 Rickettsia sibirica 246 Aquifex aeolicus VF5 Wolinella succinogenes DSM 1740	two-component hybrid sensor and regulator [Leptospira interrogans serovar Lai str. 56601] gb AAN48944.1 two-component hybrid sensor and regulator [Leptospira interrogans serovar lai str. 56601] hypothetical protein SO2593 [Shewanella oneidensis MR-1] gb AAN55623.1 conserved hypothetical protein [Shewanella oneidensis MR-1] unknown [Rickettsia sibirica 246] ref ZP_00142707.1 hypothetical protein [Rickettsia sibirica 246] hypothetical protein aq_563 [Aquifex aeolicus VF5] gb AAC06808.1 hypothetical protein [Aquifex aeolicus VF5] pir G70350 conserved hypothetical protein aq_563 - Aquifex aeolicus hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes]				2.7.3.- 1.4.1.2 1.4.1.2 2.7.3.-

12829, 12830, 12831, 12832, 12833, 12834	20807293 48853434 48856692 48831001	33 68 40 38	1.00E-39 3.00E-73 4.00E-15 2.00E-53	Thermoanaerobacter tengcongensis MB4 Cytophaga hutchinsonii Cytophaga hutchinsonii Magnetococcus sp. MC-1	Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Thermoanaerobacter tengcongensis MB4] gb AAM24068.1 Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Thermoanaerobacter tengcongensis MB4] sp Q8RBK5 PURL_THETN Phosphoribosylformylglycinamide synthase II (FGAM synthase II)			6.3.5.3 2.7.7.24
12835, 12836	53712955	50	2.00E-41	Bacteroides fragilis YCH46	COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii] COG0304: 3-oxoacyl-(acyl-carrier-protein) synthase [Cytophaga hutchinsonii]			2.7.3.- 3.1.3.25
12837, 12838	34557246	55	3.00E-78	Wolinella succinogenes DSM 1740	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] sulfite synthesis pathway protein CysQ [Bacteroides fragilis YCH46]			2.7.3.-
12839, 12840	34557246	33	3.00E-32	Wolinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]			2.7.3.-
12843, 12844	45658172	30	2.00E-31	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 Flocruz L1-130	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]			2.7.3.-
12847, 12848	48846045	43	2.00E-22	Geobacter metallireducens GS	serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70895.1 serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			2.7.3.-
12849, 12850	48846045	34	1.00E-09	Geobacter metallireducens GS	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]			
1285, 1286	48853435	70	5.00E-55	Cytophaga hutchinsonii	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]	Prochlorococcus marinus MIT9313 complete genome; segment 1/7	94	1.00E-06
12851, 12852	53796794	41	9.00E-20	Chloroflexus aurantiacus	COG1088: dTDP-D-glucose 4,6-dehydratase [Cytophaga hutchinsonii]			4.2.1.46 1.1.1.20
12857, 12858	28974235	41	4.00E-43	Campylobacter fetus	COG0517: FOG: CBS domain [Chloroflexus aurantiacus] putative putative two-component sensor Cf0035 [Campylobacter fetus]			5 2.7.3.-

12859, 12860	23129844	29	1.00E-11	Nostoc punctiforme PCC 73102	COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102]			2.7.3.-
12861, 12862	48846045	48	1.00E-20	Geobacter metallireducens GS-15	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]			2.7.3.-
12863, 12864	23012315	49	4.00E-22	Magnetospirillum magnetotacticum MS-1	COG0834: ABC-type amino acid transport/signal transduction systems, periplasmic component/domain [Magnetospirillum magnetotacticum MS-1]			4.2.-
12865, 12866	21674940	48	2.00E-31	Chlorobium tepidum TLS	hypothetical protein CT2131 [Chlorobium tepidum TLS] gb AAM73347.1			
12867, 12868	40062786	31	1.00E-09	uncultured bacterium 439	conserved domain protein [uncultured bacterium 439]			
1287, 1288	AAY80126	29	2.00E-17	Methanosarcina barkeri str. fusaro	Desc:Sphaerotilus natans SnaBI endonuclease protein SEQ ID NO:4. Org:Sphaerotilus natans			
12871, 12872	48841399	28	2.00E-07	Methanosarcina barkeri str. fusaro	COG2244: Membrane protein involved in the export of O-antigen and teichoic acid [Methanosarcina barkeri str. fusaro]			
12873, 12874	14591370	35	2.00E-08	Pyrococcus horikoshii OT3	transcriptional regulator [Pyrococcus horikoshii OT3]			
12875, 12876	ABP73922	46	5.00E-53	Pyrococcus horikoshii	spi059256[REG7_PYRHO HTH-type transcriptional regulator lrpA dbj BAA30704.1 141aa long hypothetical transcriptional regulator [Pyrococcus horikoshii OT3] pir H71037 probable transcription regulator - Pyrococcus horikoshii			4.2.1.36
12877, 12878	32477370	35	5.00E-19	Rhodopirella baltica SH 1	Desc:Candida albicans essential protein SEQ ID NO 7759. Org:Candida albicans			
12879, 12880	30249527	50	7.00E-28	Nitrosomonas europaea ATCC 19718	phosphoribosylaminoimidazole-succinocarboxamide synthase [Rhodopirella baltica SH 1] emb CAD7744.1.1 phosphoribosylaminoimidazole-succinocarboxamide synthase [Pirella sp.]			6.3.2.6
12881, 12882	41724578	30	4.00E-24	Dechloromonas aromatica RCB	putative transposase [Nitrosomonas europaea ATCC 19718] emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718]			
12883, 12884	48855825	29	9.00E-18	Cytophaga hutchinsonii	COG0842: ABC-type multidrug transport system, permease component [Dechloromonas aromatica RCB]			
12885, 12886	15603871	37	2.00E-40	Pasteurella multocida subsp. multocida str. Pm70	COG0304: 3-oxoacyl-(acyl-carrier-protein) synthase [Cytophaga hutchinsonii]			2.3.1.41

12887, 12888	29348444	36	1.00E-26	Bacteroides thetaiotaomicron VPI-5482	carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO78141.1 carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482]			
12889, 12890 12891, 12892	45658026	36	2.00E-13	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	CMP-N-acetylneuraminic acid synthetase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711786.1 Probable acylneuraminase cytidyltransferase [Leptospira interrogans serovar Lai str. 56601] gb AAN4804.1 Probable acylneuraminase cytidyltransferase [Leptospira interrogans serovar lai str. 56601] gb AAS70749.1 CMP-N- acetylneuraminic acid synthetase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			2.7.7.43
12893, 12894	48853351	63	1.00E-50	Cytophaga hutchinsonii	COG4804: Uncharacterized conserved protein [Cytophaga hutchinsonii] conserved hypothetical protein TIGR00486 [Campylobacter coli RM2228] gb EAL57503.1 conserved hypothetical protein TIGR00486 [Campylobacter coli RM2228]			
12895, 12896	5740646	50	5.00E-29	Campylobacter lari RM2100	UDP-N-acetylmuramoylalanine-D-glutamate 2, 6-diaminopimelate ligase [Campylobacter lari RM2100] gb EAL55039.1 UDP-N-acetylmuramoylalanine- D-glutamate 2, 6-diaminopimelate ligase [Campylobacter lari RM2100]			6.3.2.13
12897, 12898	34556481	37	1.00E-15	Wolinella succinogenes DSM 1740	hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes]			
12899, 12900	34556481	49	6.00E-55	Wolinella succinogenes DSM 1740	hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes]			2.7.3.-
129, 130	48854463	55	1.00E-35	Cytophaga hutchinsonii	COG0193: Peptidyl-tRNA hydrolase [Cytophaga hutchinsonii]			3.1.1.29
12901, 12902	57505271	43	4.00E-41	Campylobacter upsallensis RM3195	nicotinate (nicotinamide) nucleotide adenyltransferase [Campylobacter upsallensis RM3195] gb EAL53192.1 nicotinate (nicotinamide) nucleotide adenyltransferase [Campylobacter upsallensis RM3195]			2.7.7.18
12903, 12904	32263376	59	2.00E-53	Helicobacter hepaticus ATCC 51449	phosphoenolpyruvate synthase [Helicobacter hepaticus ATCC 51449] ref NP_861355.1 phosphoenolpyruvate synthase [Helicobacter hepaticus ATCC 51449]			2.7.9.2
12905, 12906	45658435	52	6.00E-65	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	adenylate/guanylate cyclase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS71158.1 adenylate/guanylate cyclase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			4.6.1.2

12907, 12908	AAU3593 1	56	2.00E-18		Desc:Helicobacter pylori cellular proliferation protein #244. Org:Helicobacter pylori			1.17.4.1
12909, 12910 12911, 12912 12913, 12914	56479307 48853884 14531035	35 37 37	5.00E-13 5.00E-29 2.00E-07	Azoarcus sp. EbN1 Cytophaga hutchinsonii Flavobacterium johnsoniae	transposition helper protein [Azoarcus sp. EbN1] ref YP_160652.1 transposition helper protein [Azoarcus sp. EbN1] ref YP_160194.1 transposition helper protein [Azoarcus sp. EbN1] ref YP_158869.1 transposition helper protein [Azoarcus sp. EbN1] ref YP_158141.1 transposition helper protein [Azoarcus sp. EbN1] ref YP_157415.1 transposition helper protein [Azoarcus sp. EbN1] ref YP_157215.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI09995.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI09751.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI09293.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI07968.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI07240.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI06514.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI06314.1 transposition helper protein [Azoarcus sp. EbN1] emb CAI10704.1 IstB, ATP-binding protein [Azoarcus sp. EbN1] emb CAI10643.1 transposase OrfB protein [Azoarcus sp. EbN1] emb CAI10603.1 orfB protein, similar to Isr3 COG3225: ABC-type uncharacterized transport system involved in gliding motility, auxiliary component [Cytophaga hutchinsonii] gliding motility protein GldG [Flavobacterium johnsoniae]			
12915, 12916, 12917, 12918	34558438 48833884	46 28	9.00E-56 2.00E-11	Wolinella succinogenes DSM 1740 Magnetococcus sp. MC-1	CYTOCHROME C BIOGENESIS PROTEIN (YCF5) [Wolinella succinogenes DSM 1740] emb CAE11153.1 CYTOCHROME C BIOGENESIS PROTEIN (YCF5) [Wolinella succinogenes] COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] 3-DEOXY-D-MANNO-OCTULOSONIC-ACID TRANSFERASE KDTA [Wolinella succinogenes DSM 1740] emb CAE11114.1 3-DEOXY-D-MANNO-OCTULOSONIC-ACID TRANSFERASE KDTA [Wolinella succinogenes]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 4/6	92 4.00E-08	
12919, 12920	34558399	42	6.00E-18	Wolinella succinogenes DSM 1740	Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] gb AAK81185.1 Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] pir F97299 sensory transduction protein containing HD_GYP domain [Imported] - Clostridium acetobutylicum			2.4.99.-
12921, 12922	15896496	44	3.00E-39	Clostridium acetobutylicum ATCC 824	molybdenum transport protein ModE [Chlorobium tepidum TLS]			
12923, 12924	21674362	40	5.00E-41	Chlorobium tepidum TLS	gbl AAM72769.1 molybdenum transport protein ModE [Chlorobium tepidum TLS]			

12925, 12926	17231298	26	5.00E-16	Nostoc sp. PCC 7120	hypothetical protein alr3806 [Nostoc sp. PCC 7120] pir JAG2281 hypothetical protein alr3806 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75505.1 alr3806 [Nostoc sp. PCC 7120]			
12929, 12930	29346209	24	4.00E-10	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0799 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75906.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
1293, 1294	53712627	38	2.00E-26	Bacteroides fragilis YCH46	putative RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD48085.1 putative RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46]			
12931, 12932	57241729	48	7.00E-25	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54399.1 conserved hypothetical protein [Campylobacter lari RM2100]			
12935, 12936	46141858	35	2.00E-30	Methanococcus burtonii DSM 6242	COG0598: Mg2+ and Co2+ transporters [Methanococcus burtonii DSM 6242]			
12939, 12940	34104254	32	3.00E-12	Chromobacterium violaceum ATCC 12472	conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_902615.1 hypothetical protein CV2945 [Chromobacterium violaceum ATCC 12472]			
12941, 12942	48858108	61	3.00E-36	Clostridium thermocellum ATCC 27405	COG0281: Malic enzyme [Clostridium thermocellum ATCC 27405]			1.1.1.38
12943, 12944	29346750	34	2.00E-13	Bacteroides thetaiotaomicron VPI-5482	putative lipopolysaccharide biosynthesis glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76447.1 putative lipopolysaccharide biosynthesis glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]			
12947, 12948	48854416	49	2.00E-72	Cytophaga hutchinsonii Wolinella succinogenes DSM 1740	COG3275: Putative regulator of cell autolysis [Cytophaga hutchinsonii]			2.7.3.-
12949, 12950	34557884	33	2.00E-17	Bacteroides fragilis YCH46	DIGUANYLATE CYCLASE [Wolnella succinogenes DSM 1740] emb CAE10599.1 DIGUANYLATE CYCLASE [Wolnella succinogenes]			2.7.3.-
1295, 1296	53712627	37	6.00E-26	Bacteroides fragilis YCH46	putative RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD48085.1 putative RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46]			
12951, 12952	48862623	22	2.00E-09	Microbulifer degradans 2-40	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Microbulifer degradans 2-40]			2.1.1.-
12955, 12956	57237984	53	2.00E-47	Campylobacter jejuni RM1221	tRNA pseudouridine synthase B [Campylobacter jejuni RM1221] gb AAW35567.1 tRNA pseudouridine synthase B [Campylobacter jejuni RM1221]			4.2.1.70
12957, 12958	34557269	58	7.00E-82	Wolnella succinogenes DSM 1740	ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolnella succinogenes DSM 1740] emb CAE09984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolnella succinogenes]			3.6.1.-

12959, 12960	57237231	53	2.00E-53	Campylobacter jejuni RM1221	DNA adenine methylase [Campylobacter jejuni RM1221] gb AAW34814.1 DNA adenine methylase [Campylobacter jejuni RM1221]			2.1.1.72
12961, 12962	48846045	40	3.00E-42	Geobacter metallireducens GS	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]			2.7.3.-
12963, 12964	48891870	48	5.00E-56	Trichodesmium erythraeum IMS101	COG0566: rRNA methylases [Trichodesmium erythraeum IMS101] conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228]			2.1.1.-
12965, 12966	57169064	31	1.00E-25	Campylobacter coli RM2228	ATP-BINDING PROTEIN-ATPases involved in chromosome partitioning [Wollinella succinogenes DSM 1740] emb CAE10672.1 ATP-BINDING PROTEIN-ATPases involved in chromosome partitioning [Wollinella succinogenes]			
12967, 12968	34557957	41	5.00E-37	Wollinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes] COG3279: Response regulator of the LysR/AigR family [Cytophaga hutchinsonii]			2.7.3.-
12969, 12970	34556560	35	5.00E-48	Wollinella succinogenes DSM 1740	PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wollinella succinogenes DSM 1740] emb CAE09198.1 PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wollinella succinogenes]			5.1.3.-
12971, 12972	34556483	56	3.00E-38	Campylobacter coli RM2228	3'(2') 5'-bisphosphate nucleotidase [Campylobacter coli RM2228] gb EAL56330.1 3'(2') 5'-bisphosphate nucleotidase [Campylobacter coli RM2228]	Aquifex aeolicus VF5 section 16 of 109 of the complete genome	87 4.00E-14	3.1.3.25
12973, 12974	57168975	63	6.00E-80	Wollinella succinogenes DSM 1740	PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10693.1 PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wollinella succinogenes]			2.3.2.-
12975, 12976	34557978	46	5.00E-62	Alvinella pompejana epibiont 7G3	succinylornithine transaminase [Alvinella pompejana epibiont 7G3]			2.6.1.11
12979, 12980	34558829	44	2.00E-47	Wollinella succinogenes DSM 1740	hypothetical protein WS0394 [Wollinella succinogenes DSM 1740] emb CAE09540.1 conserved hypothetical protein [Wollinella succinogenes]			
12981, 12982	34556825	39	2.00E-35					

12983, 12984	15678576	38	2.00E-18	Methanothermobacter thermautotrophicus str. Delta H	sensory transduction regulatory protein [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85054.1 sensory transduction regulatory protein [Methanothermobacter thermotrophicus str. Delta H] pi D69172 sensory transduction regulatory protein - Methanobacterium thermautotrophicum (strain Delta H)			2.7.3.-
12985, 12986	34557975	57	1.00E-72	Wolinella succinogenes DSM 1740	AAA FAMILY ATPASE [Wolinella succinogenes DSM 1740] emb CAE10690.1 AAA FAMILY ATPASE [Wolinella succinogenes]			
12987, 12988	34557975	67	9.00E-67	Wolinella succinogenes DSM 1740	AAA FAMILY ATPASE [Wolinella succinogenes DSM 1740] emb CAE10690.1 AAA FAMILY ATPASE [Wolinella succinogenes]	Helicobacter hepaticus ATCC 51449 section 2 of 6 of the complete genome	93	1.00E-13 3.4.24.-
12989, 12990	45658172	45	9.00E-44	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70895.1 serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			3.1.3.16
12991, 12992	46201501	28	7.00E-12	Magnetospirillum magnetotacticum MS-1	COG2208: Serine phosphatase RsbU, regulator of sigma subunit [Magnetospirillum magnetotacticum MS-1]			
12993, 12994	37519590	31	3.00E-38	Gloeobacter violaceus PCC 7421	HlyB/MsbA family ABC transporter [Gloeobacter violaceus PCC 7421] db JBAC87962.1 HlyB/MsbA family ABC transporter [Gloeobacter violaceus PCC 7421]			3.4.21.-
12997, 12998	48856940	37	5.00E-19	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]			
12999, 13000	48478360	30	4.00E-12	Picrophilus torridus DSM 9790	thiamin-phosphate pyrophosphorylase [Picrophilus torridus DSM 9790] gb AAT43873.1 thiamin-phosphate pyrophosphorylase [Picrophilus torridus DSM 9790]			2.5.1.3
13001, 13002	27804856	29	7.00E-10	Myxococcus xanthus	putative histidine kinase [Myxococcus xanthus]			
13003, 13004	46578599	30	2.00E-19	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	radical SAM domain protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94666.1 radical SAM domain protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			
13007, 13008	48832299	43	7.00E-42	Magnetococcus sp. MC-1	COG2206: HD-GYP domain [Magnetococcus sp. MC-1]			
13009, 13010	39958006	44	1.00E-23	Geobacter sulfurreducens PCA	sigma-54 dependent DNA-binding response regulator [Geobacter sulfurreducens PCA] gb AAR36307.1 sigma-54 dependent DNA-binding response regulator [Geobacter sulfurreducens PCA]			2.7.-

13011,	57233639	45	7.00E-17	Dehalococcoides	DNA internalization-related competence protein ComEC/Rec2 [Dehalococcoides ethenogenes 195]				
13012									
13013,									
13014	46155955	38	6.00E-29	Haemophilus somnus 2336	COG2249: Putative NADPH-quinone reductase (modulator of drug activity)				1.6.99-
13015,									
13016	28211915	38	2.00E-08	Clostridium tetani E88	imidazolonepropionase [Clostridium tetani E88]				3.5.2.7
13019,									
13020	15605808	37	1.00E-15	Aquifex aeolicus VF5	hypothetical protein aq_268 [Aquifex aeolicus VF5] gb AAC06590.1				
13025,									
13026	48788644	47	2.00E-43	Burkholderia fungorum LB400	hypothetical protein aq_268 - Aquifex aeolicus				2.3.2.6
13027,									
13028	29347026	41	8.00E-41	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT1616 [Bacteroides thetaiotaomicron VPI-5482]				
13029,									
13030	28896908	41	1.00E-19	Vibrio parahaemolyticus RIMD 2210633	general secretion pathway protein E [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58397.1 general secretion pathway protein E [Vibrio parahaemolyticus]				
13033,									
13034	51572906	60	2.00E-31	Borrelia garinii PBI	peptide chain release factor 2 [Borrelia garinii PBI] ref YP_072523.1 peptide chain release factor 2 [Borrelia garinii PBI]				
13035,									
13036	53714646	34	4.00E-23	Bacteroides fragilis YCH46	putative outer membrane protein [Bacteroides fragilis YCH46]				
13037,									
13038	57505272	50	1.00E-27	Campylobacter upsaliensis RM3195	glyceraldehyde-3-phosphate dehydrogenase, type I [Campylobacter upsaliensis RM3195]				1.2.1.12
13039,									
13040	53718408	29	7.00E-09	Burkholderia pseudomallei K96243	hypothetical protein BPSL0769 [Burkholderia pseudomallei K96243]				
13041,									
13042	17231298	26	2.00E-15	Nostoc sp. PCC 7120	hypothetical protein air3806 [Nostoc sp. PCC 7120] pir AG2281 hypothetical protein air3806 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75505.1				
13047,									
13048	53714415	72	3.00E-80	Bacteroides fragilis YCH46	dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46]				2.4.1.83
13049,									
13050	34557635	47	1.00E-53	Wolffia succinogenes DSM 1740	RND PUMP PROTEIN [Wolffia succinogenes DSM 1740]				

13051, 13052	34558004	54	9.00E-85	Wolinella succinogenes DSM 1740	RNA POLYMERASE ALPHA SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10719.1 RNA POLYMERASE ALPHA SUBUNIT [Wolinella succinogenes] sp Q7M8F7 RPOA_WOLSU DNA-directed RNA polymerase alpha chain (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit)				2.7.7.6	
13053, 13054	29335929	28	5.00E-08	Bacteroides thetaiotaomicron	Tram-like [Bacteroides thetaiotaomicron] ref NP_818968.1 Tram-like protein [Bacteroides thetaiotaomicron]					
13055, 13056	34556523	55	3.00E-25	Wolinella succinogenes DSM 1740	hypothetical protein WS0069 [Wolinella succinogenes DSM 1740] emb CAE09238.1 conserved hypothetical protein [Wolinella succinogenes]					
13057, 13058	34556524	41	4.00E-18	Wolinella succinogenes DSM 1740	hypothetical protein WS0070 [Wolinella succinogenes DSM 1740] emb CAE09239.1 hypothetical protein [Wolinella succinogenes] PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]				2.3.1.12 8	
13059, 13060	34557782	38	3.00E-31	Wolinella succinogenes DSM 1740	hypothetical protein MM2979 [Methanosarcina mazei Go1] gb AAM32675.1 hypothetical protein [Methanosarcina mazei Goe1]				2.7.3.-	
13061, 13062	21229081	52	4.00E-66	Methanosarcina mazei Go1	hypothetical protein [Methanosarcina mazei Goe1]					
13063, 13064	53712881	33	2.00E-22	Bacteroides fragilis YCH46	hypothetical protein BF1590 [Bacteroides fragilis YCH46] db BAD48339.1 conserved hypothetical protein [Bacteroides fragilis YCH46]					
13065, 13066	34556560	45	3.00E-21	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] acetylglutamate kinase [Helicobacter hepaticus ATCC 51449] ref NP_859710.1 acetylglutamate kinase [Helicobacter hepaticus ATCC 51449] sp Q7VJR4 ARGB_HELHP Acetylglutamate kinase (NAG kinase) (AGK) (N-acetyl-L-glutamate 5-phosphotransferase)				2.7.3.-	
13069, 13070	32261726	60	4.00E-42	Helicobacter hepaticus ATCC 51449	COG1216: Predicted glycosyltransferases [Cytophaga hutchinsonii]					2.7.2.8
1307, 1308	48854748	55	4.00E-90	Cytophaga hutchinsonii	hypothetical protein WS0063 [Wolinella succinogenes DSM 1740] emb CAE09232.1 conserved hypothetical protein [Wolinella succinogenes]					2.4.1.-
13071, 13072	34556517	47	5.00E-42	Wolinella succinogenes DSM 1740	COG3019: Predicted metal-binding protein [Rhodospirillum rubrum] hypothetical protein all7133 [Nostoc sp. PCC 7120] db BAB78217.1 all7133 [Nostoc sp. PCC 7120] pir AE2494 hypothetical protein all7133 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha					
13073, 13074	48764124	42	3.00E-25	Rhodospirillum rubrum						
13075, 13076	17233149	36	3.00E-32	Nostoc sp. PCC 7120						
13077, 13078	23475535	53	5.00E-51	Desulfovibrio desulfuricans G20						

13079, 13080	23466453	41	4.00E-30	Haemophilus sommus 129PT	COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Haemophilus somnus 129PT]				
13085, 13086	45250013	67	3.00E-84	Aneurinibacillus thermoaerophilus	dTDP-glucose 4,6-dehydratase [Aneurinibacillus thermoaerophilus]				4.2.1.46
13087, 13088	53728940	33	1.00E-08	Actinobacillus pleuropneumoniae serovar 1 str. 4074	COG0561: Predicted hydrolases of the HAD superfamily [Actinobacillus pleuropneumoniae serovar 1 str. 4074]				
1309, 1310	29347685	65	3.00E-61	Bacteroides thetaiotaomicron VPI-5482	thymidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77382.1 thymidine kinase [Bacteroides thetaiotaomicron VPI-5482]				2.7.1.21
13095, 13096	48862944	42	3.00E-40	Microbulbifer degradans 2-40	COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Microbulbifer degradans 2-40]				
13097, 13098	AAU3592 8	60	8.00E-40		Desc:Helicobacter pylori cellular proliferation protein #241. Org:Helicobacter pylori				4.6.1.4
13101, 13102	57241323	49	8.00E-21	Campylobacter lari RM2100	hypothetical protein CLA1225 [Campylobacter lari RM2100] gb EAL55019.1 hypothetical protein CLA1225 [Campylobacter lari RM2100]				
13103, 13104	57241291	51	5.00E-41	Campylobacter lari RM2100	cell division protein (ftsK) [Campylobacter lari RM2100] gb EAL54987.1 cell division protein (ftsK) [Campylobacter lari RM2100]				
13105, 13106	56419990	55	9.00E-53	Geobacillus kaustophilus HTA426	recombinase of Bh.Int-like element [Geobacillus kaustophilus HTA426] dbj BAD75740.1 recombinase of Bh.Int-like element [Geobacillus kaustophilus HTA426]				2.7.7.49
13107, 13108	32262431	61	1.00E-84	Helicobacter hepaticus ATCC 51449	3-dehydroquinase synthase [Helicobacter hepaticus ATCC 51449] ref NP_860413.1 3-dehydroquinase synthase [Helicobacter hepaticus ATCC 51449] sp Q7VHT1 AROB_HELHP 3-dehydroquinase synthase				
13109, 13110	34557844	26	5.00E-22	Wolinella succinogenes DSM 1740	MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10559.1 MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes]			82	1.00E-11 4.2.3.4
1311, 1312	18308986	31	2.00E-31	Clostridium perfringens str. 13	DNA repair and genetic recombination protein [Clostridium perfringens str. 13] dbj BAB79710.1 DNA repair and genetic recombination protein [Clostridium perfringens str. 13] sp Q8XPF9 RECF_CLOPE DNA replication and repair protein refC				
13113, 13114	31239345	36	7.00E-17	Anopheles gambiae	ENSANGP00000018355 [Anopheles gambiae] gb EAA14826.1 ENSANGP00000018355 [Anopheles gambiae str. PEST] ref XP_553245.1 ENSANGP00000018355 [Anopheles gambiae str. PEST]				3.1.-.-

13115, 13116	12744764	33	7.00E-13	<i>Pichia pastoris</i>	PR-aminimidazolesuccinocarboxamide synthase [Pichia pastoris] sp Q9C1J4 PUR7_PICPA Phosphoribosylamidoimidazole-succinocarboxamide synthase (SAICAR synthetase)				6.3.2.6
13119, 13120	34557698	37	4.00E-24	<i>Wollinella succinogenes</i> DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10413.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes]				
13121, 13122	23014414	31	3.00E-21	<i>Magnetospirillum magnetotacticum</i> MS-1	COG0643: Chemotaxis protein histidine kinase and related kinases [Magnetospirillum magnetotacticum MS-1]				
13125, 13126	54309698	53	3.00E-49	<i>Photobacterium profundum</i> SS9	hypothetical deoxyguanosinetriphosphatetriphosphohydrolase [Photobacterium profundum SS9] emb CAG20916.1 hypothetical deoxyguanosinetriphosphatetriphosphohydrolase [Photobacterium profundum]				3.1.5.1
13127, 13128	11499442	40	4.00E-25	<i>Archaeoglobus fulgidus</i> DSM 4304	NADH oxidase (noxA-5) [Archaeoglobus fulgidus DSM 4304] gb AAB89398.1 NADH oxidase (noxA-5) [Archaeoglobus fulgidus DSM 4304] pir A69482 NADH oxidase (noxA-5) homolog - Archaeoglobus fulgidus				1.6.-.-
13131, 13132	56708505	50	4.00E-77	<i>Francisella tularensis</i> subsp. tularensis Schu 4	dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis Schu 4] emb CAG46097.1 dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis] gb AAS60264.1 sugar dehydratase [Francisella tularensis subsp. tularensis]				4.2.1.-
13135, 13136	46580167	23	5.00E-08	<i>Desulfovibrio vulgaris</i> subsp. vulgaris str. Hildenborough	site-specific recombinase, phage integrase family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96234.1 site-specific recombinase, phage integrase family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]				
13137, 13138	34557245	34	1.00E-35	<i>Wollinella succinogenes</i> DSM 1740	TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wollinella succinogenes DSM 1740] emb CAE09960.1 TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wollinella succinogenes]				2.7.3.-
13139, 13140	9655557	40	1.00E-29	<i>Vibrio cholerae</i> O1 biovar eltor str. N16961	periplasmic binding protein-related protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_230734.1 periplasmic binding protein-related protein [Vibrio cholerae O1 biovar eltor str. N16961] pir A82245 periplasmic binding protein-related protein VC1089 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				
13141, 13142	15607008	38	4.00E-22	<i>Aquifex aeolicus</i> VF5	hypothetical protein aq_2027 [Aquifex aeolicus VF5] gb AAC07788.1 hypothetical protein [Aquifex aeolicus VF5] pir A70474 conserved hypothetical protein aq_2027 - Aquifex aeolicus sp O67821 YK27_AQUAE Hypothetical protein AQ_2027				
13143, 13144	51244727	38	8.00E-31	<i>Desulfotalea psychrophila</i> LSV54	hypothetical protein DP0875 [Desulfotalea psychrophila LSV54] emb CAG35604.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]				4.-.-.-

13145, 13146	34556479	45	1.00E-55	Wolnella succinogenes DSM 1740	POSSIBLE NUCLEOTIDYLTRANSFERASE [Wolnella succinogenes DSM 1740] emb CAE09194.1 POSSIBLE NUCLEOTIDYLTRANSFERASE [Wolnella succinogenes]			2.7.7.59
13147, 13148	34556778	52	1.00E-32	Wolnella succinogenes DSM 1740	THIF, MOEB, HESA FAMILY PROTEIN [Wolnella succinogenes DSM 1740] emb CAE09493.1 THIF, MOEB, HESA FAMILY PROTEIN [Wolnella succinogenes]			
13149, 13150	18309954	41	8.00E-28	Clostridium perfringens str. 13	probable histidinol phosphatase [Clostridium perfringens str. 13] dbj BAB80678.1 probable histidinol phosphatase [Clostridium perfringens str. 13]			
13151, 13152	34557884	46	1.00E-28	Wolnella succinogenes DSM 1740	DIGUANYLATE CYCLASE [Wolnella succinogenes DSM 1740] emb CAE10599.1 DIGUANYLATE CYCLASE [Wolnella succinogenes]			2.7.3.-
13153, 13154	45656100	41	1.00E-39	Leptospira Interrogans serovar Copenhageni str. Floeruz L1-130	photoproduct lyase [Leptospira Interrogans serovar Copenhageni str. Floeruz L1-130] gb AAS68823.1 photoproduct lyase [Leptospira Interrogans serovar Copenhageni str. Floeruz L1-130]			4.1.99.-
13155, 13156	34557419	47	5.00E-21	Wolnella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolnella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolnella succinogenes]			2.7.3.-
13157, 13158	57241192	37	3.00E-16	Campylobacter lari RM2100	fructose-1,6-bisphosphatase [Campylobacter lari RM2100] gb EAL54888.1 fructose-1,6-bisphosphatase [Campylobacter lari RM2100]			3.1.3.11
13163, 13164	34556519	42	3.00E-37	Wolnella succinogenes DSM 1740	PUTATIVE DIMETHYLADENOSINE TRANSFERASE 16S RRNA DIMETHYLASEEC 2.1.1. [Wolnella succinogenes DSM 1740] emb CAE09234.1 PUTATIVE DIMETHYLADENOSINE TRANSFERASE 16S RRNA DIMETHYLASEEC 2.1.1. [Wolnella succinogenes]			2.1.1.-
1317, 1318	53736083	52	2.00E-59	Crocospaera watsonii WH 8501	COG0463: Glycosyltransferases involved in cell wall biogenesis [Crocospaera watsonii WH 8501]			2.4.1.83
13171, 13172	52425081	39	9.00E-30	Mannheimia succiniciproducens MBEL55E	hypothetical protein MS1026 [Mannheimia succiniciproducens MBEL55E] gb AAU37633.1 unknown [Mannheimia succiniciproducens MBEL55E]			2.1.1.72
13173, 13174	52425081	50	9.00E-45	Mannheimia succiniciproducens MBEL55E	hypothetical protein MS1026 [Mannheimia succiniciproducens MBEL55E] gb AAU37633.1 unknown [Mannheimia succiniciproducens MBEL55E] (3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase [Geobacter sulfurreducens PCA] gb AAR3564.1 (3R)-hydroxymyristoyl-(acyl-carrier- protein) dehydratase [Geobacter sulfurreducens PCA] sp P61453 FABZ_GEOSL (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase ((3R)-hydroxymyristoyl ACP dehydratase)			2.1.1.72
13175, 13176	39997363	63	1.00E-35	Geobacter sulfurreducens PCA				4.2.1.-

13177, 13178	45520556	30	4.00E-12	Methylobacillus flagellatus KT	COG0835: Chemotaxis signal transduction protein [Methylobacillus flagellatus KT]			
13179, 13180	15606118	43	6.00E-35	Aquifex aolicus VF5	glycogen synthase [Aquifex aolicus VF5] gb AAC06894.1 glycogen synthase [Aquifex aolicus VF5] pir C70363 glycogen synthase - Aquifex aolicus spi O66935 GLGA_AQUAE Glycogen synthase (Starch) [bacterial glycogen] synthase)			2.4.1.21
13185, 13186	53711526	42	1.00E-30	Bacteroides fragilis YCH46	shikimate kinase [Bacteroides fragilis YCH46] dbj BAD46984.1 shikimate kinase [Bacteroides fragilis YCH46]			2.7.1.71
13187, 13188	51573281	24	2.00E-09	Borrelia garinii PBI	lipopolysaccharide biosynthesis-related protein [Borrelia garinii PBI]			2.4.1.56
1319, 1320	48862770	46	3.00E-34	Microbulbifer degradans 2-40	ref YP_072898.1 lipopolysaccharide biosynthesis-related protein [Borrelia garinii PBI]			
13193, 13194	34558362	45	2.00E-20	Wolinella succinogenes DSM 1740	hypothetical protein Mdeg02001866 [Microbulbifer degradans 2-40]			
13199, 13200	34558118	30	1.00E-19	Wolinella succinogenes DSM 1740	PEPTIDYL-TRNA HYDROLASE [Wolinella succinogenes DSM 1740] emb CAE11077.1 PEPTIDYL-TRNA HYDROLASE [Wolinella succinogenes] spi Q7M7U8 PTH WOLSU Peptidyl-TRNA hydrolase (PTH)			3.1.1.29
13201, 13202	57168122	47	2.00E-34	Campylobacter coli RM2228	HISTIDINE KINASE SENSOR PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10833.1 HISTIDINE KINASE SENSOR PROTEIN [Wolinella succinogenes]			2.7.3.-
13203, 13204	34558265	57	3.00E-25	Wolinella succinogenes DSM 1740	signal-transducing protein, histidine kinase [Campylobacter coli RM2228] gb EAL57165.1 signal-transducing protein, histidine kinase [Campylobacter coli RM2228]			2.7.3.-
13205, 13206	34558265	47	3.00E-62	Wolinella succinogenes DSM 1740	PUTATIVE HEMOLYSIN [Wolinella succinogenes DSM 1740] emb CAE10980.1 PUTATIVE HEMOLYSIN [Wolinella succinogenes]			
13207, 13208	45524550	33	7.00E-25	Crocospaera watsonii WH 8501	PUTATIVE HEMOLYSIN [Wolinella succinogenes DSM 1740] emb CAE10980.1 PUTATIVE HEMOLYSIN [Wolinella succinogenes]			
13209, 13210	34557184	50	4.00E-48	Wolinella succinogenes DSM 1740	hypothetical protein Cwat03005121 [Crocospaera watsonii WH 8501]			
1321, 1322	23471862	33	5.00E-15	Pseudomonas syringae pv. syringae B728a	BH0401 PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09899.1 BH0401 PROTEIN [Wolinella succinogenes]			
13211, 13212	34556743	49	5.00E-54	Wolinella succinogenes DSM 1740	COG3172: Predicted ATPase/kinase involved in NAD metabolism [Pseudomonas syringae pv. syringae B728a]			
					hypothetical protein WS0307 [Wolinella succinogenes DSM 1740] emb CAE09458.1 hypothetical protein [Wolinella succinogenes]			

13213, 13214	16519917	39	6.00E-55	Rhizobium sp. NGR234	Y4qJ [Rhizobium sp. NGR234] gb AAB92465.1 Y4qJ [Rhizobium sp. NGR234] sp P55631 Y4QJ_RHISN Putative transposase Y4QJ				
13215, 13216	53762765	32	1.00E-23	Ralstonia eutropha JMP134	COG1073: Hydrolases of the alpha/beta superfamily [Ralstonia eutropha JMP134]				
13217, 13218	15602076	36	4.00E-18	Pasteurella multocida subsp. multocida str. Pm70	hypothetical protein PM0211 [Pasteurella multocida subsp. multocida str. Pm70] gb AAK02295.1 unknown [Pasteurella multocida subsp. multocida str. Pm70] sp Q9CP49 Y211_PASMU Hypothetical UPF0276 protein PM0211				
13227, 13228	23114483	37	3.00E-34	Desulfotobacterium hafnense DCB-2	COG2931: RTX toxins and related Ca2+-binding proteins [Desulfotobacterium hafnense DCB-2]				
13231, 13232	29604946	34	2.00E-13	Streptomyces avermitilis MA-4680	putative esterase [Streptomyces avermitilis MA-4680] ref NP_822479.1 putative esterase [Streptomyces avermitilis MA-4680]				
13233, 13234	20808597	55	9.00E-57	Thermoanaerobacter tengcongensis MB4	Thioredoxin reductase [Thermoanaerobacter tengcongensis MB4] gb AAM25372.1 Thioredoxin reductase [Thermoanaerobacter tengcongensis MB4]				1.6.4.5
13235, 13236	34558248	24	8.00E-17	Wolinella succinogenes DSM 1740	METHYL-ACCEPTING CHEMOTAXIS PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10863.1 METHYL-ACCEPTING CHEMOTAXIS PROTEIN [Wolinella succinogenes]				
13237, 13238	34763541	52	6.00E-58	Fusobacterium nucleatum subsp. vincentii ATCC 49256	SWF/SNF family helicase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA23925.1 SWF/SNF family helicase [Fusobacterium nucleatum subsp. vincentii ATCC 49256]				3.6.1.3
13239, 13240	48856112	38	4.00E-44	Cytophaga hutchinsonii	COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
13241, 13242	48856112	40	3.00E-24	Cytophaga hutchinsonii	COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
13243, 13244	13928880	35	3.00E-29	Rattus norvegicus	plasma glutamate carboxypeptidase [Rattus norvegicus] gb AAC72384.1 hematopoietic lineage switch 2 related protein [Rattus norvegicus]				
13247, 13248	30250110	47	1.00E-46	Nitrosomonas europaea ATCC 19718	hypothetical protein NE2176 [Nitrosomonas europaea ATCC 19718] emb CAD86087.1 conserved hypothetical protein [Nitrosomonas europaea ATCC 19718]				
1325, 1326	21232295	49	3.00E-36	Xanthomonas campestris pv. campestris str. ATCC 33913	monofunctional biosynthetic peptidoglycan transglycosylase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM42136.1 monofunctional biosynthetic peptidoglycan transglycosylase [Xanthomonas campestris pv. campestris str. ATCC 33913] sp Q8P6V1 MTGA_XANCP Monofunctional biosynthetic peptidoglycan transglycosylase (Monofunctional TGase)				2.4.2.-

13255, 13256	34556928	54	4.00E-66	Wol nella succin ogenes DSM 1740	PUTATIVE GAMMA-GLUTAMYL KINASE [Wol nella succinogenes DSM 1740] emb CAE09643.1 PUTATIVE GAMMA-GLUTAMYL KINASE [Wol nella succinogenes] sp Q7MA27 PROB_WOLSU Glutamate 5-kinase (Gamma-glutamyl kinase) (GK)			2.7.2.11
13257, 13258	57168109	38	8.00E-22	Campylobacter coli RM2228	signal-transducing protein, histidine kinase, putative [Campylobacter coli RM2228] gb EAL57152.1 signal-transducing protein, histidine kinase, putative [Campylobacter coli RM2228]			2.7.3.-
13261, 13262	48833864	46	6.00E-25	Magnetococcus sp. MC-1	COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Magnetococcus sp. MC-1]			2.7.3.-
13265, 13266	53712431	37	5.00E-34	Bacteroides fragilis YCH46	hypothetical protein BF1139 [Bacteroides fragilis YCH46] dbj BAD47889.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
1327, 1328	42557748	61	1.00E-31	uncultured crenarchaeote	putative threonine synthase [uncultured crenarchaeote]			4.2.99.2
13271, 13272	20089001	40	7.00E-13	Methanosarcina acetivorans C2A	nucleotidyltransferase [Methanosarcina acetivorans C2A] gb AAM03556.1 nucleotidyltransferase [Methanosarcina acetivorans str. C2A]			2.7.7.-
13273, 13274	20088978	26	2.00E-14	Methanosarcina acetivorans C2A	hypothetical protein MA0079 [Methanosarcina acetivorans C2A] gb AAM03533.1 hypothetical protein (multi-domain) [Methanosarcina acetivorans str. C2A]			
13275, 13276	37520689	23	3.00E-10	Gloeobacter viola ceus PCC 7421	hypothetical protein glf1120 [Gloeobacter violaceus PCC 7421] dbj BAC89061.1 glf1120 [Gloeobacter violaceus PCC 7421]			
13277, 13278	6967633	46	6.00E-29	Campylobacter jejuni subsp. jejuni NCTC 11168	putative endonuclease [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81431 probable endonuclease Cj0139 [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281350.1 putative endonuclease [Campylobacter jejuni subsp. jejuni NCTC 11168]			3.1.21.-
13279, 13280	54303177	46	5.00E-26	Photobacterium profundum SS9	hypothetical protein PBPRB1504 [Photobacterium profundum SS9] emb CAG23370.1 hypothetical protein [Photobacterium profundum] putative zinc metallo protease [Bdellovibrio bacteriovorus HD100] emb CAE81073.1 putative zinc metallo protease [Bdellovibrio bacteriovorus HD100]			3.4.24.-
13281, 13282	42525039	31	3.00E-20	Bdellovibrio bacteriovorus HD100	putative EntE, Peptide arylatase [Photobacterium profundum SS9] emb CAG20073.1 putative EntE, Peptide arylatase [Photobacterium profundum] [Photobacterium profundum]			6.2.1.1
13285, 13286	54308855	26	8.00E-07	Photobacterium profundum SS9	hypothetical protein WS2113 [Wol nella succinogenes DSM 1740] emb CAE11111.1 hypothetical protein [Wol nella succinogenes] COG1373: Predicted ATPase (AAA+ superfamily) [Methanosarcina barkeri str. fusaro]			3.1.3.16
13287, 13288	34558396	33	1.00E-33	Wol nella succin ogenes DSM 1740				
13289, 13290	48837872	44	4.00E-56	Methanosarcina barkeri str. fusaro				

1329, 1330	57169027	34	9.00E-24	Campylobacter coli RM2228	type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228] gb EAL56262.1 type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228]			2.1.1.72
13293, 13294	34557679	50	2.00E-25	Wolinnella succinogenes DSM 1740	hypothetical protein WS1318 [Wolinnella succinogenes DSM 1740] emb CAE10394.1 hypothetical protein [Wolinnella succinogenes]			1.---
13297, 13298	48864174	32	3.00E-14	Microbulbifer degradans 2-40	hypothetical protein Mdeg02000547 [Microbulbifer degradans 2-40]			
133, 134	21227241	30	4.00E-11	Methanosarcina mazel Go1	Dolichyl-phosphate mannosyl transferase related protein [Methanosarcina mazel Go1] gb AAM30835.1 Dolichyl-phosphate mannosyl transferase related protein [Methanosarcina mazel Go1]			2.---
13301, 13302	57241730	36	5.00E-13	Campylobacter lari RM2100	hypothetical protein CLA0161 [Campylobacter lari RM2100] gb EAL54400.1 hypothetical protein CLA0161 [Campylobacter lari RM2100]			
13303, 13304	57167861	27	7.00E-10	Campylobacter coli RM2228	membrane protein, putative [Campylobacter coli RM2228] gb EAL57647.1 membrane protein, putative [Campylobacter coli RM2228]			
13305, 13306	53715232	39	1.00E-09	Bacteroides fragilis YCH46	putative secreted sulfatase ydeN precursor [Bacteroides fragilis YCH46] dbj BAD50690.1 putative secreted sulfatase ydeN precursor [Bacteroides fragilis YCH46]			
13307, 13308	48856591	26	8.00E-08	Cytophaga hutchinsonii	COG0823: Periplasmic component of the Tol biopolymer transport system [Cytophaga hutchinsonii]			
13309, 13310	48855914	38	4.00E-20	Cytophaga hutchinsonii	COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii]			
1331, 1332	57169027	36	2.00E-22	Campylobacter coli RM2228	type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228] gb EAL56262.1 type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228]			2.1.1.72
13313, 13314	32261607	31	2.00E-08	Helicobacter hepaticus ATCC 51449	hypothetical protein HH0060 [Helicobacter hepaticus ATCC 51449] ref NP_859591.1 hypothetical protein HH0060 [Helicobacter hepaticus ATCC 51449]			
13315, 13316	31195913	46	3.00E-47	Anopheles gambiae	ENSANGP00000000411 [Anopheles gambiae] related to 5' to 3' DNA helicase [Desulfotalea psychrophila Lsv54] emb CAG36716.1 related to 5' to 3' DNA helicase [Desulfotalea psychrophila Lsv54]			
13317, 13318	51245839	32	6.00E-21	Desulfotalea psychrophila Lsv54	glycosyl transferase [Rhodopirellula baltica SH 1] emb CAD72671.1 glycosyl transferase [Pirellula sp.]			3.6.1.-
13321, 13322	32471993	34	5.00E-21	Rhodopirellula baltica SH 1	CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinnella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinnella succinogenes]			
13323, 13324	34556616	37	7.00E-21	Wolinnella succinogenes DSM 1740				

13325,	34556616	42	1.00E-40	Wolinella succinogenes DSM 1740	CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes]			
13326				Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]			
13327,	48853894	40	7.00E-37	Pediococcus pentosaceus ATCC 25745	COG2344: AT-rich DNA-binding protein [Pediococcus pentosaceus ATCC 25745]			
13329,	48870017	33	5.00E-22					2.7.7.-
13330								
13331,								
13332								
13333,				Porphyromonas gingivalis W83	cysteine peptidase, putative [Porphyromonas gingivalis W83] ref NP_905889.1 cysteine peptidase, putative [Porphyromonas gingivalis W83]			
13334	34397727	40	2.00E-35					
13335,				Bacillus halodurans C-125	modification methylase [Bacillus halodurans C-125] dbj BAB07723.1 modification methylase [Bacillus halodurans C-125] pir D84150 modification methylase BH4004 [imported] - Bacillus halodurans (strain C-125)			2.1.1.72
13336	15616566	51	6.00E-59					
13337,				Lactococcus lactis subsp. lactis bv. diacetylactis	restriction enzyme [Lactococcus lactis subsp. lactis bv. diacetylactis] gb AAC77902.1 LlaKR21 restriction enzyme [Lactococcus lactis]			3.1.21.4
13338	8489196	31	6.00E-24					
13339,	48832337	37	2.00E-42	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			2.7.3.-
13340								
13341,	48855815	53	2.00E-45	Cytophaga hutchinsonii	COG1600: Uncharacterized Fe-S protein [Cytophaga hutchinsonii]			
13342								
13343,	48831001	24	6.00E-14	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			
13344				Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	aspartate ammonia-lyase, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96243.1 aspartate ammonia-lyase, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			4.3.1.1
13345,	46580176	42	6.00E-33					
13346				Campylobacter jejuni RM1221	DNA-binding response regulator [Campylobacter jejuni RM1221] gb AAW36097.1 DNA-binding response regulator [Campylobacter jejuni RM1221]			
13347,	57238514	30	3.00E-10					
13348				Wolinella succinogenes DSM 1740	hypothetical protein WS1256 [Wolinella succinogenes DSM 1740] emb CAE10335.1 conserved hypothetical protein [Wolinella succinogenes]			
13349,	34557620	58	6.00E-74					
13350				Cytophaga hutchinsonii	hypothetical protein Chut02001830 [Cytophaga hutchinsonii]			
1335,	48855491	44	2.00E-30		hypothetical protein PBPPA1826 [Photobacterium profundum SS9]			
1336				Photobacterium profundum SS9	hypothetical protein [Photobacterium profundum]			
13351,	54309012	30	2.00E-08					
13352								

13353, 13354	30020374	40	1.00E-27	NADP+	Succinate-semialdehyde dehydrogenase [NADP+] [Bacillus cereus ATCC 14579] gb AAP09206.1 Succinate-semialdehyde dehydrogenase [NADP+] [Bacillus cereus ATCC 14579]				1.2.1.3
13357, 13358	34557573	39	1.00E-55	Wolinella succinogenes DSM 1740	SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes]	Leptospira interrogans serovar lai str. 56601 chromosome I, section 229 of 397 of the complete sequence	90	7.00E-07	2.7.3.-
13359, 13360	34556471	36	3.00E-36	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09186.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]				2.7.3.-
13361, 13362	53759644	29	7.00E-23	Methylobacillus flagellatus KT	hypothetical protein Mflag03001521 [Methylobacillus flagellatus KT]				
13363, 13364	48856479	60	3.00E-69	Cytophaga hutchinsonii	COG0179: 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) [Cytophaga hutchinsonii]				4.1.1.-
13365, 13366	48855764	31	4.00E-22	Cytophaga hutchinsonii	COG5316: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
13367, 13368	15605806	47	1.00E-28	Aquifex aerolicus VF5	hypothetical protein aq_265 [Aquifex aerolicus VF5] gb AAC06589.1 hypothetical protein [Aquifex aerolicus VF5] pir C70324 conserved hypothetical protein aq_265 - Aquifex aerolicus				2.7.3.-
13369, 13370	57505466	48	5.00E-49	Campylobacter upsaliensis RM3195	aminoacyl-histidine dipeptidase [Campylobacter upsaliensis RM3195] gb EAL53077.1 aminoacyl-histidine dipeptidase [Campylobacter upsaliensis RM3195]				3.4.13.3
1337, 1338	20803924	28	8.00E-15	Mesorhizobium loti	HYPOTHETICAL PROTEIN [Mesorhizobium loti]				
13371, 13372	48833400	40	3.00E-22	Magnetococcus sp. MC-1	COG0500: SAM-dependent methyltransferases [Magnetococcus sp. MC-1]				
13373, 13374	21228207	29	1.00E-11	Methanosarcina mazel Go1	putative glycosyltransferase [Methanosarcina mazel Go1] gb AAM31801.1 putative glycosyltransferase [Methanosarcina mazel Go1]				2.4.1.-
13375, 13376	34557966	55	1.00E-55	Wolinella succinogenes DSM 1740	ATP-DEPENDENT HELICASE [Wolinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wolinella succinogenes] Histidyl-tRNA synthetase [Thermoanaerobacter tengcongensis MB4] gb AAM24457.1 Histidyl-tRNA synthetase [Thermoanaerobacter tengcongensis MB4] sp Q8RA18 SYH_THETN Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HisRS)				3.6.1.-
13377, 13378	20807682	44	1.00E-60	Thermoanaerobact er tengcongensis MB4					6.1.1.21

13379, 13380	53715401	37	8.00E-20	Bacteroides fragilis YCH46	ribosomal large subunit pseudouridine synthase D [Bacteroides fragilis YCH46] dbj BAD50859.1 ribosomal large subunit pseudouridine synthase D [Bacteroides fragilis YCH46]			4.2.1.70
13381, 13382	53756922	51	7.00E-74	Methylococcus capsulatus str. Bath	heavy metal efflux pump, Czca family [Methylococcus capsulatus str. Bath] ref YP_115121.1 heavy metal efflux pump, Czca family [Methylococcus capsulatus str. Bath]			
13383, 13384	9949348	56	2.00E-28	Pseudomonas aeruginosa PAO1	peptidyl-prolyl cis-trans isomerase A [Pseudomonas aeruginosa PAO1] ref NP_251917.1 peptidyl-prolyl cis-trans isomerase A [Pseudomonas aeruginosa PAO1] sp Q59641 PPIA_PSEAE Peptidyl-prolyl cis-trans isomerase A precursor (PPIase A) (Rotamase A) (Cyclophilin A) pir G83243 peptidyl-prolyl cis-trans isomerase A PA3227 [imported] - Pseudomonas aeruginosa (strain PAO1)		5.2.1.8	
13385, 13386	46580489	34	1.00E-21	Desulfovibrio vulgaris subsp. vulgaris str.	oligopeptide-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96557.1 oligopeptide-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			
13387, 13388	48833864	39	3.00E-35	Magnetococcus sp. MC-1	COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Magnetococcus sp. MC-1]			2.7.3.-
13389, 13390	34556565	36	2.00E-26	Wolinella succinogenes DSM 1740	PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09280.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes] emb CAD23185.1 putative transcriptional regulator protein [Wolinella succinogenes]			
1339, 1340	48853838	47	1.00E-28	Cytophaga hutchinsonii	COG1522: Transcriptional regulators [Cytophaga hutchinsonii]			
13391, 13392	24373599	34	4.00E-09	Shewanella oneidensis MR-1	hypothetical protein SO2039 [Shewanella oneidensis MR-1] gb AAN55086.1 conserved domain protein [Shewanella oneidensis MR-1]			
13393, 13394	34557297	53	8.00E-34	Wolinella succinogenes DSM 1740	PUTATIVE TRANSPORTER [Wolinella succinogenes DSM 1740] emb CAE10012.1 PUTATIVE TRANSPORTER [Wolinella succinogenes]			1.8.-
13395, 13396	53730423	45	1.00E-32	Dechloromonas aromatica RCB	COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB]			
13399, 13400	32451220	52	5.00E-21	Bacteroides sp. 139	putative dTDP-dehydrohamnose reductase [Bacteroides sp. 139]			1.1.1.13 3
13401, 13402	19704339	32	2.00E-18	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Transcriptional regulator, TetR family [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95200.1 Transcriptional regulator, TetR family [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			
13403, 13404	48853332	28	2.00E-10	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]			

13405, 13406	56709007	30	2.00E-20	Silicibacter pomeroyi DSS-3	cytochrome cd1 nitrite reductase [Silicibacter pomeroyi DSS-3] gb AAV97357.1 cytochrome cd1 nitrite reductase [Silicibacter pomeroyi DSS-3]			
13407, 13408	34557573	54	8.00E-48	Wolinella succinogenes DSM 1740	SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes]			2.7.3.-
1341, 1342	20806566	53	2.00E-68	Thermoanaerobacter tengcongensis MB4	Seryl-tRNA synthetase [Thermoanaerobacter tengcongensis MB4] gb AAM2334.1 Seryl-tRNA synthetase [Thermoanaerobacter tengcongensis MB4] sp Q8RDJ5 SYS_THEIN Seryl-tRNA synthetase (Seryl-tRNA ligase) (SerRS)			6.1.1.11
13411, 13412	34556560	42	6.00E-73	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]			
13413, 13414	34557407	40	2.00E-51	Wolinella succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10122.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes]			2.7.3.-
13415, 13416	48860860	59	1.00E-100	Microbulbifer degradans 2-40	COG0439: Biotin carboxylase [Microbulbifer degradans 2-40]			6.3.4.6
13417, 13418	34557494	60	1.00E-81	Wolinella succinogenes DSM 1740	PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes DSM 1740] emb CAE10209.1 PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes]	Wolinella succinogenes, complete genome; segment 4/7	84	4.00E-08 6.3.5.-
13419, 13420	13508081	28	9.00E-20	Mycoplasma pneumoniae M129	type I restriction enzyme HsdM [Mycoplasma pneumoniae M129] gb AAB96142.1 type I restriction enzyme HsdM [Mycoplasma pneumoniae M129] pir S73820 type I restriction enzyme hsdM - Mycoplasma pneumoniae (strain ATCC 29342) sp P75436 T1MD_MYCPN Putative type I restriction enzyme MpnORFDP M protein (M.MpnORFDP) (H91_orf543)			2.1.1.72
13421, 13422	AAU3570	1	2.00E-81		Desc:Helicobacter pylori cellular proliferation protein #14. Org:Helicobacter pylori			2.7.9.2
13425, 13426	37678843	47	9.00E-53	Vibrio vulnificus YJ016	hypothetical protein VV0659 [Vibrio vulnificus YJ016] db BAC93423.1 conserved hypothetical protein [Vibrio vulnificus YJ016]			
13427, 13428	53714594	42	1.00E-29	Bacteroides fragilis YCH46	LacI family transcriptional regulator [Bacteroides fragilis YCH46] db BAD50052.1 LacI family transcriptional regulator [Bacteroides fragilis YCH46]			
13429, 13430	34557684	51	2.00E-38	Wolinella succinogenes DSM 1740	PHOSPHOTYROSINE PROTEIN PHOSPHATASE [Wolinella succinogenes DSM 1740] emb CAE10399.1 PHOSPHOTYROSINE PROTEIN PHOSPHATASE [Wolinella succinogenes]			3.1.3.48
1343, 1344	48854902	41	5.00E-34	Cytophaga hutchinsonii	COG0845: Membrane-fusion protein [Cytophaga hutchinsonii]			

13431, 13432	16078046	51	8.00E-67	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU09810 [Bacillus subtilis subsp. subtilis str. 168] emb CAA74443.1 hypothetical protein [Bacillus subtilis] emb CAB12820.1 yhaZ [Bacillus subtilis subsp. subtilis str. 168] pir D69820 hypothetical protein yhaZ - Bacillus subtilis				
13433, 13434	20092636	40	7.00E-22	Methanosarcina acetivorans C2A	hypothetical protein MA3840 [Methanosarcina acetivorans C2A] gb AAM07191.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A]				
13437, 13438	48855764	39	3.00E-18	Cytophaga hutchinsonii	COG5316: Uncharacterized conserved protein [Cytophaga hutchinsonii] putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] gb AAO78416.1 putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482]				
13439, 13440	29348719	59	5.00E-24	Bacteroides thetaiotaomicron VPI-5482	hydrogenase maturation protein HypF [Shewanella oneidensis MR-1] gb AAN55141.1 hydrogenase maturation protein HypF [Shewanella oneidensis MR-1]				
13441, 13442	24373654	45	3.00E-57	Shewanella oneidensis MR-1	MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10559.1 MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes]				
13445, 13446	34557844	25	2.00E-21	Wolinella succinogenes DSM 1740	SULFATE ADENYLYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE10944.1 SULFATE ADENYLYLTRANSFERASE [Wolinella succinogenes]				2.7.7.4
13447, 13448	34558229	46	4.00E-63	Wolinella succinogenes DSM 1740	DNA-binding response regulator RprY [Alvinella pompejana epibiont 6C6] transcriptional regulator, Crp family [Porphyromonas gingivalis W83] ref NP_905705.1 transcriptional regulator, Crp family [Porphyromonas gingivalis W83]				2.7.3.-
13449, 13450	34558806	31	6.00E-13	Alvinella pompejana epibiont 6C6	COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii]				
1345, 1346	34397542	33	1.00E-31	Porphyromonas gingivalis W83	hypothetical protein WS0587 [Wolinella succinogenes DSM 1740] emb CAE09719.1 conserved hypothetical protein [Wolinella succinogenes]				
13457, 13458	48855914	52	5.00E-21	Cytophaga hutchinsonii	APOLIPOPROTEIN N-ACYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09249.1 APOLIPOPROTEIN N-ACYLTRANSFERASE [Wolinella succinogenes] sp Q7MAR3 LNT_WOLSU Apolipoprotein N- acyltransferase (ALP N-acyltransferase)				2.3.1.-
13459, 13460	34557004	52	5.00E-39	Wolinella succinogenes DSM 1740	hypothetical protein PBPR3401 [Photobacterium profundum SS9] emb CAG21685.1 conserved hypothetical protein [Photobacterium profundum]				
13461, 13462	34556534	40	2.00E-51	Wolinella succinogenes DSM 1740					
13463, 13464	54310467	31	6.00E-14	Photobacterium profundum SS9					

13465,	48863717	26	2.00E-19	Microbulbifer	COG2308: Uncharacterized conserved protein [Microbulbifer degradans 2-40]				
13466				degradans 2-40					
13467,	48863716	40	1.00E-48	Microbulbifer	COG1305: Transglutaminase-like enzymes, putative cysteine proteases [Microbulbifer degradans 2-40]				
13468				degradans 2-40					
13469,				Helicobacter	hypothetical protein HH0949 [Helicobacter hepaticus ATCC 51449]				
13470	32262499	50	5.00E-09	hepaticus ATCC 51449	ref NP_860480.1 hypothetical protein HH0949 [Helicobacter hepaticus ATCC 51449]				
1347,				Geobacter	hypothetical protein GSU0981 [Geobacter sulfurreducens PCA]				
1348	39996084	36	2.00E-22	sulfurreducens PCA	gb AAK34308.1 conserved hypothetical protein [Geobacter sulfurreducens PCA]				
13471,				Campylobacter	phosphoglucosamine mutase [Campylobacter upsaliensis RM3195]				
13472	57242727	65	1.00E-102	upsaliensis RM3195	gb EAL53440.1 phosphoglucosamine mutase [Campylobacter upsaliensis RM3195]			83	3.00E-15 5.4.2.-
13473,				Campylobacter	probable transcription regulator Cj0571 [Campylobacter lari RM2100]				
13474	57240278	42	1.00E-41	lari RM2100	gb EAL55392.1 probable transcription regulator Cj0571 [Campylobacter lari RM2100]				
13475,				Magnetococcus sp.	COG2602: Beta-lactamase class D [Magnetococcus sp. MC-1]				3.5.2.6
13476	48834051	49	2.00E-24	MC-1					
13477,				Shewanella	hypothetical protein SO1851 [Shewanella oneidensis MR-1] gb AAN54903.1 conserved hypothetical protein [Shewanella oneidensis MR-1]				
13478	24373416	77	2.00E-81	oneidensis MR-1	related to ATP-dependent helicase [Desulfotalea psychrophila LSV54]			89	3.00E-08 2.1.1.-
13481,				Desulfotalea	emb CAG36812.1 related to ATP-dependent helicase [Desulfotalea psychrophila LSV54]				
13482	51245835	35	3.00E-41	psychrophila LSV54	two-component hybrid sensor and regulator [Nostoc sp. PCC 7120]				3.-.-.-
13489,				Nostoc sp. PCC	pir AB2276 two-component hybrid sensor and regulator air3761 [imported] - Nostoc sp. (strain PCC 7120) db BAB75460.1 two-component hybrid sensor and regulator [Nostoc sp. PCC 7120]				
13490	17231253	36	9.00E-26	7120				95	1.00E-07 2.7.3.-
1349,				Bacteroides	histidinol-phosphate aminotransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75309.1 histidinol-phosphate aminotransferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8ABA8 HIS8_BACTN Histidinol-phosphate aminotransferase [imidazole acetol-phosphate transaminase]				
1350	29345612	48	6.00E-83	VPI-5482				87	5.00E-08 2.6.1.9
13493,				Desulfotalea	hypothetical protein DP1553 [Desulfotalea psychrophila LSV54]				
13494	51245405	41	2.00E-30	psychrophila LSV54	emb CAG36282.1 unknown protein [Desulfotalea psychrophila LSV54]				

13495, 13496	34332886	28	4.00E-19	12472	Chromobacterium violaceum ATCC	conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_903131.1 hypothetical protein CV3461 [Chromobacterium violaceum ATCC 12472]			2.7.3.-
13497, 13498	34558788	33	4.00E-35	6C6	Alvinella pompejana epibiont	TPR domain protein [Alvinella pompejana epibiont 6C6]			
135, 136	48855435	48	3.00E-24	hutchinsonii	Cytophaga hutchinsonii	COG0777: Acetyl-CoA carboxylase beta subunit [Cytophaga hutchinsonii]			6.4.1.2
13503, 13504	3511126	37	1.00E-37	aegyptius	Haemophilus aegyptius	HaeIV restriction/modification system [Haemophilus aegyptius]			
13505, 13506	23130584	36	6.00E-19	PCC 73102	Nostoc punctiforme	COG0816: Predicted endonuclease involved in recombination (possible Holliday junction resolvase in Mycoplasmas and B. subtilis) [Nostoc punctiforme PCC 73102]			
13507, 13508	15606156	38	6.00E-38	VF5	Aquifex aeolicus	hypothetical protein aq_775 [Aquifex aeolicus VF5] gb AAC06941.1 hypothetical protein [Aquifex aeolicus VF5] pir A70368 conserved hypothetical protein aq_775 - Aquifex aeolicus			4.-.-.-
13509, 13510	24373682	35	1.00E-25	Shewanella oneidensis MR-1	Shewanella oneidensis MR-1	purine-binding chemotaxis protein CheW [Shewanella oneidensis MR-1] gb AAN55169.1 purine-binding chemotaxis protein CheW [Shewanella oneidensis MR-1]			2.7.3.-
1351, 1352	23112865	41	1.00E-35	hafnense DCB-2	Desulfitobacterium hafnense DCB-2	COG4636: Uncharacterized protein conserved in cyanobacteria [Desulfitobacterium hafnense DCB-2]			
13511, 13512	13357672	38	5.00E-13	str. ATCC 700970	Ureaplasma parvum serovar 3	phosphoglycolate phosphatase [Ureaplasma parvum serovar 3 str. ATCC 700970] gb AAF30521.1 phosphoglycolate phosphatase [Ureaplasma parvum serovar 3 str. ATCC 700970] pir F82931 phosphoglycolate phosphatase UU115 [imported] - Ureaplasma urealyticum			3.1.3.18
13513, 13514	32261701	51	1.00E-38	51449	Helicobacter hepaticus ATCC	transcription elongation factor GreA [Helicobacter hepaticus ATCC 51449] ref NP_859685.1 transcription elongation factor GreA [Helicobacter hepaticus ATCC 51449]			
13515, 13516	48846821	30	2.00E-17	15	Geobacter metallireducens GS	COG0639: Diadenosine tetraphosphatase and related serine/threonine protein phosphatases [Geobacter metallireducens GS-15]			3.1.3.16
13521, 13522	52550386	43	9.00E-20	GZfos3D4	uncultured archaeon	putative glycerate kinase [uncultured archaeon GZfos3D4]			1.1.1.81
13523, 13524	48863830	47	7.00E-30	degradans 2-40	Microbulbifer degradans 2-40	COG0463: Glycosyltransferases involved in cell wall biogenesis [Microbulbifer degradans 2-40]			
13525, 13526	34557111	35	1.00E-08	1740	Wolinella succinogenes DSM	hypothetical protein WS0700 [Wolinella succinogenes DSM 1740] emb CAE09826.1 hypothetical protein [Wolinella succinogenes]			

13529, 13530	29142624	28	2.00E-20	Salmonella enterica subsp. enterica serovar Typhi Ty2	putative aminotransferase CobD [Salmonella enterica subsp. enterica serovar Typhi Ty2] ref NP_455220.1 putative aminotransferase CobD [Salmonella enterica subsp. enterica serovar Typhi str. CT18] gb AAO69826.1 putative aminotransferase CobD [Salmonella enterica subsp. enterica serovar Typhi Ty2] emb CAD05121.1 putative aminotransferase CobD [Salmonella enterica subsp. enterica serovar Typhi] pir AG0581 probable aminotransferase CobD cobD [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) sp Q8Z8H8 COBD_SALT1 Threonine-phosphate decarboxylase (L-threonine-O-3-phosphate decarboxylase)			2.6.1.9
13533, 13534 13535, 13536	29348161 53691857	53 39	1.00E-87 3.00E-43	Bacteroides thetaiotaomicron VPI-5482 Desulfovibrio desulfuricans G20	primosomal protein N' (replication factor Y) [Bacteroides thetaiotaomicron VPI-5482] gb AAO77858.1 primosomal protein N' (replication factor Y) [Bacteroides thetaiotaomicron VPI-5482] COG1876: D-alanyl-D-alanine carboxypeptidase [Desulfovibrio desulfuricans G20]			
13537, 13538	32469350	53	4.00E-25	Francisella tularensis subsp. novicida	unknown [Francisella tularensis subsp. novicida] GUANYLATE KINASE [Wolinella succinogenes DSM 1740] emb CAE09349.1 GUANYLATE KINASE [Wolinella succinogenes] sp Q7MAK5 KGUA_WOLSU Guanylate kinase (GMP kinase) COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] DNA polymerase III, alpha subunit [Porphyromonas gingivalis W83] ref NP_904390.1 DNA polymerase III, alpha subunit [Porphyromonas gingivalis W83]	Francisella tularensis subsp. novicida strain FSC040 region of difference 1 (RD1), complete sequence	88 2.00E-07	2.7.4.8
13539, 13540 13541, 13542	34556634 48856940	53 33	4.00E-57 1.00E-15	Wolinella succinogenes DSM 1740 Cytophaga hutchinsonii	2-HYDROXY-6-OXOHEPTA-2,4-DIENOATE HYDROLASE [Wolinella succinogenes DSM 1740] emb CAE09579.1 2-HYDROXY-6-OXOHEPTA-2,4-DIENOATE HYDROLASE [Wolinella succinogenes] D-ALANYL-D-ALANINE-ADDING ENZYME [Wolinella succinogenes DSM 1740] emb CAE09578.1 D-ALANYL-D-ALANINE-ADDING ENZYME [Wolinella succinogenes] COG4191: Signal transduction histidine kinase regulating C4-dicarboxylate transport system [Magnetococcus sp. MC-1]			2.7.7.7
13545, 13546	34396222	60	1.00E-102	Porphyromonas gingivalis W83	2-HYDROXY-6-OXOHEPTA-2,4-DIENOATE HYDROLASE [Wolinella succinogenes DSM 1740] emb CAE09579.1 2-HYDROXY-6-OXOHEPTA-2,4-DIENOATE HYDROLASE [Wolinella succinogenes] D-ALANYL-D-ALANINE-ADDING ENZYME [Wolinella succinogenes DSM 1740] emb CAE09578.1 D-ALANYL-D-ALANINE-ADDING ENZYME [Wolinella succinogenes] COG4191: Signal transduction histidine kinase regulating C4-dicarboxylate transport system [Magnetococcus sp. MC-1]			6.3.2.15
13549, 13550	34556864	48	8.00E-46	Wolinella succinogenes DSM 1740	2-HYDROXY-6-OXOHEPTA-2,4-DIENOATE HYDROLASE [Wolinella succinogenes DSM 1740] emb CAE09579.1 2-HYDROXY-6-OXOHEPTA-2,4-DIENOATE HYDROLASE [Wolinella succinogenes] D-ALANYL-D-ALANINE-ADDING ENZYME [Wolinella succinogenes DSM 1740] emb CAE09578.1 D-ALANYL-D-ALANINE-ADDING ENZYME [Wolinella succinogenes] COG4191: Signal transduction histidine kinase regulating C4-dicarboxylate transport system [Magnetococcus sp. MC-1]			2.7.3.-
13551, 13552 13553, 13554 13555, 13556	34556863 48833776 5360168	48 36 32	1.00E-22 3.00E-33 9.00E-37	Wolinella succinogenes DSM 1740 Magnetococcus sp. MC-1 Flavobacterium johnsoniae	2-HYDROXY-6-OXOHEPTA-2,4-DIENOATE HYDROLASE [Wolinella succinogenes DSM 1740] emb CAE09579.1 2-HYDROXY-6-OXOHEPTA-2,4-DIENOATE HYDROLASE [Wolinella succinogenes] D-ALANYL-D-ALANINE-ADDING ENZYME [Wolinella succinogenes DSM 1740] emb CAE09578.1 D-ALANYL-D-ALANINE-ADDING ENZYME [Wolinella succinogenes] COG4191: Signal transduction histidine kinase regulating C4-dicarboxylate transport system [Magnetococcus sp. MC-1] GldB [Flavobacterium johnsoniae]			

13559, 13560	57237231	52	2.00E-65	Campylobacter jejuni RM1221	DNA adenine methylase [Campylobacter jejuni RM1221] gb AAW34814.1 DNA adenine methylase [Campylobacter jejuni RM1221]			2.1.1.72
13561, 13562	48856760	45	3.00E-33	Cytophaga hutchinsonii	COG2062: Phosphohistidine phosphatase SixA [Cytophaga hutchinsonii]			3.1.3.-
13563, 13564	52550557	39	7.00E-55	uncultured archaeon GZfos9E5	predicted P-loop ATPase [uncultured archaeon GZfos9E5]			
13565, 13566	34557232	37	8.00E-16	Wolinella succinogenes DSM 1740	NIFS PROTEIN (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE09947.1 NIFS PROTEIN (FRAGMENT) [Wolinella succinogenes]			4.4.1.-
13567, 13568	57169090	35	3.00E-12	Campylobacter coli RM2228	N-terminal HTH domain of molybdenum-binding protein family [Campylobacter coli RM2228] gb EAL56239.1 N-terminal HTH domain of molybdenum-binding protein family [Campylobacter coli RM2228]			
13569, 13570	21673339	26	5.00E-14	Chlorobium tepidum TLS	hypothetical protein CT0504 [Chlorobium tepidum TLS] gb AAM71746.1 hypothetical protein [Chlorobium tepidum TLS]			
1357, 1358	47569655	62	3.00E-09	Bacillus cereus G9241	prophage LambdaSa2, HNH endonuclease family protein [Bacillus cereus G9241] gb EAL12072.1 prophage LambdaSa2, HNH endonuclease family protein [Bacillus cereus G9241]			
13573, 13574	34556738	52	9.00E-87	Wolinella succinogenes DSM 1740	SUCCINYLORNITHINE TRANSAMINASE [Wolinella succinogenes DSM 1740] emb CAE09453.1 SUCCINYLORNITHINE TRANSAMINASE [Wolinella succinogenes] sp Q7MAE6 ARGD_WOLSU Acetylornithine aminotransferase (ACOAT)			2.6.1.11
13575, 13576	34556738	53	9.00E-57	Wolinella succinogenes DSM 1740	SUCCINYLORNITHINE TRANSAMINASE [Wolinella succinogenes DSM 1740] emb CAE09453.1 SUCCINYLORNITHINE TRANSAMINASE [Wolinella succinogenes] sp Q7MAE6 ARGD_WOLSU Acetylornithine aminotransferase (ACOAT)			2.6.1.11
13577, 13578	48853920	49	2.00E-30	Cytophaga hutchinsonii	COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii]			
13579, 13580	34558448	56	2.00E-25	Wolinella succinogenes DSM 1740	ANTHRANILATE SYNTHASE COMPONENT II [Wolinella succinogenes DSM 1740] emb CAE11163.1 ANTHRANILATE SYNTHASE COMPONENT II [Wolinella succinogenes]			4.1.3.27
13583, 13584	15893748	27	9.00E-10	Clostridium acetobutylicum ATCC 824	Transcriptional regulator, AcrR family [Clostridium acetobutylicum ATCC 824] gb AAK78437.1 Transcriptional regulator, AcrR family [Clostridium acetobutylicum ATCC 824] pir B96956 transcription regulator, AcrR family [[imported] - Clostridium acetobutylicum]			
13585, 13586	34557295	24	1.00E-13	Wolinella succinogenes DSM 1740	hypothetical protein WS0905 [Wolinella succinogenes DSM 1740] emb CAE10010.1 hypothetical protein [Wolinella succinogenes]			

13587, 13588	19705009	30	1.00E-30	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Oxidoreductase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93803.1 Oxidoreductase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			1.1.1.-
13589, 13590	57238414	50	3.00E-40	Campylobacter jejuni RM1221	nucleotide phosphoribosyltransferase, putative [Campylobacter jejuni RM1221] gb AAW35997.1 nucleotide phosphoribosyltransferase, putative [Campylobacter jejuni RM1221] emb CAB73797.1 putative nucleotide phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir G81281 probable nucleotide phosphoribosyltransferase C 1370 [Imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282516.1 putative nucleotide phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168]			2.4.2.22
1359, 1360	47569655	39	4.00E-13	Bacillus cereus G9241	prophage LambdaSa2, HNH endonuclease family protein [Bacillus cereus G9241] gb EAL12072.1 prophage LambdaSa2, HNH endonuclease family protein [Bacillus cereus G9241]			
13591, 13592	48893877	30	7.00E-12	Trichodesmium erythraeum IMS101	COG0642: Signal transduction histidine kinase [Trichodesmium erythraeum IMS101]			2.7.3.-
13593, 13594	34557246	57	3.00E-61	Wolinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]			2.7.3.-
13597, 13598	45528155	59	9.00E-23	Crocospaera watsonii WH 8501	COG0662: Mannose-6-phosphate isomerase [Crocospaera watsonii WH 8501]			
13599, 13600	53731618	68	4.00E-61	Methanococcoides burtonii DSM 6242	COG0577: ABC-type antimicrobial peptide transport system, permease component [Methanococcoides burtonii DSM 6242]			
13601, 13602	53731618	75	3.00E-88	Methanococcoides burtonii DSM 6242	COG0577: ABC-type antimicrobial peptide transport system, permease component [Methanococcoides burtonii DSM 6242]			
13603, 13604	27366052	37	2.00E-40	Vibrio vulnificus CMCP6	ABC-type amino acid transport, signal transduction systems, periplasmic component/domain [Vibrio vulnificus CMCP6] gb AAO11107.1 ABC-type amino acid transport, signal transduction systems, periplasmic component/domain [Vibrio vulnificus CMCP6]			
13605, 13606	17545857	43	4.00E-31	Ralstonia solanacearum GMI1000	PUTATIVE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum GMI1000] emb CAD14840.1 PUTATIVE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum]			
13607, 13608	32261983	41	3.00E-08	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_859966.1 hypothetical protein HH0435 [Helicobacter hepaticus ATCC 51449] gb AAD30109.1 membrane-associated protein map18 [Helicobacter hepaticus]			

13609, 13610	23126603	34	9.00E-38	Nostoc punctiforme PCC 73102	COG0834: ABC-type amino acid transport/signal transduction systems, periplasmic component/domain [Nostoc punctiforme PCC 73102]			
1361, 1362	48856375	37	3.00E-27	Cytophaga hutchinsonii	COG0568: DNA-directed RNA polymerase, sigma subunit (sigma70/sigma32) [Cytophaga hutchinsonii]			
13611, 13612	46578435	29	7.00E-42	Desulfovibrio vulgaris subsp. vulgaris str.	methyl-accepting chemotaxis protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AA594502.1 methyl-accepting chemotaxis protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			2.7.3.-
13613, 13614	21226648	30	6.00E-11	Methanosarcina mazel Go1	hypothetical protein MM0546 [Methanosarcina mazel Go1] gb AAM30242.1 conserved protein [Methanosarcina mazel Go1]			
13615, 13616	54024734	40	8.00E-38	Nocardia farcinica IFM 10152	putative restriction-modification system endonuclease [Nocardia farcinica IFM 10152] dbj BAD57612.1 putative restriction-modification system endonuclease [Nocardia farcinica IFM 10152]			3.1.21.3
13619, 13620	48855496	42	1.00E-64	Cytophaga hutchinsonii	COG0514: Superfamily II DNA helicase [Cytophaga hutchinsonii]			3.6.1.-
13621, 13622	57238514	34	4.00E-21	Campylobacter jejuni RM1221	DNA-binding response regulator [Campylobacter jejuni RM1221]			2.7.3.-
13623, 13624	42522455	41	5.00E-27	Bdellovibrio bacteriovorus HD100	cell wall surface anchor family protein [Bdellovibrio bacteriovorus HD100] emb CAE78828.1 cell wall surface anchor family protein [Bdellovibrio bacteriovorus HD100]			
13629, 13630	46019826	40	2.00E-46	Streptococcus thermophilus	putative cytosine-specific methyltransferase [Streptococcus thermophilus]			2.1.1.73
1363, 1364	48853840	32	9.00E-25	Cytophaga hutchinsonii	COG0438: Glycosyltransferase [Cytophaga hutchinsonii]			
13631, 13632	57240720	47	3.00E-48	Campylobacter lari RM2100	biotin--acetyl-CoA-carboxylase ligase [Campylobacter lari RM2100] gb EAL55113.1 biotin--acetyl-CoA-carboxylase ligase [Campylobacter lari RM2100]			6.3.4.15
13635, 13636	53765153	35	4.00E-16	Anabaena variabilis ATCC 29413	COG1975: Xanthine and CO dehydrogenases maturation factor, XdhC/CoxF family [Anabaena variabilis ATCC 29413]			
13637, 13638	57241988	42	4.00E-19	Campylobacter upsaliensis RM3195	folypolyglutamate synthase (folC) [Campylobacter upsaliensis RM3195] gb EAL53961.1 folypolyglutamate synthase (folC) [Campylobacter upsaliensis RM3195]			6.3.2.17
13641, 13642	54302389	55	6.00E-88	Photobacterium profundum SS9	hypothetical protein PBPRB0710 [Photobacterium profundum SS9] emb CAG22582.1 hypothetical protein [Photobacterium profundum SS9]			6.3.2.3
13643, 13644	54302390	56	3.00E-46	Photobacterium profundum SS9	hypothetical carboxypeptidase G2 [Photobacterium profundum SS9] emb CAG22583.1 hypothetical carboxypeptidase G2 [Photobacterium profundum]			3.4.17.1 1

13645,	29347044	39	4.00E-26	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT1634 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76741.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
13646					unnamed protein product [Homo sapiens] emb CAD97795.1 hypothetical protein [Homo sapiens]				3.7.1.2
13647,	31291	59	8.00E-74	Homo sapiens	conserved hypothetical protein [Campylobacter coli RM2228]				
13648				Campylobacter coli RM2228	gb EAL56657.1 conserved hypothetical protein [Campylobacter coli RM2228]				
13651,				Synechococcus elongatus PCC 6301	hypothetical protein syc0173_c [Synechococcus elongatus PCC 6301] dbj BAD78363.1 hypothetical protein [Synechococcus elongatus PCC 6301]				2.7.3.-
13652	57168696	42	1.00E-23	Campylobacter coli RM2228	probable membrane protein Cj0152c [Campylobacter lari RM2100] gb EAL54499.1 probable membrane protein Cj0152c [Campylobacter lari RM2100]				
13653,	56750182	33	2.00E-08	Campylobacter lari RM2100	conserved hypothetical protein; putative sensory transduction histidine kinase [Acinetobacter sp. ADP1] emb CAG69864.1 conserved hypothetical protein; putative sensory transduction histidine kinase [Acinetobacter sp. ADP1]				2.7.3.-
13654				Acinetobacter sp. ADP1	putative membrane protein [Staphylococcus aureus subsp. aureus MRSA252] emb CAG40924.1 putative membrane protein [Staphylococcus aureus subsp. aureus MRSA252]				
13655,	57241387	30	2.00E-18	Staphylococcus aureus subsp. MRSA252	DNA-binding response regulator [Campylobacter jejuni RM1221] gb AAW35678.1 DNA-binding response regulator [Campylobacter jejuni RM1221] emb CAB73477.1 putative two-component regulator [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282370.1 putative two-component regulator [Campylobacter jejuni subsp. jejuni NCTC 11168] pir A81329 probable two-component regulator Cj1223c [imported] - Campylobacter jejuni (strain NCTC 11168)				
13656	50086176	25	3.00E-14	Campylobacter jejuni RM1221	COG0265: Trypsin-like serine proteases, typically periplasmic, contain C- terminal PDZ domain [Cytophaga hutchinsonii]				87 6.00E-12 2.7.3.-
13659,				Cytophaga hutchinsonii	Highly conserved protein containing a domain related to cellulase catalytic domain and a thioredoxin domain [Clostridium acetobutylicum ATCC 824]				3.4.21.-
13660	49484088	22	1.00E-07	Clostridium acetobutylicum ATCC 824	gb AAK81471.1 Highly conserved protein containing a domain related to cellulase catalytic domain and a thioredoxin domain [Clostridium acetobutylicum ATCC 824] pir D97335 hypothetical protein CAC3546 [imported] - Clostridium acetobutylicum				2.7.4.9
13663,				Sinorhizobium meliloti 1021	PUTATIVE TWO 2-COMPONENT RECEIVER DOMAINS PROTEIN [Sinorhizobium meliloti 1021] emb CAC46578.1 PUTATIVE TWO 2- COMPONENT RECEIVER DOMAINS PROTEIN [Sinorhizobium meliloti]				
13664	15896782	37	2.00E-45						
13667,	57238095	49	6.00E-35						
13668									
1367,	48853600	36	4.00E-31						
1368									
13673,									
13674									
13675,									
13676	15965752	32	5.00E-17						

13677, 13678	34556483	61	1.00E-105	Wollinella succinogenes DSM 1740	PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wollinella succinogenes DSM 1740] emb CAE09198.1 PUTATIVE UDP- GLUCURONIC ACID EPIMERASE [Wollinella succinogenes]	B.thuringiensis PK1 & cap genes, putative	85	3.00E-18	5.1.3.-
13683, 13684	3122989	70	5.00E-52	Escherichia coli	UDP-glucose 6-dehydrogenase (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) gb AAC45829.1 hypothetical uridine-5'-diphosphoglucose dehydrogenase [Escherichia coli]	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	88	5.00E-09	1.1.1.22
13685, 13686	57240662	39	7.00E-33	Campylobacter lari RM2100	response regulator [Campylobacter lari RM2100] gb EAL55055.1 response regulator [Campylobacter lari RM2100]				2.7.3.-
13689, 13690	57240337	55	2.00E-46	Campylobacter lari RM2100	HIT family protein [Campylobacter lari RM2100] gb EAL55451.1 HIT family protein [Campylobacter lari RM2100]				3.6.1.17
1369, 1370	53797583	49	9.00E-52	Chloroflexus aurantiacus	COG1200: RecG-like helicase [Chloroflexus aurantiacus]				3.6.1.-
13693, 13694	42525039	34	9.00E-20	Bdellovibrio bacteriovorus HD100	putative zinc metallo protease [Bdellovibrio bacteriovorus HD100] emb CAE81073.1 putative zinc metallo protease [Bdellovibrio bacteriovorus HD100]				3.4.24.-
13695, 13696	52548588	28	1.00E-11	uncultured archaeon GZfos17F1	FOG TPR repeat [uncultured archaeon GZfos17F1]				
137, 138	39997183	41	3.00E-42	Geobacter sulfurreducens PCA	ADP-heptose synthase [Geobacter sulfurreducens PCA] gb AAR35461.1 ADP-heptose synthase [Geobacter sulfurreducens PCA] sp Q74BF6 HLDE_GEOSL Bifunctional protein hldE [Includes: D-beta-D- heptose 7-phosphate kinase (D-beta-D-heptose 7-phosphotransferase); D- beta-D-heptose 1-phosphate adenosyltransferase]				2.7.-:-
13703, 13704	34557665	47	5.00E-27	Wollinella succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wollinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wollinella succinogenes]				2.7.3.-
13705, 13706	34556560	52	1.00E-31	Wollinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes]				
13707, 13708	23123945	27	3.00E-24	Nostoc punctiforme PCC 73102	COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102]				2.7.3.-
1371, 1372	48853483	45	3.00E-29	Cytophaga hutchinsonii	COG0566: rRNA methylases [Cytophaga hutchinsonii]				2.1.1.34
13713, 13714	48854978	52	3.00E-68	Cytophaga hutchinsonii	COG1410: Methionine synthase 1, cobalamin-binding domain [Cytophaga hutchinsonii]				2.1.1.13

13715, 13716	13472325	32	6.00E-23	Mesorhizobium loti MAFF303099	endo-1,3-1,4-beta-glycanase [Mesorhizobium loti MAFF303099] dbj BAB49678.1 endo-1,3-1,4-beta-glycanase [Mesorhizobium loti MAFF303099]			3.2.1.-
13717, 13718	34557931	67	3.00E-73	Wolinella succinogenes DSM 1740	PUTATIVE TRANSCRIPTION REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10646.1 PUTATIVE TRANSCRIPTION REGULATOR [Wolinella succinogenes]			2.1.1.63
13719, 13720	48846313	38	7.00E-11	Geobacter metallireducens GS-15	COG1450: Type II secretory pathway, component PulD [Geobacter metallireducens GS-15]			
13721, 13722	15606636	27	4.00E-10	Aquifex aeolicus VF5	hypothetical protein aq_1473 [Aquifex aeolicus VF5] gb AAC07420.1 putative protein [Aquifex aeolicus VF5] pir A70428 hypothetical protein aq_1473 - Aquifex aeolicus			
13725, 13726	46201088	66	1.00E-97	Magnetospirillum magnetotacticum MS-1	COG2192: Predicted carbamoyl transferase, NodU family [Magnetospirillum magnetotacticum MS-1]	Prochlorococcus marinus MED4 complete genome; segment 4/5	86 2.00E-10	2.7.3.-
13729, 13730	34555660	30	1.00E-27	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]			2.7.3.-
1373, 1374	48855091	36	2.00E-31	Cytophaga hutchinsonii	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii]			2.7.3.-
13731, 13732	29347060	37	4.00E-17	Bacteroides thetalaotomicron VPI-5482	putative teichoic acid biosynthesis protein F [Bacteroides thetalaotomicron VPI-5482] gb AAO76757.1 putative teichoic acid biosynthesis protein F [Bacteroides thetalaotomicron VPI-5482]			
13733, 13734	48853891	58	8.00E-40	Cytophaga hutchinsonii	COG4948: L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily [Cytophaga hutchinsonii]			
13735, 13736	32262912	55	1.00E-44	Helicobacter hepaticus ATCC 51449	lipopolysaccharid core biosynthesis protein [Helicobacter hepaticus ATCC 51449] ref NP_860892.1 lipopolysaccharid core biosynthesis protein [Helicobacter hepaticus ATCC 51449]			2.7.7.3
13737, 13738	39996754	36	6.00E-45	Geobacter sulfurreducens PCA	response regulator, putative [Geobacter sulfurreducens PCA] gb AAR35028.1 response regulator, putative [Geobacter sulfurreducens PCA]			2.7.3.-
13739, 13740	54302806	45	3.00E-40	Photobacterium profundum SS9	hypothetical protein PBPRB1127 [Photobacterium profundum SS9] emb CAG22999.1 conserved hypothetical protein [Photobacterium profundum]			

13741, 13742	6968536	54	2.00E-66	Campylobacter jejuni subsp. jejuni NCTC 11168	tRNA pseudouridine synthase B [Campylobacter jejuni subsp. jejuni NCTC 11168] pir A81314 pseudouridylate synthase (EC 4.2.1.70) tRNA-specific Cj1102 [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282250.1 tRNA pseudouridine synthase B [Campylobacter jejuni subsp. jejuni NCTC 11168] sp Q9PNJ2 TRUB_CAMJE tRNA pseudouridine synthase B (tRNA pseudouridine 55 synthase) (Psi55 synthase) (Pseudouridylate synthase) (Uracil hydrolyase)				4.2.1.70
13747, 13748 1375, 1376	57242478	32	2.00E-15	Campylobacter upsallensis RM3195	type I restriction-modification system, M subunit, putative [Campylobacter upsallensis RM3195] gb EAL53546.1 type I restriction-modification system, M subunit, putative [Campylobacter upsallensis RM3195]				
	46486686	26	1.00E-17	Lyngbya majuscula	JamP [Lyngbya majuscula]				2.3.1.38
13751, 13752 13757, 13758 13759, 13760 13765, 13766	51244502 ABU0094 8 48836151 57168617	71 32 46 25	1.00E-107 5.00E-30 1.00E-63 2.00E-09	Desulfotalea psychrophila LSV54 Thermobifida fusca Campylobacter coli RM2228	probable DNA gyrase, subunit A [Desulfotalea psychrophila LSV54] emb CAG35379.1 probable DNA gyrase, subunit A [Desulfotalea psychrophila LSV54] Desc:S. pneumoniae type 4 strain protein from coding region #517. Org:Streptococcus pneumoniae type 4 strain COG0210: Superfamily I DNA and RNA helicases [Thermobifida fusca] HsdM [Campylobacter coli RM2228] gb EAL56578.1 HsdM [Campylobacter coli RM2228] conserved hypothetical protein [Streptomyces coelicolor A3(2)] ref NP_627953.1 hypothetical protein SCO3763 [Streptomyces coelicolor A3(2)]			95	6.00E-07 5.99.1.3
13769, 13770 13775, 13776	10432467 4234793	26 40	7.00E-13 5.00E-38	Streptomyces coelicolor A3(2) Leptospira borgpetersenii	ref NP_627953.1 hypothetical protein SCO3763 [Streptomyces coelicolor A3(2)] unknown [Leptospira borgpetersenii]				
13779, 13780 13783, 13784	33347983 53712412	32 48	6.00E-07 5.00E-35	Enterobacteria phage RB49 Bacteroides fragilis YCH46	gp2 DNA end protector protein [Enterobacteria phage RB49] ref NP_891702.1 gp2 DNA end protector protein [Enterobacteria phage RB49] adenylate kinase [Bacteroides fragilis YCH46] dbj BAD47870.1 adenylate kinase [Bacteroides fragilis YCH46]				2.7.4.3
13785, 13786	29347006	51	3.00E-45	Bacteroides thetaiotaomicron VPI-5482	putative sulfatase yidJ [Bacteroides thetaiotaomicron VPI-5482] gb AAO76703.1 putative sulfatase yidJ [Bacteroides thetaiotaomicron VPI-5482]				3.1.6.6

13787, 13788	29347006	49	3.00E-44	Bacteroides thetalaotomicron VPI-5482	putative sulfatase yidJ [Bacteroides thetalaotomicron VPI-5482] gb AAO76703.1 putative sulfatase yidJ [Bacteroides thetalaotomicron VPI-5482]			3.1.6.6
13789, 13790	57241143	57	7.00E-99	Campylobacter lari RM2100	DNA ligase, NAD-dependent [Campylobacter lari RM2100] gb EAL54839.1 DNA ligase, NAD-dependent [Campylobacter lari RM2100]			6.5.1.2
13791, 13792	48853636	39	6.00E-33	Cytophaga hutchinsonii	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii]			2.7.3.-
13795, 13796	48833622	23	3.00E-19	Magnetococcus sp. MC-1	COG0840: Methyl-accepting chemotaxis protein [Magnetococcus sp. MC-1] hypothetical protein OB2759 [Oceanobacillus ihayensis HTE831]			
13797, 13798	23100214	37	9.00E-08	Oceanobacillus ihayensis HTE831	hypothetical protein OB2759 [Oceanobacillus ihayensis HTE831] dbj BAC14715.1 hypothetical conserved protein [Oceanobacillus ihayensis HTE831]			3.1.3.15
13799, 13800	34556616	40	9.00E-64	Wolinella succinogenes DSM 1740	CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes]			
13801, 13802	34556616	38	4.00E-29	Wolinella succinogenes DSM 1740	CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes]			
13805, 13806	32170824	52	2.00E-24	Sphingomonas elodea	αTDP-D-glucose-4,6-dehydratase [Sphingomonas elodea]			4.2.1.46
13807, 13808	56783471	69	3.00E-61	Campylobacter jejuni	sugar-1-phosphate nucleotidyltransferase [Campylobacter jejuni]	Nostoc sp. PCC 7120 DNA, complete genome	93	3.00E-07
13813, 13814	23475504	33	3.00E-33	Desulfovibrio desulfuricans G20	COG2348: Uncharacterized protein involved in methicillin resistance [Desulfovibrio desulfuricans G20]			
13819, 13820	ABB8477 1	42	1.00E-35		DescDNA polymerase III holoenzyme delta subunit related protein SEQ ID:144. Org: Cytophaga hutchinsonii			
13821, 13822	34557329	35	4.00E-23	Wolinella succinogenes DSM 1740	hypothetical protein WS0940 [Wolinella succinogenes DSM 1740] emb CAE10044.1 conserved hypothetical protein [Wolinella succinogenes]			2.7.3.-
13823, 13824	37677003	22	7.00E-11	Vibrio vulnificus YJ016	hypothetical protein VVA1343 [Vibrio vulnificus YJ016] dbj BAC97369.1 conserved hypothetical protein [Vibrio vulnificus YJ016]			
13827, 13828	48854305	51	6.00E-22	Cytophaga hutchinsonii	COG0026: Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase) [Cytophaga hutchinsonii]			4.1.1.21

1383, 1384	29349052	41	2.00E-45	Bacteroides thetaiotaomicron VPI-5482	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacteroides thetaiotaomicron VPI-5482] gblAAO78749.1 UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacteroides thetaiotaomicron VPI-5482]				6.3.2.15
13831, 13832	48856007	42	1.00E-34	Cytophaga hutchinsonii	COG0308: Aminopeptidase N [Cytophaga hutchinsonii]				3.4.11.-
13833, 13834	46164951	32	3.00E-37	Pseudomonas aeruginosa UCBPP PA14	COG2831: Hemolysin activation/secretion protein [Pseudomonas aeruginosa UCBPP-PA14]				
13835, 13836	53765608	47	7.00E-68	Anabaena variabilis ATCC 29413	COG4096: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Anabaena variabilis ATCC 29413]				3.1.21.3
13837, 13838	57241290	57	3.00E-46	Campylobacter lari RM2100	Uncharacterized BCR, YceG family COG1559 [Campylobacter lari RM2100] gblEAL54986.1 Uncharacterized BCR, YceG family COG1559 [Campylobacter lari RM2100]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6	97	3.00E-11	4.---
13839, 13840	6967998	25	9.00E-08	Campylobacter jejuni subsp. jejuni NCTC 11168	putative periplasmic protein [Campylobacter jejuni subsp. jejuni NCTC 11168] pir B81399 probable periplasmic protein Cj0530 [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281714.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni NCTC 11168]				
13841, 13842	28210082	31	6.00E-14	Clostridium tetani E88	exodeoxyribonuclease V alpha chain [Clostridium tetani E88] gblAAO34963.1 exodeoxyribonuclease V alpha chain [Clostridium tetani E88]				3.1.11.5
13843, 13844	53713270	53	5.00E-84	Bacteroides fragilis YCH46	helicase domain protein [Bacteroides fragilis YCH46] dbj BAD48728.1 helicase domain protein [Bacteroides fragilis YCH46]				
13847, 13848	15965752	33	7.00E-17	Sinorhizobium meliloti 1021	PUTATIVE TWO 2-COMPONENT RECEIVER DOMAINS PROTEIN [Sinorhizobium meliloti 1021] emb CAC46578.1 PUTATIVE TWO 2-COMPONENT RECEIVER DOMAINS PROTEIN [Sinorhizobium meliloti]				
1385, 1386	53799051	41	5.00E-15	Chloroflexus aurantiacus	COG0500: SAM-dependent methyltransferases [Chloroflexus aurantiacus]				
13851, 13852	3183059	44	4.00E-55	Anthopleura japonica	Arginine kinase (AK) dbj BAA22888.1 arginine kinase [Anthopleura japonica]				2.7.3.3
13857, 13858	11692716	28	2.00E-14	Methanothermobacter ther woolfeii prophage psiM100	unknown [Methanothermobacter woolfeii prophage psiM100] ref NP_071813.1 unknown [Methanothermobacter woolfeii prophage psiM100]				
13859, 13860	11497405	38	6.00E-55	Borrelia burgdorferi B31	adenine specific DNA methyltransferase [Borrelia burgdorferi B31] gblAAF07736.1 adenine specific DNA methyltransferase [Borrelia burgdorferi B31]				

13861, 13862, 13863, 13864	29349444 34396491	38 53	8.00E-25 2.00E-54	Bacteroides thetaiotaomicron VPI-5482 Porphyromonas gingivalis W83	hypothetical protein BT4036 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79141.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] GTP-binding protein [Porphyromonas gingivalis W83] ref NP_904658.1 GTP-binding protein [Porphyromonas gingivalis W83]				
13865, 13866, 13867, 13868, 13869, 13870	28170140 48854120 48854120	83 39 52	1.00E-84 3.00E-19 3.00E-68	Vibrio vulnificus Cytophaga hutchinsonii Cytophaga hutchinsonii	dTDP-6-deoxy-D-xylo-4-hexulose-3,5-epimerase [Vibrio vulnificus] COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii] COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii]	80	6.00E-37	5.1.3.13	
1387, 1388	53715621	59	1.00E-34	Bacteroides fragilis YCH46 Wolinella succinogenes DSM 1740	hypothetical protein BF4341 [Bacteroides fragilis YCH46] dbj BAD51079.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			6.2.1.3	
13871, 13872	34558477	47	5.00E-10	Wolinella succinogenes DSM 1740	hypothetical protein WS2202 [Wolinella succinogenes DSM 1740] emb CAE11192.1 hypothetical protein [Wolinella succinogenes]				

13873, 13874	15678369	31	8.00E-26	Methanothermobacter thermautotrophicus str. Delta H	coenzyme F420-reducing hydrogenase, beta subunit homolog [Methanothermobacter thermautotrophicus str. Delta H] gb AAB84847.1 coenzyme F420-reducing hydrogenase, beta subunit homolog [Methanothermobacter thermautotrophicus str. Delta H] pir H69143 coenzyme F420-reducing hydrogenase, beta subunit homolog - Methanobacterium thermoautotrophicum (strain Delta H)				1.12.99. 1
13875, 13876	23111747	42	9.00E-65	Desulfotobacterium hafniense DCB-2	COG1032: Fe-S oxidoreductase [Desulfotobacterium hafniense DCB-2] ispD/ispF bifunctional enzyme [Campylobacter jejuni RM1221] gb AAW36203.1 ispD/ispF bifunctional enzyme [Campylobacter jejuni RM1221]				1.97.1.4
13877, 13878	57238620	47	3.00E-49	Campylobacter jejuni RM1221					2.7.7.60
13879, 13880								Desulfotalea psychrophila Lsv54 chromosome	82 6.00E-15
13881, 13882	26987128	38	1.00E-29	Pseudomonas putida KT2440	sensory box protein [Pseudomonas putida KT2440] gb AAN66017.1 sensory box protein [Pseudomonas putida KT2440]				2.7.3.-
13887, 13888	57240449	55	1.00E-35	Campylobacter lari RM2100	transcription-repair coupling factor [Campylobacter lari RM2100] gb EAL55563.1 transcription-repair coupling factor [Campylobacter lari RM2100]				
1389, 1390	48853834	69	2.00E-68	Cytophaga hutchinsonii	COG0536: Predicted GTPase [Cytophaga hutchinsonii]				
13891, 13892	56420320	60	1.00E-51	Geobacillus kaustophilus HTA426	glutathione peroxidase [Geobacillus kaustophilus HTA426] dbj BAD76070.1 glutathione peroxidase [Geobacillus kaustophilus HTA426]				1.11.1.9
13893, 13894	34557957	35	2.00E-40	Wolinella succinogenes DSM 1740	ATP-BINDING PROTEIN-ATPases involved in chromosome partitioning [Wolinella succinogenes DSM 1740] emb CAE10672.1 ATP-BINDING PROTEIN-ATPases involved in chromosome partitioning [Wolinella succinogenes]				
13895, 13896	48832078	47	3.00E-56	Magnetococcus sp. MC-1	COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Magnetococcus sp. MC-1]				2.7.3.-
13897, 13898	53712612	39	3.00E-38	Bacteroides fragilis YCH46	O-succinylbenzoic acid-CoA ligase [Bacteroides fragilis YCH46] dbj BAD48070.1 O-succinylbenzoic acid-CoA ligase [Bacteroides fragilis YCH46]				6.2.1.26
13899, 13900	1197006	46	2.00E-54	Bacteroides fragilis	unknown protein [Bacteroides fragilis] gb AA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for insertion sequence element IS4351 (Transposon TN4551)				

13903, 13904	29350114	32	2.00E-13	Bacteroides thetaiotaomicron VPI-5482	putative anti-sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79811.1 putative anti-sigma factor [Bacteroides thetaiotaomicron VPI-5482]				
13905, 13906	53712242	39	1.00E-29	Bacteroides fragilis YCH46	RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] db BAD47700.1 RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46]				
13907, 13908	52548364	54	7.00E-67	uncultured archaeon GZfos11H11	pyruvate-formate lyase-activating enzyme [uncultured archaeon GZfos11H11]				1.97.1.4
13909, 13910	16077588	66	3.00E-42	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU05210 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12328.1 ydel [Bacillus subtilis subsp. subtilis str. 168] pir C69778 hypothetical protein ydel - Bacillus subtilis db BAA19356.1 FUNCTION UNKNOWN. [Bacillus subtilis]			91 1.00E-06	
1391, 1392	15896321	28	2.00E-20	Clostridium acetobutylicum ATCC 824	Glycosyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK81010.1 Glycosyltransferase [Clostridium acetobutylicum ATCC 824] pir G97277 glycosyltransferase [imported] - Clostridium acetobutylicum				2.4.1.-
13913, 13914	21232334	47	2.00E-21	Xanthomonas campestris pv. campestris str. ATCC 33913	DNA-damage-inducible protein d [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM42175.1 DNA-damage-inducible protein d [Xanthomonas campestris pv. campestris str. ATCC 33913]				
13915, 13916	52009462	45	2.00E-26	Silicibacter sp. TM1040	COG0834: ABC-type amino acid transport/signal transduction systems, periplasmic component/domain [Silicibacter sp. TM1040]				
13917, 13918	34556541	42	5.00E-36	Wolinella succinogenes DSM 1740	ANTHRANILATE SYNTHASE COMPONENT I [Wolinella succinogenes DSM 1740] emb CAE09256.1 ANTHRANILATE SYNTHASE COMPONENT I [Wolinella succinogenes]				4.1.3.27
13919, 13920	57236934	41	4.00E-47	Campylobacter jejuni RM1221	RNA pseudouridylylase synthase family protein [Campylobacter jejuni RM1221] gb AAW34517.1 RNA pseudouridylylase synthase family protein [Campylobacter jejuni RM1221]				4.2.1.70
13921, 13922	34557444	39	2.00E-44	Wolinella succinogenes DSM 1740	hypothetical protein WS1061 [Wolinella succinogenes DSM 1740] emb CAE10159.1 conserved hypothetical protein [Wolinella succinogenes]				
13923, 13924	21673510	31	6.00E-26	Chlorobium tepidum TLS	type I restriction system specificity protein [Chlorobium tepidum TLS] gb AAM71917.1 type I restriction system specificity protein [Chlorobium tepidum TLS]				3.1.21.3

13927, 13928	46580432	27	6.00E-30	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	hypothetical protein DVU2025 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96500.1 conserved hypothetical protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] ribosomal protein L5 [Campylobacter jejuni RM1221] gb AAW36285.1 ribosomal protein L5 [Campylobacter jejuni RM1221] emb CAB73681.1 50S ribosomal protein L5 [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282821.1 50S ribosomal protein L5 [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81267 50S ribosomal protein L5 Cj1695c [imported] - Campylobacter jejuni (strain NCTC 11168) sp Q9PLY3 RL5_CAMJE 50S ribosomal protein L5	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 6/8	78	5.00E-16	
13929, 13930	57238702	71	1.00E-66	Campylobacter jejuni RM1221	COG1959: Predicted transcriptional regulator [Thiobacillus denitrificans ATCC 25259]				
1393, 1394	52007674	34	2.00E-10	Thiobacillus denitrificans ATCC					
13931, 13932	34558795	43	4.00E-68	Alvinella pompejana epibiont	TonB-dependent receptor [Alvinella pompejana epibiont 6C6]				
13933, 13934	54302657	29	3.00E-11	Photobacterium profundum SS9	hypothetical outer membrane receptor protein [Photobacterium profundum SS9] emb CAG22850.1 hypothetical outer membrane receptor protein [Photobacterium profundum]				
13935, 13936	32262400	47	4.00E-32	Helicobacter hepaticus ATCC	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860382.1 hypothetical protein HH0851 [Helicobacter hepaticus ATCC 51449]				
13937, 13938	34556481	46	4.00E-57	Wolinella succinogenes DSM	hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes]				
13939, 13940	34104648	54	3.00E-51	Chromobacterium violaceum ATCC	probable sensory transduction protein [Chromobacterium violaceum ATCC 12472] ref NP_903011.1 probable sensory transduction protein [Chromobacterium violaceum ATCC 12472]				
13943, 13944	57240289	56	1.00E-59	Campylobacter lari	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55403.1 conserved hypothetical protein [Campylobacter lari RM2100]				
13945, 13946	57240288	46	6.00E-60	Campylobacter lari	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55402.1 conserved hypothetical protein [Campylobacter lari RM2100]				
13947, 13948	34557884	29	5.00E-29	Wolinella succinogenes DSM	DIGUANYLATE CYCLASE [Wolinella succinogenes DSM 1740] emb CAE10599.1 DIGUANYLATE CYCLASE [Wolinella succinogenes]				2.7.3.-
13949, 13950	34557771	35	3.00E-13	Wolinella succinogenes DSM	hypothetical protein WS1424 [Wolinella succinogenes DSM 1740] emb CAE10486.1 hypothetical protein [Wolinella succinogenes]				

1395, 1396	48853997	27	9.00E-11	Cytophaga hutchinsonii	COG2825: Outer membrane protein [Cytophaga hutchinsonii] DNA-binding response regulator [Campylobacter jejuni RM1221]				
13953, 13954	57238514	26	1.00E-07	Campylobacter jejuni RM1221	gb AAW36097.1 DNA-binding response regulator [Campylobacter jejuni RM1221]				
13955, 13956	34557410	52	3.00E-30	Wolinella succinogenes DSM 1740	hypothetical protein WS1024 [Wolinella succinogenes DSM 1740] emb CAE10125.1 conserved hypothetical protein [Wolinella succinogenes]				
13957, 13958	48831642	48	4.00E-54	Magnetococcus sp. MC-1	COG1876: D-alanyl-D-alanine carboxypeptidase [Magnetococcus sp. MC-1] hydrogenase isoenzymes formation protein [Helicobacter hepaticus ATCC 51449] ref NP_859853.1 hydrogenase isoenzymes formation protein [Helicobacter hepaticus ATCC 51449]				
13959, 13960	32261870	59	6.00E-91	Helicobacter hepaticus ATCC 51449	COG1876: D-alanyl-D-alanine carboxypeptidase [Magnetococcus sp. MC-1] hydrogenase isoenzymes formation protein [Helicobacter hepaticus ATCC 51449] ref NP_859853.1 hydrogenase isoenzymes formation protein [Helicobacter hepaticus ATCC 51449]				
13963, 13964	34558493	72	1.00E-105	Wolinella succinogenes DSM 1740	PUTATIVE ZINC PROTEASE [Wolinella succinogenes DSM 1740] emb CAE11208.1 PUTATIVE ZINC PROTEASE [Wolinella succinogenes]			81	5.00E-20 3.4.-
13965, 13966	34557072	34	5.00E-10	Wolinella succinogenes DSM 1740	TWO COMPONENT RESPONSE REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09787.1 TWO COMPONENT RESPONSE REGULATOR [Wolinella succinogenes]				
13967, 13968	21229067	42	2.00E-15	Methanosarcina mazel Go1	hypothetical sensory transduction histidine kinase [Methanosarcina mazel Go1] gb AAM32661.1 hypothetical sensory transduction histidine kinase [Methanosarcina mazel Go1]				2.7.3.-
13969, 13970	46142558	55	1.00E-29	Methanococcoides burtonii DSM 6242	COG0784: FOG: CheY-like receiver [Methanococcoides burtonii DSM 6242]				2.7.3.-
13971, 13972	15898132	28	2.00E-11	Sulfolobus solifataricus P2	hypothetical protein SSO1289 [Sulfolobus solifataricus P2] gb AAK41527.1 Conserved hypothetical protein [Sulfolobus solifataricus P2] pir H90283 conserved hypothetical protein [imported] - Sulfolobus solifataricus				
13973, 13974	32263234	59	1.00E-46	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861213.1 hypothetical protein HH1682 [Helicobacter hepaticus ATCC 51449]				2.7.3.-
13977, 13978	34557252	43	2.00E-17	Wolinella succinogenes DSM 1740	hypothetical protein WS0858 [Wolinella succinogenes DSM 1740] emb CAE09967.1 hypothetical protein [Wolinella succinogenes]				
13979, 13980	29346175	31	6.00E-28	Bacteroides thetaiotaomicron VPI-5482	putative protease [Bacteroides thetaiotaomicron VPI-5482] gb AAO75872.1 putative protease [Bacteroides thetaiotaomicron VPI-5482]				3.4.21.-

13983, 13984 13985, 13986	51246876 ABG9157 1	61 39	2.00E-76 7.00E-55	Desulfotalea psychrophila Lsv54 	related to pseudouridine synthase [Desulfotalea psychrophila Lsv54] emb CAG37753.1 related to pseudouridine synthase [Desulfotalea psychrophila Lsv54] Desc:Purine/pyrimidine triphosphate type nucleotidyltransferase #156. Org:Aquifex aeolicus			4.2.1.70 2.7.7.13	
13987, 13988 13989, 13990 1399, 1400	51246976 57242307 53713469	50 47 50	5.00E-61 8.00E-44 2.00E-66	Desulfotalea psychrophila Lsv54 Campylobacter upsaliensis RM3195 Bacteroides fragilis YCH46	probable reverse transcriptase/maturase family protein [Desulfotalea psychrophila Lsv54] emb CAG37869.1 probable reverse transcriptase/maturase family protein [Desulfotalea psychrophila Lsv54] transcription termination factor NusA [Campylobacter upsaliensis RM3195] gb EAL53769.1 transcription termination factor NusA [Campylobacter upsaliensis RM3195] putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1 putative helicase [Bacteroides fragilis YCH46]	Podospora anserina race A mitochondrial DNA class II intron downstream of alpha-sen DNA near Col gene 5'end	89	6.00E-07	2.7.7.49
13991, 13992	 39936986	 43	 5.00E-45	 Rhodopseudomona s palustris CGA009	putative dTDP-glucose 4,6-dehydratase [Rhodopseudomonas palustris CGA009] emb CAE29366.1 putative dTDP-glucose 4,6-dehydratase [Rhodopseudomonas palustris CGA009]				4.2.1.46
13993, 13994	 15897644	 50	 2.00E-73	 Sulfolobus solfataricus P2	GTP binding protein [Sulfolobus solfataricus P2] emb CAB57559.1 gtp- binding protein [Sulfolobus solfataricus] gb AAK41039.1 GTP binding protein [Sulfolobus solfataricus P2] pir H90222 GTP binding protein [Imported] - Sulfolobus solfataricus				
13997, 13998	 45658464	 38	 2.00E-19	 Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711217.1 two-component hybrid sensor and regulator [Leptospira Interrogans serovar Lai str. 56601] gb AAN48235.1 two-component hybrid sensor and regulator [Leptospira interrogans serovar lai str. 56601] gb AAS71187.1 histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			2.7.3.-	
13999, 14000	 34556470	 52	 2.00E-58	 Wolinetella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT REGULATOR [Wolinetella succinogenes DSM 1740] emb CAE09185.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinetella succinogenes]			2.7.-	
14001, 14002	 34556469	 33	 6.00E-25	 Wolinetella succinogenes DSM 1740	hypothetical protein WS0010 [Wolinetella succinogenes DSM 1740] emb CAE09184.1 conserved hypothetical protein [Wolinetella succinogenes]				
14003, 14004	 45547576	 46	 8.00E-53	 Rubrobacter xylanophilus DSM 8941	COG0539: Ribosomal protein S1 [Rubrobacter xylanophilus DSM 9941]	Photobacterium profundum SS9; segment 9/12	91	6.00E-07	2.7.7.8

14005, 14006	57241144	51	2.00E-49	Campylobacter lari RM2100	hemolysin A [Campylobacter lari RM2100] gb EAL54840.1 hemolysin A [Campylobacter lari RM2100]			
14007, 14008	47567784	37	4.00E-34	Bacillus cereus G9241	helicase/SNF2 family domain protein [Bacillus cereus G9241] gb EAL13804.1 helicase/SNF2 family domain protein [Bacillus cereus G9241]			2.7.7.-
14009, 14010	34557966	53	4.00E-77	Wolnella succinogenes DSM 1740	ATP-DEPENDENT HELICASE [Wolnella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wolnella succinogenes]			3.6.1.-
1401, 1402	53712307	46	1.00E-26	Bacteroides fragilis YCH46	putative lipoprotein [Bacteroides fragilis YCH46] db BAD47765.1 putative lipoprotein [Bacteroides fragilis YCH46]			
14011, 14012	37521458	33	7.00E-13	Gloeobacter violaceus PCC 7421	hypothetical protein gll1889 [Gloeobacter violaceus PCC 7421] db BAC89830.1 gll1889 [Gloeobacter violaceus PCC 7421]			
14015, 14016	46578677	32	8.00E-16	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	universal stress protein family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94744.1 universal stress protein family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			
14017, 14018	48856414	25	2.00E-08	Cytophaga hutchinsonii	hypothetical protein Chut02000132 [Cytophaga hutchinsonii]			
14019, 14020	57240764	45	4.00E-39	Campylobacter lari RM2100	proline dipeptidase TC0863 [Campylobacter lari RM2100] gb EAL55157.1 proline dipeptidase TC0863 [Campylobacter lari RM2100]			3.4.11.9
14021, 14022	29349461	53	1.00E-77	Bacteroides thetaiotaomicron VPI-5482	putative membrane transport protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79158.1 putative membrane transport protein [Bacteroides thetaiotaomicron VPI-5482]			
14023, 14024	23474422	29	2.00E-25	Desulfovibrio desulfuricans G20	COG0840: Methyl-accepting chemotaxis protein [Desulfovibrio desulfuricans G20]			
14025, 14026	57241251	53	1.00E-63	Campylobacter lari RM2100	response regulator (ompR) [Campylobacter lari RM2100] gb EAL54947.1 response regulator (ompR) [Campylobacter lari RM2100]			2.7.3.-
14027, 14028	57241252	44	7.00E-29	Campylobacter lari RM2100	signal-transducing protein, histidine kinase [Campylobacter lari RM2100] gb EAL54948.1 signal-transducing protein, histidine kinase [Campylobacter lari RM2100]			2.7.3.-
14029, 14030	48856174	40	4.00E-49	Cytophaga hutchinsonii	COG2912: Uncharacterized conserved protein [Cytophaga hutchinsonii]			
1403, 1404	13471790	52	3.00E-39	Mesorhizobium loti MAFF303099	hypothetical protein mlr1881 [Mesorhizobium loti MAFF303099] db BAB49143.1 mlr1881 [Mesorhizobium loti MAFF303099]			
14033, 14034	48856384	46	1.00E-20	Cytophaga hutchinsonii	hypothetical protein Chut02000101 [Cytophaga hutchinsonii]			

14035, 14036	30249663	38	4.00E-40	Nitrosomonas europaea ATCC 19718	possible msrA, pms; peptide methionine sulfoxide reductase [Nitrosomonas europaea ATCC 19718]			1.8.4.6
14037, 14038	29349974	37	4.00E-46	Bacteroides thetaiotaomicron VPI-5482	two-component system response regulator protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79671.1 two-component system response regulator protein [Bacteroides thetaiotaomicron VPI-5482]			3.1.1.61
14039, 14040	34558828	27	5.00E-27	Alvinella pompejana epibiont 7G3	KIAA1005 protein [Alvinella pompejana epibiont 7G3] hypothetical protein MA4540 [Methanosarcina acetivorans C2A] gb AAM07879.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A]			
14041, 14042	20093324	42	1.00E-26	Methanosarcina acetivorans C2A	type I restriction-modification system, R subunit [Methylococcus capsulatus str. Bath] ref YP_114328.1 type I restriction-modification system, R subunit [Methylococcus capsulatus str. Bath]			3.4.24.-
14043, 14044	53757541	49	4.00E-65	Methylococcus capsulatus str. Bath				3.1.21.3
14045, 14046	15668834	38	2.00E-16	Methanocaldococ- cus jannaschii DSM 2661	Inosine-5'-monophosphate dehydrogenase (guaB) [Methanocaldococcus jannaschii DSM 2661] gb AAB98648.1 inosine-5'-monophosphate dehydrogenase (guaB) [Methanocaldococcus jannaschii DSM 2661] pir E64381 conserved hypothetical protein MJ0653 - Methanococcus jannaschii sp Q58069 V653_METJA Hypothetical protein MJ0653 hypothetical protein BT3247 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78353.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			1.1.1.20 5
14047, 14048	29348656	38	6.00E-36	Bacteroides thetaiotaomicron VPI-5482				
14049, 14050	45681861	25	6.00E-09	Mesorhizobium sp. BNC1	COG3919: Predicted ATP-grasp enzyme [Mesorhizobium sp. BNC1]			
1405, 1406	46142700	35	1.00E-29	Methanococcoides burtonii DSM 6242	COG0642: Signal transduction histidine kinase [Methanococcoides burtonii DSM 6242]			2.7.3.-
14051, 14052	48832299	46	1.00E-46	Magnetococcus sp. MC-1	COG2206: HD-GYP domain [Magnetococcus sp. MC-1]			
14053, 14054	48832299	44	2.00E-44	Magnetococcus sp. MC-1	COG2206: HD-GYP domain [Magnetococcus sp. MC-1]			
14057, 14058	29654169	40	4.00E-37	Coxiella burnetii RSA 493	glycosyl transferase, group 1 family protein [Coxiella burnetii RSA 493] gb AAO90375.1 glycosyl transferase, group 1 family protein [Coxiella burnetii RSA 493]			
14061, 14062	20806796	27	1.00E-13	Thermoanaerobact- er tengcongensis MB4	predicted glycosyltransferases [Thermoanaerobacter tengcongensis MB4] gb AAM23571.1 predicted glycosyltransferases [Thermoanaerobacter tengcongensis MB4]			2.4.1.-

14063, 14064	29610237	28	4.00E-18	Streptomyces avermitilis MA-4680	putative glycosyltransferase [Streptomyces avermitilis MA-4680] ref NP_827749.1 putative glycosyltransferase [Streptomyces avermitilis MA-4680]				2.4.1.83
14065, 14066	48854768	37	2.00E-20	Cytophaga hutchinsonii	COG2319: FOG: WD40 repeat [Cytophaga hutchinsonii]				
14067, 14068	6968471	43	5.00E-57	Campylobacter jejuni subsp. jejuni NCTC 11168	possible transferase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir H81305 probable transferase Cj1035c [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282185.1 possible transferase [Campylobacter jejuni subsp. jejuni NCTC 11168] sp Q9PNQ6 ATE_CAMJE Putative arginyl- tRNA-protein transferase (R-transferase) (Arginyltransferase)			2.3.2.8	
14069, 14070	34558373	56	8.00E-64	Wolinella succinogenes DSM 1740	UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE GLMU [Wolinella succinogenes DSM 1740] emb CAE11088.1 UDP-N- ACETYLGLUCOSAMINE PYROPHOSPHORYLASE GLMU [Wolinella succinogenes]			2.7.7.23	
1407, 1408	53731556	33	5.00E-27	Methanococcoides burtonii DSM 6242	COG0642: Signal transduction histidine kinase [Methanococcoides burtonii DSM 6242]			2.7.3.-	
14071, 14072	34556560	54	5.00E-65	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]				
14073, 14074	32262189	42	3.00E-35	Helicobacter hepaticus ATCC 51449	3-Deoxy-D-manno-octulosonic-acid transferase [Helicobacter hepaticus ATCC 51449] ref NP_860171.1 3-Deoxy-D-manno-octulosonic-acid transferase [Helicobacter hepaticus ATCC 51449]			2.4.99.-	
14081, 14082	48862648	34	1.00E-10	Microbulifer degradans 2-40	COG0705: Uncharacterized membrane protein (homolog of Drosophila rhomboid) [Microbulifer degradans 2-40]				
14085, 14086	23474440	28	9.00E-17	Desulfovibrio desulfuricans G20	COG0714: MoxR-like ATPases [Desulfovibrio desulfuricans G20]				
14087, 14088	33861847	44	2.00E-43	Prochlorococcus marinus subsp. pastoris str. CCMP1986	tRNA methyl transferase:tRNA (5-methylaminomethyl)-2-thiouridy... [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19750.1 tRNA methyl transferase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]			2.1.1.61	
14089, 14090	49236207	47	2.00E-35	Moorella thermoacetica ATCC 39073	COG0301: Thiamine biosynthesis ATP pyrophosphatase [Moorella thermoacetica ATCC 39073]				
1409, 1410	45658173	32	2.00E-14	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	hypothetical protein L1C12325 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711602.1 hypothetical protein LA1421 [Leptospira interrogans serovar Lai str. 56601] gb AAN48620.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS70896.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				

14091,	23125625	28	6.00E-09	Nostoc punctiforme PCC 73102	COG0514: Superfamily II DNA helicase [Nostoc punctiforme PCC 73102]				3.1.21.3
14092,	46140259	52	3.00E-31	Dechloromonas aromatica RCB	COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB]				2.7.3.-
14095,	53713780	37	2.00E-41	Bacteroides fragilis YCH46	cobalamin biosynthesis protein CobD [Bacteroides fragilis YCH46]				
14096,	46201931	46	5.00E-24	Magnetospirillum magnetotacticum MS-1	COG2199: FOG: GGDEF domain [Magnetospirillum magnetotacticum MS-1]				2.7.3.-
14097,	558266	66	8.00E-74	Wolinella succinogenes	orf [Wolinella succinogenes] pir[S50154 hypothetical protein 2 - Wolinella succinogenes]				
14098,	24375871	34	5.00E-16	Shewanella oneidensis MR-1	hypothetical protein SO4391 [Shewanella oneidensis MR-1] gb AA57358.1				
14099,	16077106	46	1.00E-60	Bacillus subtilis subsp. subtilis str. 168	methionyl-tRNA synthetase [Bacillus subtilis subsp. subtilis str. 168] emb CAB11814.1 methionyl-tRNA synthetase [Bacillus subtilis subsp. subtilis str. 168] sp P37465 SYM_BACSU Methionyl-tRNA synthetase (Methionine-tRNA ligase) (MetRS) pir S86067 methionine-tRNA ligase (EC 6.1.1.10) metS - Bacillus subtilis db BAA05273.1 methionyl-tRNA synthetase [Bacillus subtilis]				6.1.1.10
14101,	48855475	64	2.00E-35	Cytophaga hutchinsonii	COG5557: Polysulphide reductase [Cytophaga hutchinsonii]				
14102,	57168693	55	6.00E-67	Campylobacter coli RM2228	translation initiation factor IF-2 [Campylobacter coli RM2228] gb EAL56654.1 translation initiation factor IF-2 [Campylobacter coli RM2228]	Ureaplasma parvum serovar 3 str. ATCC 700970 section 30 of 59 of the complete genome	94	4.00E-11	3.6.1.48
14103,	20809124	49	6.00E-34	Thermoanaerobacter tengcongensis MB4	NAD/FAD-utilizing enzyme apparently involved in cell division [Thermoanaerobacter tengcongensis MB4] gb AAM25899.1 NAD/FAD-utilizing enzyme apparently involved in cell division [Thermoanaerobacter tengcongensis MB4] sp Q8R6K9 GIA2_THETN Glucose inhibited division protein A 2				
14104,	57241681	63	4.00E-97	Campylobacter lari RM2100	DNA gyrase, B subunit [Campylobacter lari RM2100] gb EAL54351.1 DNA gyrase, B subunit [Campylobacter lari RM2100]	Campylobacter lari serotype T64 DNA gyrase subunit B (gyrB) gene, partial cds	87	2.00E-13	5.99.1.3

1411, 1412	45658174	42	1.00E-09	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	hypothetical protein LIC12326 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70897.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				
14113, 14114	53729993	29	2.00E-08	Dechloromonas aromatica RCB	COG3038: Cytochrome B561 [Dechloromonas aromatica RCB]				
14115, 14116	57242136	27	7.00E-25	Campylobacter upsallensis RM3195	signal-transducing protein, histidine kinase [Campylobacter upsallensis RM3195] gb EAL54109.1 signal-transducing protein, histidine kinase [Campylobacter upsallensis RM3195]				2.7.3.-
14117, 14118	34557558	53	2.00E-55	Wolinella succinogenes DSM 1740	PUTATIVE AMINOTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE10273.1 PUTATIVE AMINOTRANSFERASE [Wolinella succinogenes]				4.4.1.-
14119, 14120	16264212	44	1.00E-22	Sinorhizobium melloti 1021	hypothetical protein SMb20482 [Sinorhizobium melloti 1021] pir H95899 hypothetical protein [imported] - Sinorhizobium melloti (strain 1021) magaplasmid pSymB emb CAC48864.1 HYPOTHETICAL PROTEIN [Sinorhizobium melloti 1021]				
14121, 14122	56478430	43	9.00E-56	Azoarcus sp. EbN1	putative acetyltransferase [Azoarcus sp. EbN1] emb CAI09118.1 putative acetyltransferase [Azoarcus sp. EbN1]				6.-.-.-
14123, 14124	2118361	61	1.00E-53	Haemophilus influenzae R2846	formate-tetrahydrofolate ligase (EC 6.3.4.3) - Clostridium cylindrosporium sp Q07064 FTHS_CLOCY Formate-tetrahydrofolate ligase (Formyltetrahydrofolate synthetase) (FHS) (FTHFS) gb AAA23239.1 N10- CHO-H4folate synthetase	Clostridium perfringens str. 13 DNA, complete genome	89	4.00E-19	6.3.4.3
14125, 14126	42629381	43	3.00E-25	Helicobacter hepaticus ATCC 51449	hypothetical protein Hfl103001140 [Haemophilus influenzae R2846] lipid A biosynthesis protein LpxK [Helicobacter hepaticus ATCC 51449] ref NP_860540.1 lipid A biosynthesis protein LpxK [Helicobacter hepaticus ATCC 51449]				2.7.1.13 0
1413, 1414	24214122	45	2.00E-34	Leptospira interrogans serovar Lai str. 56601	Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601]				
14135, 14136	34558237	36	7.00E-39	Wolinella succinogenes DSM 1740	hypothetical protein WS1946 [Wolinella succinogenes DSM 1740] emb CAE10952.1 hypothetical protein [Wolinella succinogenes]				
14137, 14138	53684899	27	4.00E-12	Desulfotobacterium hafnense DCB-2	COG2234: Predicted aminopeptidases [Desulfotobacterium hafnense DCB- 2]				3.4.17.2 1
14139, 14140	15605874	22	2.00E-12	Aquifex aerophilus VF5	hypothetical protein aq_367 [Aquifex aerophilus VF5] gb AAC06656.1 hypothetical protein [Aquifex aerophilus VF5] pir G70332 conserved hypothetical protein aq_367 - Aquifex aerophilus				

14141, 14142	15611181	56	1.00E-103	Helicobacter pylori J99	PHOSPHOENOLPYRUVATE SYNTHASE [Helicobacter pylori J99] gb AAD05690.1 PHOSPHOENOLPYRUVATE SYNTHASE [Helicobacter pylori J99] pir E71972 pyruvate, water dikinase (EC 2.7.9.2) - Helicobacter pylori (strain J99) spiQ92MV4 PPSA_HELPJ Phosphoenolpyruvate synthase (Pyruvate, water dikinase) (PEP synthase)			2.7.9.2
14143, 14144	49237143	36	2.00E-12	Moorella thermoacetica ATCC 39073	COG0701: Predicted permeases [Moorella thermoacetica ATCC 39073]			
14147, 14148	17940062	40	9.00E-36	Leptospira interrogans	unknown [Leptospira Interrogans]			2.4.1.-
14149, 14150	11499239	44	2.00E-07	Archaeoglobus fulgidus DSM 4304	tungsten formylmethanofuran dehydrogenase, subunit G (fwdG) [Archaeoglobus fulgidus DSM 4304] gb AAB89607.1 tungsten formylmethanofuran dehydrogenase, subunit G (fwdG) [Archaeoglobus fulgidus DSM 4304] pir H69455 tungsten formylmethanofuran dehydrogenase, subunit G (fwdG) homolog - Archaeoglobus fulgidus thiamine monophosphate synthase [Helicobacter hepaticus ATCC 51449] ref NP_861359.1 thiamine monophosphate synthase [Helicobacter hepaticus ATCC 51449]			1.2.99.5
14153, 14154	32263380	46	5.00E-40	Geobacter metallireducens GS	COG0761: Penicillin tolerance protein [Geobacter metallireducens GS-15]			2.5.1.3
14157, 14158	15607028	33	7.00E-10	Aquifex aeolicus VF5	2-acylglycerophosphoethanolamine acyltransferase [Aquifex aeolicus VF5] gb AAC07802.1 2-acylglycerophosphoethanolamine acyltransferase [Aquifex aeolicus VF5] pir E70476 2-acylglycerophosphoethanolamine acyltransferase - Aquifex aeolicus			6.2.1.20
14159, 14160	53715403	26	4.00E-09	Bacteroides fragilis YCH46	transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD50861.1 transcriptional regulator [Bacteroides fragilis YCH46]			
14161, 14162	34557963	45	2.00E-36	Wolinella succinogenes DSM 1740	FLAVOPROTEIN [Wolinella succinogenes DSM 1740] emb CAE10678.1 FLAVOPROTEIN [Wolinella succinogenes]			
14163, 14164	37526735	57	6.00E-26	Photobacterium luminescens subsp. laumondii TTO1	hypothetical protein plu2845 [Photobacterium luminescens subsp. laumondii TTO1] emb CAE15219.1 unnamed protein product [Photobacterium luminescens subsp. laumondii TTO1]			
14165, 14166	57505678	32	1.00E-07	Campylobacter upsaliensis RM3195	conserved hypothetical protein [Campylobacter upsaliensis RM3195] gb EAL52739.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195]			
1417, 1418	48728708	32	1.00E-16	Pseudomonas fluorescens PfO-1	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Pseudomonas fluorescens PfO-1]			

14171, 14172	52842621	31	3.00E-10	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	AMPC cephalosporinase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28473.1 AMPC cephalosporinase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56657.1 conserved hypothetical protein [Campylobacter coli RM2228]				
14175, 14176	57168696	43	1.00E-26	Campylobacter coli RM2228	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE10055.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]				2.7.3.-
14177, 14178	34557340	39	6.00E-67	Wolinella succinogenes DSM 1740	COG1799: Uncharacterized protein conserved in bacteria [Desulfotobacterium hafnense DCB-2]				
14181, 14182	53684633	25	2.00E-07	Desulfotobacterium hafnense DCB-2	PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wolinella succinogenes DSM 1740] emb CAE09198.1 PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wolinella succinogenes]	B.thuringiensis PK1 & cap genes, putative	85	2.00E-18	5.1.3.-
14185, 14186	34556483	64	5.00E-84	Wolinella succinogenes DSM 1740	3'(2'),5'-bisphosphate nucleotidase [Campylobacter coli RM2228] gb EAL56330.1 3'(2'),5'-bisphosphate nucleotidase [Campylobacter coli RM2228]	Aquifex aeolicus VF5 section 16 of 109 of the complete genome	87	4.00E-14	3.1.3.25
14187, 14188	57168975	62	3.00E-81	Campylobacter coli RM2228	DNA-directed RNA polymerase beta' chain [Bacteroides fragilis YCH46] db BAD50934.1 DNA-directed RNA polymerase beta' chain [Bacteroides fragilis YCH46]	Bacteroides fragilis YCH46 DNA, complete genome	85	6.00E-10	2.7.7.6
14189, 14190	53715476	56	4.00E-81	Bacteroides fragilis YCH46	hypothetical protein AF2325 [Archaeoglobus fulgidus DSM 4304] gb AAB88946.1 A. fulgidus predicted coding region AF2325 [Archaeoglobus fulgidus DSM 4304] pir E69540 hypothetical protein AF2325 - Archaeoglobus fulgidus				
1419, 1420	11499906	27	2.00E-08	Archaeoglobus fulgidus DSM 4304	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]				
14191, 14192	48854613	28	3.00E-24	Cytophaga hutchinsonii	COG3129: Predicted SAM-dependent methyltransferase [Cytophaga hutchinsonii]				2.7.3.-
14193, 14194	48856096	52	5.00E-85	Cytophaga hutchinsonii	hypothetical protein BT3112 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78218.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
14195, 14196	29348521	48	3.00E-25	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3112 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78218.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
14197, 14198	29348521	45	7.00E-38	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein [Staphylococcus aureus]				
14199, 14200	57207874	32	4.00E-12	Staphylococcus aureus					

14201, 14202	34557348	38	6.00E-18	Wolnella succinogenes DSM 1740	HECB PRECURSOR [Wolnella succinogenes DSM 1740] emb CAE10063.1 HECB PRECURSOR [Wolnella succinogenes]				
14203, 14204	53714768	31	5.00E-12	Bacteroides fragilis YCH46	hypothetical protein BF3483 [Bacteroides fragilis YCH46] dbj BAD50226.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
14205, 14206	20808521	30	3.00E-22	Thermoanaerobact er tengcongensis MB4	NADH:flavin oxidoreductases, Old Yellow Enzyme family [Thermoanaerobacter tengcongensis MB4] gb AAM25296.1 NADH:flavin oxidoreductases, Old Yellow Enzyme family [Thermoanaerobacter tengcongensis MB4]				1.6.-
1421, 1422	21673804	38	9.00E-47	Chlorobium tepidum TLS	carbohydrate kinase, PfkB family [Chlorobium tepidum TLS] gb AAM7221.1 carbohydrate kinase, PfkB family [Chlorobium tepidum TLS]				2.7.1.15
14211, 14212	AAW9827 0	50	2.00E-67		Desc:H. pylori GHPO 442 protein. Org:Helicobacter pylori				1.4.99.1
14213, 14214	57159872	29	4.00E-17	Thermococcus kodakaraensis	NADH:ubiquinone oxidoreductase, NADH-binding subunit F [Thermococcus kodakaraensis] ref YP_184026.1 NADH:ubiquinone oxidoreductase, NADH- binding subunit F [Thermococcus kodakaraensis]				1.6.5.3
14215, 14216	53691858	56	1.00E-86	Desulfovibrio desulfuricans G20	hypothetical protein Ddes0200066 [Desulfovibrio desulfuricans G20]				
14217, 14218	46581597	44	1.00E-23	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	lipoprotein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS97665.1 lipoprotein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]				
14223, 14224	23130537	45	4.00E-17	Nostoc punctiforme PCC 73102	COG0778: Nitroreductase [Nostoc punctiforme PCC 73102]				
14227, 14228	34557966	57	8.00E-46	Wolnella succinogenes DSM 1740	ATP-DEPENDENT HELICASE [Wolnella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wolnella succinogenes]				3.6.1.-
14231, 14232	28211368	28	1.00E-13	Clostridium tetani E88	hypothetical protein CTC01714 [Clostridium tetani E88] conserved protein [Clostridium tetani E88]				
14233, 14234	32263376	65	5.00E-72	Helicobacter hepaticus ATCC 51449	phosphoenolpyruvate synthase [Helicobacter hepaticus ATCC 51449] ref NP_861355.1 phosphoenolpyruvate synthase [Helicobacter hepaticus ATCC 51449]				2.7.9.2
14235, 14236	AAW8997 9	61	3.00E-53		Desc:Protein encoded by clone d11 ORF2. Org:Helicobacter pylori				1.2.7.3
14237, 14238	55733904	41	1.00E-36	Oryza sativa (japonica cultivar- group)	putative glycosyltransferase [Oryza sativa (japonica cultivar-group)] ref XP_475798.1 putative glycosyltransferase [Oryza sativa (japonica cultivar-group)]				

14239, 14240	48846045	37	4.00E-38	15	Geobacter metallireducens GS-	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]				2.7.3.-
14241, 14242	30249663	34	2.00E-29	19718	Nitrosomonas europaea ATCC	possible msrA, pms; peptide methionine sulfoxide reductase [Nitrosomonas europaea ATCC 19718] emb CAD85612.1 possible msrA, pms; peptide methionine sulfoxide reductase [Nitrosomonas europaea ATCC 19718]				1.8.4.6
14243, 14244	48855001	28	1.00E-19		Cytophaga hutchinsonii	COG2849: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				2.7.1.68
14245, 14246	53713690	55	2.00E-51		Bacteroides fragilis YCH46	dihydroorotate dehydrogenase electron transfer subunit [Bacteroides fragilis YCH46] dbj BAD49148.1 dihydroorotate dehydrogenase electron transfer subunit [Bacteroides fragilis YCH46]	Bacteroides thetataoamicron VPI-5482, section 4 of 21 of the complete genome	89	6.00E-09	1.8.2.-
14247, 14248	29346302	75	7.00E-56		Bacteroides thetataoamicron VPI-5482	dihydroorotate dehydrogenase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75999.1 dihydroorotate dehydrogenase [Bacteroides thetaiotaomicron VPI-5482]				1.3.3.1
14249, 14250	37680330	30	1.00E-26		Vibrio vulnificus YJ016	predicted signal transduction protein [Vibrio vulnificus YJ016] dbj BAC94910.1 predicted signal transduction protein [Vibrio vulnificus YJ016]				
1425, 1426	53797181	34	8.00E-21		Chloroflexus aurantiacus	COG3427: Uncharacterized conserved protein [Chloroflexus aurantiacus]				
14251, 14252	20806595	61	7.00E-68		Thermoanaerobact er tengcongensis MB4	predicted glycosylase [Thermoanaerobacter tengcongensis MB4] gb AAM23370.1 predicted glycosylase [Thermoanaerobacter tengcongensis MB4]				
14253, 14254	16077744	52	3.00E-70	168	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU06760 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12496.1 yeeA [Bacillus subtilis subsp. subtilis str. 168] pir E69792 conserved hypothetical protein yeeA - Bacillus subtilis				
14255, 14256	16077745	63	1.00E-97	168	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU06770 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12497.1 yeeB [Bacillus subtilis subsp. subtilis str. 168] gb AAB66475.1 YeeB [Bacillus subtilis] pir F69792 hypothetical protein yeeB - Bacillus subtilis				
14257, 14258	52548731	54	2.00E-88		uncultured archaeon GZfos18F2	hypothetical protein GZ18F2_10 [uncultured archaeon GZfos18F2]				
14259, 14260	48856539	31	5.00E-14		Cytophaga hutchinsonii	COG0791: Cell wall-associated hydrolases (invasion-associated proteins) [Cytophaga hutchinsonii]				

14261, 14262	34556892	80	1.00E-132	1740	Wollinella succinogenes DSM	DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wollinella succinogenes DSM 1740] emb CAE09607.1 DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wollinella succinogenes] sp Q7MA56 RPBC_WOLSU Bifunctional DNA-directed RNA polymerase, beta and beta' chain [includes: DNA-directed RNA polymerase beta chain (Transcriptase beta chain) (RNA polymerase beta subunit); DNA-directed RNA polymerase beta' chain (Transcriptase beta' chain) (RNA polymerase beta' subunit)]	Ehrlichia ruminantium RNA polymerase beta subunit (rpoB) gene, partial cds	88	4.00E-45	2.7.7.6
14263, 14264	34557246	37	7.00E-59	1740	Wollinella succinogenes DSM	SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes]				
14265, 14266	51245892	25	1.00E-06	psychrophila LSV54	Desulfotalea psychrophila LSV54	related to integrase [Desulfotalea psychrophila LSV54] emb CAG36769.1 related to integrase [Desulfotalea psychrophila LSV54]				
1427, 1428	53711500	50	2.00E-39	YCH46	Bacteroides fragilis YCH46	two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD46958.1 two-component system response regulator [Bacteroides fragilis YCH46]				2.7.3.-
14271, 14272	34558386	48	8.00E-33	1740	Wollinella succinogenes DSM	hypothetical protein WS2103 [Wollinella succinogenes DSM 1740] emb CAE11101.1 hypothetical protein [Wollinella succinogenes]				
14275, 14276	34558157	39	1.00E-12	1740	Wollinella succinogenes DSM	SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wollinella succinogenes DSM 1740] emb CAE10872.1 SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wollinella succinogenes]				
14277, 14278	48853608	41	7.00E-53	hutchinsonii	Cytophaga hutchinsonii	hypothetical protein Chu02003656 [Cytophaga hutchinsonii]				
14279, 14280	34556575	59	1.00E-104	1740	Wollinella succinogenes DSM	PUTATIVE FORMATE DEHYDROGENASE, ALPHA SUBUNIT [Wollinella succinogenes DSM 1740] emb CAE09290.1 PUTATIVE FORMATE DEHYDROGENASE, ALPHA SUBUNIT [Wollinella succinogenes]				1.2.1.2
14281, 14282	32262777	48	3.00E-42	51449	Helicobacter hepaticus ATCC	DNA processing protein DprA [Helicobacter hepaticus ATCC 51449] ref NP_860758.1 DNA processing protein DprA [Helicobacter hepaticus ATCC 51449]				
14283, 14284	29348441	41	2.00E-65	VPI-5482	Bacteroides thetaiotaomicron VPI-5482	conserved hypothetical protein, with a weak acyltransferase domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO78138.1 conserved hypothetical protein, with a weak acyltransferase domain [Bacteroides thetaiotaomicron VPI-5482]				
14287, 14288	39995706	41	7.00E-35	PCA	Geobacter sulfurreducens PCA	sensor histidine kinase [Geobacter sulfurreducens PCA] gb AAR33930.1 sensor histidine kinase [Geobacter sulfurreducens PCA]				2.7.3.-

14293, 14294	48845470	48	6.00E-43	15	Geobacter metallireducens GS	COG2353: Uncharacterized conserved protein [Geobacter metallireducens GS-15]			
14295, 14296	34556624	40	3.00E-51	1740	Wolinella succinogenes DSM	ISOLEUCYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE09339.1 ISOLEUCYL-TRNA SYNTHETASE [Wolinella succinogenes]			6.1.1.5
143, 144	32476811	47	5.00E-27	1	Rhodopirellula baltica SH 1	hypothetical protein-signal peptide prediction [Rhodopirellula baltica SH 1] emb CAD77183.1 hypothetical protein-signal peptide prediction [Pirellula sp.]			
14305, 14306	34558171	21	5.00E-08	1740	Wolinella succinogenes DSM	hypothetical protein WS1876 [Wolinella succinogenes DSM 1740] emb CAE10886.1 conserved hypothetical protein [Wolinella succinogenes]			
14307, 14308	34556981	30	4.00E-24	1740	Wolinella succinogenes DSM	hypothetical protein WS0562 [Wolinella succinogenes DSM 1740] emb CAE09696.1 conserved hypothetical protein [Wolinella succinogenes]			
14309, 14310	34556560	36	1.00E-34	1740	Wolinella succinogenes DSM	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]			2.7.3.-
1431, 1432	53711857	33	7.00E-24	YCH46	Bacteroides fragilis YCH46	beta-N-acetylglucosaminidase [Bacteroides fragilis YCH46] dbj BAD47315.1 beta-N-acetylglucosaminidase [Bacteroides fragilis YCH46]			
14311, 14312	10441471	25	7.00E-09		Lactococcus lactis subsp. lactis	abortive infection phage resistance protein abiU [Lactococcus lactis subsp. lactis]			
14313, 14314	32262189	41	8.00E-38	51449	Helicobacter hepaticus ATCC 51449	3-Deoxy-D-manno-octulosonic-acid transferase [Helicobacter hepaticus ATCC 51449] ref NP_860171.1 3-Deoxy-D-manno-octulosonic-acid transferase [Helicobacter hepaticus ATCC 51449]			2.4.99.- 2.4.1.15
14315, 14316	48854183	50	2.00E-56		Cytophaga hutchinsonii	COG0438: Glycosyltransferase [Cytophaga hutchinsonii]			1
14319, 14320	24376199	42	5.00E-19		Shewanella oneidensis MR-1	hypothetical protein SO4727 [Shewanella oneidensis MR-1] gb AA57886.1 conserved hypothetical protein [Shewanella oneidensis MR-1]			
14323, 14324	34558118	39	5.00E-35	1740	Wolinella succinogenes DSM	HISTIDINE KINASE SENSOR PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10833.1 HISTIDINE KINASE SENSOR PROTEIN [Wolinella succinogenes]			2.7.3.-
14325, 14326	57241714	34	5.00E-30		Campylobacter lari RM2100	fibrinectin/fibrinogen-binding protein, putative [Campylobacter lari RM2100] gb EAL54384.1 fibrinectin/fibrinogen-binding protein, putative [Campylobacter lari RM2100]			

14329, 14330	12512884	43	2.00E-27	Escherichia coli O157:H7	deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] ref NP_285856.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7 EDL933] ref NP_308191.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] sp Q8X8Y9 DGT_PECO57 Deoxyguanosinetriphosphate triphosphohydrolase (dGTPase) (dGTP triphosphohydrolase) pir D85500 deoxyguanosine triphosphate triphosphohydrolase [Imported] - Escherichia coli (strain O157:H7, substrain EDL933) dbj BAB33587.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] pir D90649 deoxyguanosine triphosphate triphosphohydrolase [Imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)	3.1.5.1
1433, 1434	53712575	30	9.00E-15	Bacteroides fragilis YCH46	tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] dbj BAD48033.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]	
14331, 14332	34557222	66	1.00E-114	Wolinnella succinogenes DSM 1740	PHOSPHOENOLPYRUVATE SYNTHASE [Wolinnella succinogenes DSM 1740] emb CAE09937.1 PHOSPHOENOLPYRUVATE SYNTHASE [Wolinnella succinogenes]	2.7.9.2
14333, 14334	53795932	42	3.00E-29	Chloroflexus aurantiacus	COG1941: Coenzyme F420-reducing hydrogenase, gamma subunit [Chloroflexus aurantiacus]	1.12.-
14335, 14336	46142296	63	1.00E-94	Methanococcoides burtonii DSM 6242	COG4804: Uncharacterized conserved protein [Methanococcoides burtonii DSM 6242]	
14337, 14338	53713068	28	5.00E-13	Bacteroides fragilis YCH46	hypothetical protein BF1779 [Bacteroides fragilis YCH46] dbj BAD48526.1 hypothetical protein [Bacteroides fragilis YCH46]	
14339, 14340	34557873	49	5.00E-64	Wolinnella succinogenes DSM 1740	hypothetical protein WS1545 [Wolinnella succinogenes DSM 1740] emb CAE10588.1 conserved hypothetical protein [Wolinnella succinogenes]	
14343, 14344	42780097	28	1.00E-15	Bacillus cereus ATCC 10987	helicase, SNF2 family [Bacillus cereus ATCC 10987] emb CAB40614.1 SNF2-like helicase [Bacillus cereus] gb AAS39952.1 helicase, SNF2 family [Bacillus cereus ATCC 10987]	3.6.1.3
14345, 14346	53714400	46	2.00E-41	Bacteroides fragilis YCH46	acyltransferase family protein [Bacteroides fragilis YCH46] dbj BAD49858.1 acyltransferase family protein [Bacteroides fragilis YCH46]	
14349, 14350	34557247	60	6.00E-42	Wolinnella succinogenes DSM 1740	TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolinnella succinogenes DSM 1740] emb CAE09962.1 TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolinnella succinogenes]	2.7.3.-
1435, 1436	48856980	50	5.00E-39	Cytophaga hutchinsonii	COG1522: Transcriptional regulators [Cytophaga hutchinsonii]	
14351, 14352	23467790	54	1.00E-67	Haemophilus sommus 129PT	COG0147: Anthranilate/para-aminobenzoate synthases component I [Haemophilus sommus 129PT]	4.1.3.-

14353, 14354	57240744	27	1.00E-24	Campylobacter lari RM2100	probable membrane protein Cj0124c [Campylobacter lari RM2100] gb EAL55137.1 probable membrane protein Cj0124c [Campylobacter lari RM2100]			
14355, 14356	29349623	53	3.00E-66	Bacteroides thetataoamicon VPI-5482	shikimate 5-dehydrogenase [Bacteroides thetataoamicon VPI-5482] gb AAO79320.1 shikimate 5-dehydrogenase [Bacteroides thetataoamicon VPI-5482]		1.1.1.25	
14357, 14358	38099730	26	7.00E-09	Magnaporthe grisea 70-15	hypothetical protein MG10847.4 [Magnaporthe grisea 70-15] ref XP_360535.1 hypothetical protein MG10847.4 [Magnaporthe grisea 70-15]			
14363, 14364	34396413	73	1.00E-136	Porphyromonas gingivalis W83	conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_904581.1 hypothetical protein PG0257 [Porphyromonas gingivalis W83]	Bartonella henselae strain Houston-1, complete genome	79	6.00E-26
14365, 14366	29345762	57	6.00E-32	Bacteroides thetataoamicon VPI-5482	hypothetical protein BT0352 [Bacteroides thetataoamicon VPI-5482] gb AAO75459.1 conserved hypothetical protein [Bacteroides thetataoamicon VPI-5482]			
14367, 14368	57238514	28	4.00E-26	Campylobacter jejuni RM1221	DNA-binding response regulator [Campylobacter jejuni RM1221] gb AAW36097.1 DNA-binding response regulator [Campylobacter jejuni RM1221]		2.7.3.-	
14369, 14370	34557182	52	1.00E-28	Wolinella succinogenes DSM 1740	PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09897.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes]			
14371, 14372	15894152	35	2.00E-15	Clostridium acetobutylicum ATCC 824	Two-component response regulator [Clostridium acetobutylicum ATCC 824] gb AAK7884.1 Two-component response regulator [Clostridium acetobutylicum ATCC 824] pir F97006 two-component response regulator [imported] - Clostridium acetobutylicum		3.1.1.61	
14375, 14376	48855045	36	1.00E-07	Cytophaga hutchinsonii	COG2027: D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 4) [Cytophaga hutchinsonii]		3.4.16.4	
14377, 14378	15678845	33	3.00E-22	Methanothermobacter thermautotrophicus str. Delta H	sensory transduction histidine kinase [Methanothermobacter thermotrophicus str. Delta H] gb AAB85323.1 sensory transduction histidine kinase [Methanothermobacter thermotrophicus str. Delta H] pir A69210 sensory transduction histidine kinase - Methanothermobacter thermotrophicus (strain Delta H)		2.7.3.-	
14379, 14380	32262842	47	1.00E-23	Helicobacter hepaticus ATCC 51449	ornithine acetyltransferase [Helicobacter hepaticus ATCC 51449] ref NP_860822.1 ornithine acetyltransferase [Helicobacter hepaticus ATCC 51449] sp Q93EJ3 ARGJ_HELHP Arginine biosynthesis bifunctional protein argJ [includes: Glutamate N-acetyltransferase (Ornithine acetyltransferase) (Ornithine transacetylase) (OATase); Amino-acid acetyltransferase (N-acetylglutamate synthase) (AGS)] [Contains: Arginine biosynthesis bifunctional protein argJ alpha chain; Arginine biosynthesis bifunctional protein argJ beta chain]		2.3.1.1	

14383, 14384	53713680	46	6.00E-67	Bacteroides fragilis YCH46	hypothetical protein BF2389 [Bacteroides fragilis YCH46] dbj BAD49138.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
14385, 14386	19705335	50	2.00E-36	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Ferric uptake regulation protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94129.1 Ferric uptake regulation protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			
14389, 14390	39594604	30	4.00E-24	Caenorhabditis briggsae	Hypothetical protein CBG19289 [Caenorhabditis briggsae]		6.2.1.26	
14391, 14392	34102684	46	9.00E-59	Chromobacterium violaceum ATCC 12472	conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_901044.1 hypothetical protein CV1374 [Chromobacterium violaceum ATCC 12472]			
14393, 14394	34557291	41	1.00E-36	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]		2.7.3.-	
14395, 14396	34398055	70	5.00E-49	Porphyromonas gingivalis W83	glycyl-tRNA synthetase [Porphyromonas gingivalis W83] ref NP_906216.1 glycyl-tRNA synthetase [Porphyromonas gingivalis W83]	Myroides odoratimimus metallo-beta- lactamase (MUS-1) gene, complete cds	88	2.00E-30
14397, 14398	29349019	73	4.00E-84	Bacteroides thetaiotaomicron VPI-5482	glycyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78716.1 glycyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI- 5482]			6.1.1.14
14399, 14400	48766217	66	1.00E-35	Rhodospirillum rubrum	COG0064: Asp-tRNAAsn/Glu-tRNA ^{Gln} amidotransferase B subunit (PET112 homolog) [Rhodospirillum rubrum]			6.3.5.-
14405, 14406	34558377	47	2.00E-47	Wolinella succinogenes DSM 1740	TRNA (URACIL-5-METHYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE11092.1 TRNA (URACIL-5-METHYLTRANSFERASE [Wolinella succinogenes])			2.1.1.35
14407, 14408	48854542	50	4.00E-25	Cytophaga hutchinsonii	COG1748: Saccharopine dehydrogenase and related proteins [Cytophaga hutchinsonii]			1.5.1.10
1441, 1442	47218152	49	1.00E-23	Tetraodon nigrovirdis	unnamed protein product [Tetraodon nigrovirdis]			
14413, 14414	34557661	60	1.00E-28	Wolinella succinogenes DSM 1740	hypothetical protein WS1299 [Wolinella succinogenes DSM 1740] emb CAE10376.1 hypothetical protein [Wolinella succinogenes] probable ATP-dependent DNA helicase [Azoarcus sp. EbN1] emb CAI09453.1 probable ATP-dependent DNA helicase [Azoarcus sp. EbN1]			
14419, 14420	56478765	51	1.00E-20	Azoarcus sp. EbN1				3.6.1.-

14421, 14422	57168001	27	5.00E-11	Campylobacter coli RM2228	phosphatidylserine decarboxylase-related protein [Campylobacter coli RM2228] gb EAL57044.1 phosphatidylserine decarboxylase-related protein [Campylobacter coli RM2228]			4.1.1.65
14423, 14424	21673982	44	1.00E-34	Chlorobium tepidum TLS	long-chain-fatty-acid-CoA ligase, putative [Chlorobium tepidum TLS] gb AAIM72389.1 long-chain-fatty-acid-CoA ligase, putative [Chlorobium tepidum TLS]			6.2.1.3
14425, 14426	48855640	53	1.00E-21	Cytophaga hutchinsonii	COG0714: MoxR-like ATPases [Cytophaga hutchinsonii] ABC transporter, nucleotide binding/ATPase protein [Agrobacterium tumefaciens str. C58] gb AAL41427.1 ABC transporter, nucleotide binding/ATPase protein [Agrobacterium tumefaciens str. C58] pir AE2626 hypothetical protein fbpA1 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)			
14427, 14428	17934321	40	3.00E-10	Agrobacterium tumefaciens str. C58				
14429, 14430	53688795	40	1.00E-22	Nostoc punctiforme PCC 73102	COG0500: SAM-dependent methyltransferases [Nostoc punctiforme PCC 73102]			
14431, 14432	53714606	54	1.00E-26	Bacteroides fragilis YCH46	excinuclease ABC subunit A [Bacteroides fragilis YCH46] db BAD50064.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46] related to methyl-accepting chemotaxis protein [Desulfotalea psychrophila LSv54] emb CAG35707.1 related to methyl-accepting chemotaxis protein [Desulfotalea psychrophila LSV54]	Clostridium perfringens str. 13 DNA, complete genome	88 2.00E-14	
14435, 14436	51244830	37	7.00E-07	Desulfotalea psychrophila LSV54				
14437, 14438	48856760	45	1.00E-32	Cytophaga hutchinsonii	COG2062: Phosphohistidine phosphatase SixA [Cytophaga hutchinsonii]			3.1.3.-
14439, 14440	34558171	23	3.00E-07	Wolinella succinogenes DSM 1740	hypothetical protein WS1876 [Wolinella succinogenes DSM 1740] emb CAE10886.1 conserved hypothetical protein [Wolinella succinogenes]			
14441, 14442	56461100	55	1.00E-32	Idiomarina lohiensis L2TR	Carboxynorspermidine decarboxylase [Idiomarina lohiensis L2TR] gb AAV82832.1 Carboxynorspermidine decarboxylase [Idiomarina lohiensis L2TR]			4.1.1.-
14443, 14444	57238538	59	3.00E-64	Campylobacter jejuni RM1221	carboxynorspermidine decarboxylase [Campylobacter jejuni RM1221] gb AAW36121.1 carboxynorspermidine decarboxylase [Campylobacter jejuni RM1221]			4.1.1.-
14445, 14446	53759813	39	2.00E-46	Methylobacillus flagellatus KT	COG0676: Uncharacterized enzymes related to aldose 1-epimerase [Methylobacillus flagellatus KT]			
14447, 14448	48845647	43	1.00E-46	Geobacter metallireducens GS-15	hypothetical protein Gmet02001892 [Geobacter metallireducens GS-15]			
1445, 1446	48854655	34	1.00E-11	Cytophaga hutchinsonii	hypothetical protein Chut02002321 [Cytophaga hutchinsonii]			

14451, 14452	46156514	69	1.00E-45	Haemophilus sommus 2336	COG0582: Integrase [Haemophilus somnus 2336] Desc:Haemophilus influenzae cellular proliferation protein #135. Org:Haemophilus influenzae	86	8.00E-11	Desc:Bifidobacteriu m longum NCC2705 related nucleotide sequence SEQ ID:1106. Org:Bifidobacterium longumSynthetic	
14453, 14454	AAU3549 4	43	2.00E-41	Raistonia solanacearum GMI1000	hypothetical protein RS01874 [Raistonia solanacearum GMI1000] emb[CAD13579.1] CONSERVED HYPOTHETICAL PROTEIN [Raistonia solanacearum]		2.3.1.51		
14455, 14456	17544770	33	1.00E-17	Bacteroides fragilis YCH46	hypothetical protein BF3486 [Bacteroides fragilis YCH46] dbj[BAD50229.1] conserved hypothetical protein [Bacteroides fragilis YCH46]		2.1.1.-		
14457, 14458	53714771	27	2.00E-14	Porphyromonas gingivalis W83	sensor histidine kinase [Porphyromonas gingivalis W83] ref[NP_905586.1] sensor histidine kinase [Porphyromonas gingivalis W83]				
14459, 14460	34397423	21	4.00E-12	Chloroflexus aurantiacus	COG0110: Acetyltransferase (isoleucine patch superfamily) [Chloroflexus aurantiacus]		2.3.1.-		
14463, 14464	53795087	35	9.00E-18	Desulfovibrio desulfuricans G20	COG0451: Nucleoside-diphosphate-sugar epimerases [Desulfovibrio desulfuricans G20]		5.1.3.2		
14465, 14466	53691528	35	1.00E-30	Campylobacter lari RM2100	probable transmembrane protein Cj0390 [Campylobacter lari RM2100] gb EAL54700.1 probable transmembrane protein Cj0390 [Campylobacter lari RM2100]				
14469, 14470	57241004	24	8.00E-10	Bacteroides thetaiotaomicron VPI-5482	beta-mannosidase precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO75565.1 beta-mannosidase precursor [Bacteroides thetaiotaomicron VPI-5482]		3.2.1.25		
14471, 14472	29345868	28	7.00E-22	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70895.1 serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				
14475, 14476	45658172	42	3.00E-34	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	metallo-beta-lactamase family protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS97276.1 metallo-beta-lactamase family protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]				
14477, 14478	46581208	38	2.00E-46						

14479, 14480	34557487	62	5.00E-82	Wollinella succinogenes DSM 1740	ABC TRANSPORTER, PERIPLASMIC SUBSTRATE-BINDING PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10202.1 ABC TRANSPORTER, PERIPLASMIC SUBSTRATE-BINDING PROTEIN [Wollinella succinogenes]			
14481, 14482	34557960	46	2.00E-72	Wollinella succinogenes DSM 1740	PROLINE AMINOPEPTIDASE [Wollinella succinogenes DSM 1740] emb CAE10675.1 PROLINE AMINOPEPTIDASE [Wollinella succinogenes] conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860475.1 hypothetical protein HH0944 [Helicobacter hepaticus ATCC 51449]			3.4.11.9
14483, 14484	32262494	60	3.00E-69	Helicobacter hepaticus ATCC 51449	ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes DSM 1740] emb CAE0984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes]			3.4.13.9
14485, 14486	34557269	59	1.00E-84	Wollinella succinogenes DSM 1740	fibronectin/fibrinogen-binding protein, putative [Campylobacter lari RM2100] gb EAL54384.1 fibronectin/fibrinogen-binding protein, putative [Campylobacter lari RM2100]			3.6.1.-
14487, 14488	57241714	33	3.00E-38	Campylobacter lari RM2100	membrane protein, putative [Treponema denticola ATCC 35405] gb AAS10964.1 membrane protein, putative [Treponema denticola ATCC 35405]			
14489, 14490	42525985	29	8.00E-24	Treponema denticola ATCC 35405	hypothetical protein Tery02000770 [Trichodesmium erythraeum IMS101] hypothetical protein OB2886 [Oceanobacillus theyensis HTE831] dbj BAC14842.1 hypothetical conserved protein [Oceanobacillus theyensis HTE831]			2.4.1.-
1449, 1450	48895710	38	1.00E-14	Trichodesmium erythraeum IMS101	response regulator [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94813.1 response regulator [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			
14493, 14494	23100341	40	1.00E-23	Oceanobacillus theyensis HTE831	COG0642: Signal transduction histidine kinase [Rhodospirillum rubrum] 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Bacteroides fragilis YCH46] dbj BAD47041.1 2,3-bisphosphoglycerate- independent phosphoglycerate mutase [Bacteroides fragilis YCH46]			2.7.3.-
14495, 14496	46578746	29	4.00E-19	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78525.1 2,3- bisphosphoglycerate-independent phosphoglycerate mutase [Bacteroides thetaitaomicron VPI-5482] sp Q8A287 GPMI_BACTN 2,3- bisphosphoglycerate-independent phosphoglycerate mutase (Phosphoglyceromutase) (BPG-independent PGAM) (IPGM)			5.4.2.1
14497, 14498	48763282	43	9.00E-57	Rhodospirillum rubrum	Legionella pneumophila str. Lens complete genome			96 2.00E-13 5.4.2.1
14499, 14500	53711583	61	8.00E-47	Bacteroides fragilis YCH46				
14501, 14502	29348828	63	1.00E-107	Bacteroides thetaitaomicron VPI-5482				

14505, 14506	15896782	48	2.00E-69	Clostridium acetobutylicum ATCC 824	Highly conserved protein containing a domain related to cellulase catalytic domain and a thioredoxin domain [Clostridium acetobutylicum ATCC 824] gb AAK81471.1 Highly conserved protein containing a domain related to cellulase catalytic domain and a thioredoxin domain [Clostridium acetobutylicum ATCC 824] p D97335 hypothetical protein CAC3546 [imported] - Clostridium acetobutylicum	Methanosarcina acetivorans str. C2A, section 429 of 534 of the complete genome	84	1.00E-11	2.7.4.9
14507, 14508	20809061	37	2.00E-38	Thermoanaerobact er tengcongensis MB4	ABC-type multidrug/protein/lipid transport system, ATPase component [Thermoanaerobacter tengcongensis MB4] gb AAM25836.1 ABC-type multidrug/protein/lipid transport system, ATPase component [Thermoanaerobacter tengcongensis MB4]				3.4.21.-
1451, 1452	23113094	37	5.00E-07	Desulfotobacterium hafnense DCB-2	COG0438: Glycosyltransferase [Desulfotobacterium hafnense DCB-2]				
14511, 14512	34557571	53	1.00E-88	Wolinella succinogenes DSM 1740	GLUTAMATE SYNTHASE, LARGE SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10286.1 GLUTAMATE SYNTHASE, LARGE SUBUNIT [Wolinella succinogenes]				1.4.1.13
14515, 14516	48854339	59	2.00E-94	Cytophaga hutchinsonii	COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii]				
14517, 14518	53714606	50	4.00E-76	Bacteroides fragilis YCH46	excnuclease ABC subunit A [Bacteroides fragilis YCH46] db BAD50064.1 excnuclease ABC subunit A [Bacteroides fragilis YCH46]				
14519, 14520	34557665	49	4.00E-35	Wolinella succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes]				2.7.3.-
14521, 14522	57167857	37	6.00E-14	Campylobacter coli RM2228	ferric uptake regulation protein, putative [Campylobacter coli RM2228] gb EAL57643.1 ferric uptake regulation protein, putative [Campylobacter coli RM2228]				
14525, 14526	21674678	32	1.00E-28	Chlorobium tepidum TLS	hypothetical protein CT1866 [Chlorobium tepidum TLS] gb AAM73085.1 hypothetical protein [Chlorobium tepidum TLS]				
14527, 14528	53713068	37	3.00E-11	Bacteroides fragilis YCH46	hypothetical protein BF1779 [Bacteroides fragilis YCH46] db BAD48526.1 hypothetical protein [Bacteroides fragilis YCH46]				
1453, 1454	53712397	43	6.00E-51	Bacteroides fragilis YCH46	putative glycosyltransferase [Bacteroides fragilis YCH46] gb AAD56741.1 putative glycosyltransferase [Bacteroides fragilis] db BAD47855.1 putative glycosyltransferase [Bacteroides fragilis YCH46]				
14531, 14532	26988742	44	1.00E-58	Pseudomonas putida KT2440	aminopeptidase N [Pseudomonas putida KT2440] gb AAN67631.1 aminopeptidase N [Pseudomonas putida KT2440]				3.4.11.2
14533, 14534	48855815	55	3.00E-52	Cytophaga hutchinsonii	COG1600: Uncharacterized Fe-S protein [Cytophaga hutchinsonii]				

14535, 14536	15840961	37	7.00E-13	Mycobacterium tuberculosis CDC1551	methyitransferase [Mycobacterium tuberculosis CDC1551] gb AAK45812.1 methyitransferase [Mycobacterium tuberculosis CDC1551]			
14537, 14538	42780401	54	5.00E-49	Bacillus cereus ATCC 10987	hypothetical protein BCE1327 [Bacillus cereus ATCC 10987] gb AAS40256.1 conserved hypothetical protein [Bacillus cereus ATCC 10987]			2.1.1.-
14539, 14540	15611096	44	1.00E-13	Helicobacter pylori J99	DETHIOBIOTIN SYNTHETASE [Helicobacter pylori J99] gb AAD05609.1 DETHIOBIOTIN SYNTHETASE [Helicobacter pylori J99] pir G71982 dethiobiotin synthetase - Helicobacter pylori (strain J99) sp Q9ZN34 BIOD_HELPJ Dethiobiotin synthetase (Dethiobiotin synthase) (DTB synthetase) (DTBS)			6.3.3.3
14541, 14542	53758942	46	5.00E-16	Methylococcus capsulatus str. Bath	conserved domain protein [Methylococcus capsulatus str. Bath] ref YP_113621.1 hypothetical protein MCA1152 [Methylococcus capsulatus str. Bath]			
14543, 14544	4234793	37	1.00E-43	Leptospira borgpetersenii	unknown [Leptospira borgpetersenii]			
14545, 14546	23114771	45	2.00E-57	Desulfotobacterium hafniense DCB-2	COG0451: Nucleoside-diphosphate-sugar epimerases [Desulfotobacterium hafniense DCB-2]			4.2.1.-
14547, 14548	48846045	32	5.00E-29	Geobacter metallireducens GS-15	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] serine/threonine kinase with two-component sensor domain [Nostoc sp. PCC 7120] pir AC2091 serine/threonine kinase with two-component sensor domain all2282 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73981.1 serine/threonine kinase with two-component sensor domain [Nostoc sp. PCC 7120]			2.7.3.-
14549, 14550	17229774	23	3.00E-18	Nostoc sp. PCC 7120	hypothetical protein PA4369 [Pseudomonas aeruginosa PAO1] ref ZP_00137855.2 COG1704: Uncharacterized conserved protein [Pseudomonas aeruginosa UC8PP-PA14] pir H83100 hypothetical protein PA4369 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_253059.1 hypothetical protein PA4369 [Pseudomonas aeruginosa PAO1]			
14551, 14552	15920615	36	8.00E-24	Sulfolobus tokodaii str. 7	hypothetical adenylate kinase [Sulfolobus tokodaii str. 7] sp Q9757 KCY_SULTO Cytidylate kinase (CK) (Cytidine monophosphate kinase) (CMP kinase) dbj BAB55393.1 180aa long hypothetical adenylate kinase [Sulfolobus tokodaii str. 7]			2.7.4.14

14553, 14554	52424971	76	1.00E-48	Mannheimia succiniciproducens MBEL55E	Nth protein [Mannheimia succiniciproducens MBEL55E] gb AAU37523.1 Nth protein [Mannheimia succiniciproducens MBEL55E]	Salmonella typhimurium LT2, section 67 of 220 of the complete genome	84	4.00E-098	4.2.99.1
14555, 14556	28210429	44	5.00E-57	Clostridium tetani E88	transcriptional regulatory protein [Clostridium tetani E88] gb AAO35310.1 transcriptional regulatory protein [Clostridium tetani E88]				
14557, 14558	53715867	56	7.00E-57	Bacteroides fragilis YCH46	putative xanthosine triphosphate pyrophosphatase [Bacteroides fragilis YCH46] db BAD51325.1 putative xanthosine triphosphate pyrophosphatase [Bacteroides fragilis YCH46]			2.7.7.56	
14559, 14560	48856331	41	9.00E-47	Cytophaga hutchinsonii	hypothetical protein Chut02000043 [Cytophaga hutchinsonii]				
14563, 14564	31194225	49	6.00E-28	Anopheles gambiae	ENSANGP00000000349 [Anopheles gambiae]				1.5.1.3
14565, 14566	ABP3846 9	44	4.00E-15		Desc:Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3314. Org:Staphylococcus epidermidis				2.7.6.3
14567, 14568	6968169	49	1.00E-37	Campylobacter jejuni subsp. jejuni NCTC 11168	putative 16S rRNA processing protein [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81342 probable 16S rRNA processing protein Cj0712 [Imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281884.1 putative 16S rRNA processing protein [Campylobacter jejuni subsp. jejuni NCTC 11168] sp Q9PPJ5 RIMM_CAMJE Probable 16S rRNA processing protein rimM				
14569, 14570	38099730	27	9.00E-13	Magnaporthe grisea 70-15	hypothetical protein MG10847.4 [Magnaporthe grisea 70-15] ref XP_360535.1 hypothetical protein MG10847.4 [Magnaporthe grisea 70- 15]				3.1.26.-
1457, 1458	32414055	30	4.00E-12	Neurospora crassa	hypothetical protein [Neurospora crassa] gb EAA28210.1 hypothetical protein [Neurospora crassa]				
14571, 14572	15611744	54	1.00E-46	Helicobacter pylori J99	D-ALANYL-D-ALANINE-ADDING ENZYME [Helicobacter pylori J99] gb AAD06244.1 D-ALANYL-D-ALANINE-ADDING ENZYME [Helicobacter pylori J99] pir C71903 D-alanyl-D-alanine-adding enzyme - Helicobacter pylori (strain J99)				6.3.2.15
14573, 14574	39996271	35	2.00E-34	Geobacter sulfurreducens PCA	hypothetical protein GSU1169 [Geobacter sulfurreducens PCA] gb AAR34545.1 hypothetical protein GSU1169 [Geobacter sulfurreducens PCA]				
14577, 14578	57240790	43	7.00E-39	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55183.1 conserved hypothetical protein [Campylobacter lari RM2100]				

14579,	34556686	47	1.00E-29	Wollinella succinogenes DSM 1740	hypothetical protein WS0245 [Wollinella succinogenes DSM 1740] emb CAE09401.1 conserved hypothetical protein [Wollinella succinogenes]				
14580	AAW9878								
14581,	3	37	7.00E-25		Desc:H. pylori GHPO 1210 protein. Org:Helicobacter pylori				
14582					COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Cytophaga hutchinsonii]				2.7.1.11 2
14589,	48854195	45	7.00E-26	Cytophaga hutchinsonii					
14590									
1459,				Legionella pneumophila str. Paris	protoporphyrinogen IX and coproporphyrinogen III oxidase HemY [Legionella pneumophila str. Paris] emb CAH13947.1 protoporphyrinogen IX and coproporphyrinogen III oxidase HemY [Legionella pneumophila str. Paris]				
14591,	54298730	40	7.00E-38		COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Cytophaga hutchinsonii]				
14592	48853737	25	1.00E-20	Cytophaga hutchinsonii					
14593,				Bacillus cereus	Low-affinity zinc transport protein [Bacillus cereus ATCC 14579]				
14594	30020156	26	3.00E-07	ATCC 14579					
14595,				Wollinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes]				2.7.3.-
14596	34557246	39	4.00E-32						
14599,				Polaribacter filamentus	NH(3)-dependent NAD(+) synthetase [Polaribacter filamentus]	Polaribacter filamentus NH(3)-dependent NAD(+) synthetase (nadE) gene, complete cds	86	3.00E-15	6.3.5.1
14600	36955865	74	1.00E-106						
				Legionella pneumophila subsp. pneumophila str. Philadelphia 1	hypothetical protein lpg0982 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27068.1 hypothetical protein lpg0982 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]				
14601,	52841216	28	8.00E-18						
14602									
14603,				Bacteroides fragilis	putative DNA-binding protein [Bacteroides fragilis YCH46] dbj BAD47150.1				
14604	53711692	45	9.00E-61	YCH46	putative DNA-binding protein [Bacteroides fragilis YCH46]				
14605,				Rhodospirillum rubrum	COG2199: FOG: GGDEF domain [Rhodospirillum rubrum]				
14606	48765572	38	2.00E-32						
				Wollinella succinogenes DSM 1740	PUTATIVE ABC-TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10439.1 PUTATIVE ABC-TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wollinella succinogenes]				1.8.-:-
14607,									
14608	34557724	43	6.00E-51						

14609, 14610, 14611, 14612	41718599	36	1.00E-26	Methanococcoides burtonii DSM 6242	COG0642: Signal transduction histidine kinase [Methanococcoides burtonii DSM 6242]			2.7.3.-
14613, 14614, 14615, 14616, 14617, 14618, 14619, 14620	48832069	36	1.00E-30	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			3.4.21.-
14621, 14622	52841303	41	8.00E-26	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	AbiD phage protein-like [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27155.1 AbiD phage protein-like [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			2.7.3.-
14623, 14624, 14625, 14626	48854366	38	6.00E-19	Cytophaga hutchinsonii	COG4823: Abortive infection bacteriophage resistance protein [Cytophaga hutchinsonii]			
14627, 14628	48832174	24	2.00E-10	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			
14629, 14630, 14631, 14632	51245404	34	6.00E-09	Desulfotalea psychrophila LSV54	hypothetical protein DP1552 [Desulfotalea psychrophila LSV54] emb CAG36281.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]			
14633, 14634, 14635, 14636	15606614	21	5.00E-09	Aquifex aeolicus VF5	transporter (extracellular solute binding protein family 5) [Aquifex aeolicus VF5] gb AAC07389.1 transporter (extracellular solute binding protein family 5) [Aquifex aeolicus VF5] pir C70425 transporter (extracellular solute binding protein family 5) - Aquifex aeolicus			
	18653297	35	2.00E-26	Vibrio cholerae	putative glycosyl transferase [Vibrio cholerae]			2.4.1.-
				Bacteroides thetaiotaomicron	putative long-chain-fatty-acid-CoA ligase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78656.1 putative long-chain-fatty-acid-CoA ligase [Bacteroides thetaiotaomicron VPI-5482]			6.2.1.3
	29348959	38	1.00E-26	Desulfotalea psychrophila LSV54	hypothetical protein DPPB82 [Desulfotalea psychrophila LSV54] emb CAG37926.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]			
	51247033	57	3.00E-29	Microbulbifer degradans 2-40	COG0842: Signal transduction histidine kinase [Microbulbifer degradans 2- 40]			
	48861626	40	1.00E-40	Idiomarina	Acylaminoacyl-peptidase [Idiomarina loihiensis L2TR] gb AAV81119.1			3.4.19.1
	58459387	29	2.00E-15	Idiomarina L2TR	Acylaminoacyl-peptidase [Idiomarina loihiensis L2TR]			
				Wolinella succinogenes DSM 1740	IRON-SULFUR PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10024.1 IRON-SULFUR PROTEIN [Wolinella succinogenes]			
	34557309	42	5.00E-34	Ralstonia eutropha JMP134	COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Ralstonia eutropha JMP134]			2.7.3.-

14637, 14638, 14639, 14640	34557638 48855884	63 47	1.00E-111 2.00E-23	Wolinella succinogenes DSM 1740 Cytophaga hutchinsonii	QUINOLINATE SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10353.1 QUINOLINATE SYNTHETASE [Wolinella succinogenes] COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii]				
14641, 14642	28899897	48	2.00E-42	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VPA0042 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61385.1 hypothetical protein [Vibrio parahaemolyticus]				
14643, 14644 14645, 14646	49354332 23474904	34 45	8.00E-34 2.00E-57	Mycoplasma fermentans Desulfovibrio desulfuricans G20	putative ATP-dependent DNA helicase [Mycoplasma fermentans] COG2070: Dioxygenases related to 2-nitropropane dioxygenase [Desulfovibrio desulfuricans G20]	3.6.1.- 1.13.11. 32			
14647, 14648	34557603	54	5.00E-39	Wolinella succinogenes DSM 1740	hypothetical protein WS1238 [Wolinella succinogenes DSM 1740] emb CAE10318.1 conserved hypothetical protein [Wolinella succinogenes]				
14649, 14650	34558157	44	3.00E-16	Wolinella succinogenes DSM 1740	SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes DSM 1740] emb CAE10872.1 SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes]	2.7.3.-			
1465, 1466	59963015	42	3.00E-26	Bacillus clausii KSM-K16	hypothetical protein ABC1243 [Bacillus clausii KSM-K16] dbj BAD63781.1 conserved hypothetical protein [Bacillus clausii KSM-K16]	3.4.11.5			
14651, 14652	17545258	61	3.00E-74	Ralstonia solanacearum GMI1000	PROBABLE ATP-DEPENDENT RNA HELICASE PROTEIN [Ralstonia solanacearum GMI1000] emb CAD14067.1 PROBABLE ATP-DEPENDENT RNA HELICASE PROTEIN [Ralstonia solanacearum]	2.7.7.-			
14653, 14654	46579094	35	2.00E-33	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	sensory box histidine kinase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS95161.1 sensory box histidine kinase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]	2.7.3.-			
14657, 14658	21673251	45	4.00E-48	Chlorobium tepidum TLS	iron(III) ABC transporter, ATP-binding protein, putative [Chlorobium tepidum TLS] gb AAM71658.1 iron(III) ABC transporter, ATP-binding protein, putative [Chlorobium tepidum TLS]	3.6.3.33			
14659, 14660	19705009	39	2.00E-30	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Oxidoreductase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93803.1 Oxidoreductase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]	1.1.1.21			
14661, 14662	34558468	44	2.00E-30	Wolinella succinogenes DSM 1740	PUTATIVE ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZ [Wolinella succinogenes DSM 1740] emb CAE11183.1 PUTATIVE ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZ [Wolinella succinogenes])	6.3.5.4			

14665, 14666	57242329	46	3.00E-42	Campylobacter upsaliensis RM3195	signal-transducing protein, histidine kinase [Campylobacter upsaliensis RM3195] gb EAL53791.1 signal-transducing protein, histidine kinase [Campylobacter upsaliensis RM3195]			2.7.3.-
14667, 14668	57241251	59	8.00E-67	Campylobacter lari RM2100	response regulator (ompR) [Campylobacter lari RM2100] gb EAL54947.1 response regulator (ompR) [Campylobacter lari RM2100]			2.7.3.-
14669, 14670	34557606	36	1.00E-48	Wolinella succinogenes DSM 1740	hypothetical protein WS1241 [Wolinella succinogenes DSM 1740] emb CAE10321.1 conserved hypothetical protein [Wolinella succinogenes]			3.5.1.-
1467, 1468	39936696	49	6.00E-23	Rhodopseudomonas palustris CGA009	putative Transaldolase Phosphoglucose isomerase [Rhodopseudomonas palustris CGA009] emb CAE29075.1 putative Transaldolase Phosphoglucose isomerase [Rhodopseudomonas palustris CGA009]			2.2.1.2
14671, 14672	48838846	50	3.00E-30	Methanosarcina barkeri str. fusaro	COG0457: FOG: TPR repeat [Methanosarcina barkeri str. fusaro]			
14673, 14674	33600223	29	3.00E-23	Bordetella bronchiseptica RB50	putative phosphoesterase [Bordetella bronchiseptica RB50] emb CAE31735.1 putative phosphoesterase [Bordetella bronchiseptica RB50]			
14675, 14676	42522432	41	1.00E-40	Bdellovibrio bacteriovorus HD100	ABC-type phosphonate transport protein, ATP-binding [Bdellovibrio bacteriovorus HD100] emb CAE78805.1 ABC-type phosphonate transport protein, ATP-binding [Bdellovibrio bacteriovorus HD100]			1.8.-
14677, 14678	57242034	63	1.00E-68	Campylobacter upsaliensis RM3195	uroporphyrinogen decarboxylase [Campylobacter upsaliensis RM3195] gb EAL54007.1 uroporphyrinogen decarboxylase [Campylobacter upsaliensis RM3195]			4.1.1.37
14679, 14680	28900746	38	7.00E-27	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VPA0891 [Vibrio parahaemolyticus RIMD 2210633] db BAC62234.1 hypothetical protein [Vibrio parahaemolyticus]			
14683, 14684	51244370	43	2.00E-26	Desulfotalea psychrophila LSV54	hypothetical protein DP0518 [Desulfotalea psychrophila LSV54] emb CAG35247.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]			
14685, 14686	51246963	38	2.00E-14	Desulfotalea psychrophila LSV54	hypothetical protein DP3111 [Desulfotalea psychrophila LSV54] emb CAG37840.1 hypothetical protein [Desulfotalea psychrophila LSV54]			
14687, 14688	51246963	49	2.00E-36	Desulfotalea psychrophila LSV54	hypothetical protein DP3111 [Desulfotalea psychrophila LSV54] emb CAG37840.1 hypothetical protein [Desulfotalea psychrophila LSV54]			
14689, 14690	48858932	34	9.00E-26	Clostridium thermocellum ATCC 27405	COG0842: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405]			2.7.3.-

1469, 1470	52007674	36	6.00E-16	25259	Thiobacillus denitrificans ATCC	COG1959: Predicted transcriptional regulator [Thiobacillus denitrificans ATCC 25259]			
14691, 14692	20089988	36	5.00E-11		Methanosarcina acetivorans C2A	transcriptional regulator, MarR family [Methanosarcina acetivorans C2A] gb AA04543.1 transcriptional regulator, MarR family [Methanosarcina acetivorans str. C2A]			
14693, 14694	34557604	44	4.00E-60	1740	Wolinella succinogenes DSM	TRANSCRIPTION-REPAIR COUPLING FACTOR [Wolinella succinogenes DSM 1740] emb CAE10319.1 TRANSCRIPTION-REPAIR COUPLING FACTOR [Wolinella succinogenes]			
14695, 14696	34557638	66	1.00E-106	1740	Wolinella succinogenes DSM	QUINOLINATE SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10353.1 QUINOLINATE SYNTHETASE [Wolinella succinogenes] excinuclease ABC, A subunit [Campylobacter jejuni RM1221]			
14697, 14698	57237396	79	8.00E-77		Campylobacter jejuni RM1221	gb AAW34979.1 excinuclease ABC, A subunit [Campylobacter jejuni RM1221]	Rickettsia typhi str. Wilmington complete genome	84	2.00E-12
14699, 14700	46202599	33	6.00E-27	MS-1	Magnetospirillum magnetotacticum	hypothetical protein Magn03007449 [Magnetospirillum magnetotacticum MS- 1]			
14701, 14702	54309817	71	1.00E-119		Photobacterium profundum SS9	putative UDP-glucose dehydrogenase [Photobacterium profundum SS9] emb CAG21035.1 putative UDP-glucose dehydrogenase [Photobacterium profundum]	Campylobacter jejuni	96	7.00E-13 1.1.1.22
14703, 14704	48862943	49	2.00E-59		Microbulbifer degradans 2-40	COG0845: Membrane-fusion protein [Microbulbifer degradans 2-40]			
14705, 14706	47575513	47	1.00E-76		Rubrivivax gelatinosus PM1	COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Rubrivivax gelatinosus PM1]			3.4.21.-
14707, 14708	34558477	35	5.00E-09	1740	Wolinella succinogenes DSM	hypothetical protein WS2202 [Wolinella succinogenes DSM 1740] emb CAE11192.1 hypothetical protein [Wolinella succinogenes] lipoprotein releasing system ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO78745.1 lipoprotein releasing system ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] spiQ8A1M1 OLD_BACTN Lipoprotein releasing system ATP-binding protein fold			1.8.-
14711, 14712	32471112	30	2.00E-09		Rhodopirella baltica SH 1	probable surface-associated protein cshA precursor [Rhodopirella baltica SH 1] emb CAD71782.1 probable surface-associated protein cshA precursor [Pirella sp.]			
14713, 14714	48854139	57	1.00E-49		Cytophaga hutchinsonii	COG1066: Predicted ATP-dependent serine protease [Cytophaga hutchinsonii]			
14715, 14716	51244796	45	3.00E-18		Desulfotalea psychrophila LSV54	related to ArsR-family transcription regulator [Desulfotalea psychrophila LSV54] emb CAG35673.1 related to ArsR-family transcription regulator [Desulfotalea psychrophila LSV54]			

14717,	48855926	35	1.00E-39	Cytophaga hutchinsonii	COG1091: dTDP-4-dehydrothiamine reductase [Cytophaga hutchinsonii]			1.1.1.13
14718				Bacillus cereus	Methyltransferase [Bacillus cereus ATCC 14579] gb AAP11449.1			3
14719,	30022617	51	8.00E-42	ATCC 14579	Methyltransferase [Bacillus cereus ATCC 14579]			
14720				Clostridium thermocellum	COG0500: SAM-dependent methyltransferases [Clostridium thermocellum ATCC 27405]			2.1.1.-
14721,	48859334	60	1.00E-49	ATCC 27405	hypothetical protein PBPRB0710 [Photobacterium profundum SS9]			
14722				Photobacterium profundum SS9	emb CAG22582.1 hypothetical protein [Photobacterium profundum]			
14725,	54302389	49	8.00E-42	profundum SS9	COG0747: ABC-type dipeptide transport system, periplasmic component			
14726				Cytophaga hutchinsonii	[Cytophaga hutchinsonii]			
14727,	48854027	40	4.00E-48		hypothetical protein aq_737 [Aquifex aeolicus VF5] gb AAC06915.1			
14728				Aquifex aeolicus VF5	hypothetical protein [Aquifex aeolicus VF5] pir G70364 conserved			
14729,	15606130	50	4.00E-50		hypothetical protein aq_737 - Aquifex aeolicus sp O66946 MRP_AQUAE			
14730				Bacteroides thetaiotaomicron VPI-5482	Mrp protein homolog			
1473,	29347668	39	5.00E-17		GTP-binding protein [Bacteroides thetaiotaomicron VPI-5482]			
1474				Bacillus anthracis str. 'Ames'	hypothetical protein GBAA0891 [Bacillus anthracis str. 'Ames Ancestor']			
14733,	47526177	26	5.00E-24	Ancestor	ref NP_843402.1 hypothetical protein BA0891 [Bacillus anthracis str. 'Ames']			
14734				Treponema denticola ATCC 35405	ref NP_654834.1 hypothetical protein BA_1474 [Bacillus anthracis str. 'Ames']			
14735,	42526769	26	5.00E-12		A2012] gb AAP24888.1 conserved hypothetical protein [Bacillus anthracis str. 'Ames']			
14736				Cytophaga hutchinsonii	str. 'Ames'] gb AAT30001.1 conserved hypothetical protein [Bacillus anthracis str. 'Ames Ancestor']			
14737,	48853824	48	1.00E-72		anthracis str. 'Ames Ancestor']			
14738				Cholinephosphate cytidylyltransferase/choline kinase [Treponema denticola ATCC 35405]	cholinephosphate cytidylyltransferase/choline kinase [Treponema denticola ATCC 35405] gb AAS11778.1 cholinephosphate cytidylyltransferase/choline kinase [Treponema denticola ATCC 35405]			2.7.1.32
14739,	34397911	30	2.00E-29		COG0859: ADP-heptose:LPS heptosyltransferase [Cytophaga hutchinsonii]			
14740				Porphyrromonas gingivalis W83	signal peptidase I [Porphyrromonas gingivalis W83] ref NP_906073.1 signal			3.4.21.8
14743,	53711472	52	2.00E-26		peptidase I [Porphyrromonas gingivalis W83]			9
14744				Bacteroides fragilis	signal peptidase I [Bacteroides fragilis YCH46] db BAD46930.1 signal			3.4.21.8
14745,	33355837	54	1.00E-31		peptidase I [Bacteroides fragilis YCH46]			9
14746				Enterococcus faecalis	Trsk-like protein [Enterococcus faecalis]			
14747,	57234003	60	7.00E-89		[SDet4, transposase [Dehalococcoides ethenogenes 195] gb AAW39508.1			
14748				Dehalococcoides ethenogenes 195	[SDet4, transposase [Dehalococcoides ethenogenes 195]			

14749, 14750	34557966	58	9.00E-89	Wollinella succinogenes DSM 1740	ATP-DEPENDENT HELICASE [Wollinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wollinella succinogenes]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6	92	7.00E-10	3.6.1.-
1475, 1476	56708105	33	4.00E-14	Francisella tularensis subsp. tularensis Schu 4	GDSL-like Lipase/Acylhydrolase family protein [Francisella tularensis subsp. tularensis Schu 4] emb CAG45649.1 GDSL-like Lipase/Acylhydrolase family protein [Francisella tularensis subsp. tularensis] AsnC family transcriptional regulator [Bacteroides fragilis YCH46] db BAD48864.1 AsnC family transcriptional regulator [Bacteroides fragilis YCH46]			3.1.2.-	
14751, 14752	53713406	46	3.00E-35	Bacteroides fragilis YCH46	COG0626: Cystathionine beta-lyases/cystathionine gamma-synthases [Chloroflexus aurantiacus]				4.4.1.11
14753, 14754	53798453	78	2.00E-08	Chloroflexus aurantiacus	conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56275.1 conserved hypothetical protein [Campylobacter coli RM2228]				
14757, 14758	57169040	22	1.00E-07	Campylobacter coli RM2228	hypothetical protein sil1308 [Synechocystis sp. PCC 6803] db BAA17635.1 sil1308 [Synechocystis sp. PCC 6803] pir S77301 hypothetical protein sil1308 - Synechocystis sp. (strain PCC 6803)				1.1.1.10 0
14765, 14766	28900413	42	9.00E-32	Synechocystis sp. PCC 6803	hypothetical protein VPA0558 [Vibrio parahaemolyticus RIMD 2210633] db BAC61901.1 conserved hypothetical protein [Vibrio parahaemolyticus] COG1776: Chemotaxis protein CheC, inhibitor of MCP methylation [Magnetococcus sp. MC-1]				
14767, 14768	48832346	25	5.00E-07	Vibrio parahaemolyticus RIMD 2210633 Magnetococcus sp. MC-1	conserved hypothetical protein [Silicibacter pomeroyi DSS-3] ref YP_165430.1 hypothetical protein SPO0160 [Silicibacter pomeroyi DSS- 3]				
14769, 14770	56676820	49	1.00E-50	Silicibacter pomeroyi DSS-3	unknown [Leptospira borgpetersenii]				
14771, 14772	4234793	36	1.00E-23	Leptospira borgpetersenii	hypothetical protein PP4291 [Pseudomonas putida KT2440] gb AAN69871.1 conserved hypothetical protein [Pseudomonas putida KT2440]				
14775, 14776	26990982	28	1.00E-16	Pseudomonas putida KT2440	type I restriction modification enzyme protein S [Methanosarcina acetivorans C2A] gb AAM05801.1 type I restriction modification enzyme protein S [Methanosarcina acetivorans str. C2A]				3.1.21.3
14779, 14780	20091246	46	3.00E-39	Methanosarcina acetivorans C2A	RNA pseudouridylyate synthase family protein [Campylobacter jejuni RM1221] gb AAW34517.1 RNA pseudouridylyate synthase family protein [Campylobacter jejuni RM1221]				4.2.1.70
14783, 14784	57236934	42	8.00E-28	Campylobacter jejuni RM1221					

14785, 14786	46581495	35	2.00E-10	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	hypothetical protein DVU3092 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gbl AAS97563.1 hypothetical protein DVU3092 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			
14787, 14788	20807875	48	9.00E-18	Thermoanaerobact er tengcongensis MB4	CheY-like receiver domains [Thermoanaerobacter tengcongensis MB4] gbl AAM24650.1 CheY-like receiver domains [Thermoanaerobacter tengcongensis MB4]		3.1.1.61	
14789, 14790	40741709	42	1.00E-16	Aspergillus nidulans FGSC A4	hypothetical protein AN4556.2 [Aspergillus nidulans FGSC A4] ref XP_408693.1 hypothetical protein AN4556.2 [Aspergillus nidulans FGSC A4]			
14791, 14792	57238505	37	3.00E-35	Campylobacter jejuni RM1221	hypothetical protein CJE1655 [Campylobacter jejuni RM1221] gbl AAW36088.1 conserved hypothetical protein [Campylobacter jejuni RM1221]			
14793, 14794	53713554	52	3.00E-89	Bacteroides fragilis YCH46	putative carbon-nitrogen hydrolase [Bacteroides fragilis YCH46] dbj BAD49012.1 putative carbon-nitrogen hydrolase [Bacteroides fragilis YCH46]			
14795, 14796	34557665	58	1.00E-38	Wolinella succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT)		2.7.3.-	
14801, 14802	37520430	29	2.00E-25	Gloeobacter violaceus PCC 7421	two-component sensor histidine kinase [Gloeobacter violaceus PCC 7421] dbj BAC88802.1 two-component sensor histidine kinase [Gloeobacter violaceus PCC 7421]		2.7.3.-	
14803, 14804	53713488	37	6.00E-47	Bacteroides fragilis YCH46	two-component system sensor histidine kinase [Bacteroides fragilis YCH46] dbj BAD48946.1 two-component system sensor histidine kinase [Bacteroides fragilis YCH46]		2.7.3.-	
14805, 14806	34397475	28	2.00E-13	Porphyromonas gingivalis W83	hypothetical protein PG1492 [Porphyromonas gingivalis W83] ref NP_905638.1 hypothetical protein PG1492 [Porphyromonas gingivalis W83]			
14807, 14808	34397124	77	1.00E-109	Porphyromonas gingivalis W83	D-lysine 5,6-aminomutase, beta subunit [Porphyromonas gingivalis W83] ref NP_905289.1 D-lysine 5,6-aminomutase, beta subunit [Porphyromonas gingivalis W83]	Porphyromonas gingivalis W83 section 4 of 8 of the complete genome	80 3.00E-18	5.4.3.3
14809, 14810	56460690	51	3.00E-63	Idiomarina loliensis L2TR	Zn-dependent hydrolases, glyoxylase family [Idiomarina loliensis L2TR] gbl AAV82422.1 Zn-dependent hydrolases, glyoxylase family [Idiomarina loliensis L2TR]			
1481, 1482	48838849	76	4.00E-96	Methanosarcina barkeri str. fusaro	COG4742: Predicted transcriptional regulator [Methanosarcina barkeri str. fusaro]	Methanosarcina acetivorans str. C2A, section 22 of 534 of the complete genome	81 3.00E-27	

14813, 14814	57241396	61	1.00E-38	Campylobacter lari RM2100	amidophosphoribosyltransferase [Campylobacter lari RM2100] gb JEA154508.1 amidophosphoribosyltransferase [Campylobacter lari RM2100]			2.4.2.14
14815, 14816	28974234	66	1.00E-47	Campylobacter fetus	putative two-component regulator C0034 [Campylobacter fetus]		83	8.00E-08
14817, 14818	28974235	32	2.00E-18	Campylobacter fetus	putative putative two-component sensor C0035 [Campylobacter fetus] CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes]			
14819, 14820	34556616	45	1.00E-66	Wolinella succinogenes DSM 1740	Hemolysin [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94497.1 Hemolysin [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			
14821, 14822	19703636	33	3.00E-35	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	hypothetical protein MS1396 [Mannheimia succiniciproducens MBEL55E] gb AAU38003.1 unknown [Mannheimia succiniciproducens MBEL55E]			
14823, 14824	52425451	36	6.00E-23	Mannheimia succiniciproducens MBEL55E	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii]			
14825, 14826	48856104	40	2.00E-38	Cytophaga hutchinsonii	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860522.1 hypothetical protein HH0991 [Helicobacter hepaticus ATCC 51449]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6	80	1.00E-16
14827, 14828	32262541	74	1.00E-71	Helicobacter hepaticus ATCC 51449	COG0370: Fe2+ transport system protein B [Geobacter metallireducens GS- 15]			
1483, 1484	48845148	52	3.00E-19	Geobacter metallireducens GS- 15	putative methyltransferase CmuC [Bacteroides fragilis YCH46] dbj BAD49814.1 putative methyltransferase CmuC [Bacteroides fragilis YCH46]			
14831, 14832	53714356	64	4.00E-80	Bacteroides fragilis YCH46	hypothetical protein WS0448 [Wolinella succinogenes DSM 1740] emb CAE09590.1 conserved hypothetical protein [Wolinella succinogenes] hypothetical protein, probably cold-shock inducible [Desulfotalea psychrophila LSV54] emb CAG34908.1 hypothetical protein, probably cold- shock inducible [Desulfotalea psychrophila LSV54]			
14835, 14836	34556875	35	2.00E-24	Wolinella succinogenes DSM 1740				
14841, 14842	51244031	34	1.00E-06	Desulfotalea psychrophila LSV54				

14845, 14846, 14847, 14848	29347422 53691481	34 53	9.00E-26 1.00E-74	Bacteroides thetaiotaomicron VPI-5482 Desulfovibrio desulfuricans G20	conserved hypothetical protein, putative ATPase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77119.1 conserved hypothetical protein, putative ATPase [Bacteroides thetaiotaomicron VPI-5482] COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Desulfovibrio desulfuricans G20] hypothetical protein SMU.606 [Streptococcus mutans UA159] gb AAN58344.1 hypothetical protein SMU.606 [Streptococcus mutans UA159]				
14849, 14850	24379083	33	8.00E-16	Streptococcus mutans UA159					2.7.1.-
1485, 1486	37523515	77	8.00E-77	Gloeobacter violaceus PCC 7421	rifampin ADP-ribosyl transferase [Gloeobacter violaceus PCC 7421] dbj BAC91887.1 rifampin ADP-ribosyl transferase [Gloeobacter violaceus PCC 7421]			82 6.00E-81	
14851, 14852	29346615	67	3.00E-91	Bacteroides thetaiotaomicron VPI-5482	putative ATPase, AAA family [Bacteroides thetaiotaomicron VPI-5482] gb AAO76312.1 putative ATPase, AAA family [Bacteroides thetaiotaomicron VPI-5482]				3.4.24.-
14853, 14854	16273482	54	3.00E-56	Haemophilus influenzae Rd KW20	formyltetrahydrofolate deformylase [Haemophilus influenzae Rd KW20] gb AAC23236.1 formyltetrahydrofolate deformylase (purU) [Haemophilus influenzae Rd KW20] sp Q03432 PURU_HAEIN Formyltetrahydrofolate deformylase (Formyl-FH(4) hydrolase) pir E84131 formyltetrahydrofolate deformylase (EC 3.5.1.10) - Haemophilus influenzae (strain Rd KW20)				3.5.1.10
14855, 14856	14518364	32	1.00E-19	Microscilla sp. PRE1	putative transposase [Microscilla sp. PRE1] gb AAK62881.1 MS159, putative transposase [Microscilla sp. PRE1]				
14859, 14860	56707780	57	2.00E-73	Francisella tularensis subsp. tularensis Schu 4	DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis Schu 4] emb CAG45292.1 DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis]				
14861, 14862, 14863, 14864	12512884	39	7.00E-31	Escherichia coli O157:H7 Cytophaga hutchinsonii	deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] ref NP_285856.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7 EDL933] ref NP_308191.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] sp Q8X8Y9 DGTG_ECO57 Deoxyguanosinetriphosphate triphosphohydrolase (dGTPase) (dGTP triphosphohydrolase) pir D85500 deoxyguanosine triphosphate triphosphohydrolase [imported] - Escherichia coli (strain O157:H7, substrain EDL933) dbj BAB33587.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] pir D90649 deoxyguanosine triphosphate triphosphohydrolase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)				3.1.5.1
	48553652	26	3.00E-13		COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]				

14865, 14866, 14867, 14868	34557782 48855616	27 27	8.00E-21 2.00E-13	Wollinella succinogenes DSM 1740 Cytophaga hutchinsonii	PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes] COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]			2.7.3.-
14869, 14870, 1487, 1488	20090843 48855191	43 50	6.00E-31 3.00E-51	Methanosarcina acetivorans C2A Cytophaga hutchinsonii	hypothetical protein MA1995 [Methanosarcina acetivorans C2A] gb AAM05398.1 predicted protein [Methanosarcina acetivorans str. C2A] COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-
14871, 14872	45250017	35	8.00E-40	Aneurinibacillus thermoaerophilus	putative glycosyl transferase [Aneurinibacillus thermoaerophilus] hypothetical protein PA3762 [Pseudomonas aeruginosa PAO1] ref ZP_00137160.2 COG3323: Uncharacterized protein conserved in bacteria [Pseudomonas aeruginosa UCBPP-PA14] pir A83175 hypothetical protein PA3762 [Imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_252451.1 hypothetical protein PA3762 [Pseudomonas aeruginosa PAO1]			2.4.1.-
14873, 14874	9949932	48	3.00E-23	Pseudomonas aeruginosa PAO1	hypothetical protein WS0457 [Wollinella succinogenes DSM 1740] emb CAE09599.1 conserved hypothetical protein [Wollinella succinogenes]			1.-.-.-
14879, 14880	34556884	53	2.00E-83	Wollinella succinogenes DSM 1740	alpha-cyclodextrinase [Geobacillus stearothermophilus] glycosyltransferase [Bacteroides fragilis YCH46] db BAD47233.1 glycosyltransferase [Bacteroides fragilis YCH46]			3.2.1.20
14881, 14882 14883, 14884	15375096 53711775	44 57	6.00E-18 1.00E-62	Geobacillus stearothermophilus Bacteroides fragilis YCH46	serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70895.1 serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			
14885, 14886 14887, 14888	45658172 48833325	38 28	7.00E-31 5.00E-32	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes]			2.7.3.-
14889, 14890	34557246	42	7.00E-35	Wollinella succinogenes DSM 1740	hypothetical protein WS1135 [Wollinella succinogenes DSM 1740] emb CAE10224.1 hypothetical protein [Wollinella succinogenes]			2.7.3.-
14891, 14892	34557509	64	6.00E-38	Wollinella succinogenes DSM 1740				

14895, 14896	34556516	62	3.00E-53	Wolinella succinogenes DSM 1740	hypothetical protein WS0062 [Wolinella succinogenes DSM 1740] emb CAE09231.1 conserved hypothetical protein [Wolinella succinogenes]				
14897, 14898	17936982	53	8.00E-51	Agrobacterium tumefaciens str. C58	glycosyltransferase [Agrobacterium tumefaciens str. C58] gb AAL44087.1 glycosyltransferase [Agrobacterium tumefaciens str. C58] pir AI2958 glycosyltransferase Atu3271 [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)			2.4.1.-	
14901, 14902	15893463	47	5.00E-27	Clostridium acetobutylicum ATCC 824	ABC transporter (ATP-binding protein) [Clostridium acetobutylicum ATCC 824] gb AAK78152.1 ABC transporter (ATP-binding protein) [Clostridium acetobutylicum ATCC 824] pir E96920 ABC transporter (ATP-binding protein) CAC0169 [Imported] - Clostridium acetobutylicum			1.8.-	
14903, 14904	53715141	59	1.00E-47	Bacteroides fragilis YCH46	putative long-chain-fatty-acid-CoA ligase [Bacteroides fragilis YCH46] dbj BAD50599.1 putative long-chain-fatty-acid-CoA ligase [Bacteroides fragilis YCH46]	Bacteroides thetaiotaomicron VPI-5482, section 10 of 21 of the complete genome	93	2.00E-08	6.2.1.3
14905, 14906	34557782	43	2.00E-43	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]				2.7.3.-
14909, 14910	34557184	50	2.00E-55	Wolinella succinogenes DSM 1740	BH0401 PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09899.1 BH0401 PROTEIN [Wolinella succinogenes] possible helicase [Rhodopseudomonas palustris CGA009] emb CAE27655.1 possible helicase [Rhodopseudomonas palustris CGA009]				
1491, 1492	39935283	30	1.00E-12	Rhodopseudomona s palustris CGA009	Hemolysin [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94497.1 Hemolysin [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] COG2072: Predicted flavoprotein Involved in K+ transport [Enterococcus faecium]				
14911, 14912	19703636	27	4.00E-21	Enterococcus faecium	hypothetical protein PG1236 [Porphyromonas gingivalis W83] ref NP_905423.1 hypothetical protein PG1236 [Porphyromonas gingivalis W83]				
14915, 14916	48826153	32	3.00E-09	Porphyromonas gingivalis W83	galactose-1-phosphate transferase [Lactococcus lactis subsp. cremoris] omega-3 polyunsaturated fatty acid synthase Pf1C [Photobacterium profundum SS9] emb CAG19869.1 omega-3 polyunsaturated fatty acid synthase Pf1C [Photobacterium profundum]				2.-
14917, 14918	34397259	33	9.00E-29	Lactococcus lactis subsp. cremoris					
14919, 14920	4557150	33	3.00E-15	Photobacterium profundum SS9					
14921, 14922	54308651	44	8.00E-56						

14923, 14924	34557931	68	2.00E-74	Wolinella succinogenes DSM 1740	PUTATIVE TRANSCRIPTION REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10646.1 PUTATIVE TRANSCRIPTION REGULATOR [Wolinella succinogenes]			2.1.1.63
14925, 14926	34557780	43	5.00E-21	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10495.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes]			2.7.1.1
14927, 14928	46142672	41	6.00E-19	Methanococcoides burtonii DSM 6242	COG3769: Predicted hydrolase (HAD superfamily) [Methanococcoides burtonii DSM 6242]			
14929, 14930	46142672	34	3.00E-35	Methanococcoides burtonii DSM 6242	COG3769: Predicted hydrolase (HAD superfamily) [Methanococcoides burtonii DSM 6242]			
14931, 14932	34556616	43	1.00E-49	Wolinella succinogenes DSM 1740	CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes]			
14933, 14934	20806595	61	4.00E-69	Thermoanaerobact er tengcongensis MB4	predicted glycosylase [Thermoanaerobacter tengcongensis MB4] gb AAM23370.1 predicted glycosylase [Thermoanaerobacter tengcongensis MB4]			
14937, 14938	48853894	32	1.00E-10	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]			
14939, 14940	48855730	36	1.00E-27	Cytophaga hutchinsonii	hypothetical protein Chut02000936 [Cytophaga hutchinsonii]			
14941, 14942	20092002	35	4.00E-12	Methanosarcina acetivorans C2A	moaA/nifB/pqqE family protein [Methanosarcina acetivorans C2A] gb AAM06557.1 moaA/nifB/pqqE family protein [Methanosarcina acetivorans str. C2A]			
14943, 14944	34557385	39	3.00E-35	Wolinella succinogenes DSM 1740	SELENOPHOSPHATE SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10100.1 SELENOPHOSPHATE SYNTHETASE [Wolinella succinogenes]			2.7.9.3
14945, 14946	53713487	37	2.00E-17	Bacteroides fragilis YCH46	two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD48945.1 two-component system response regulator [Bacteroides fragilis YCH46]			
14947, 14948	48855423	28	1.00E-13	Cytophaga hutchinsonii	COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii]			5.2.1.8
14951, 14952	34556738	54	2.00E-59	Wolinella succinogenes DSM 1740	SUCCINYLORNITHINE TRANSAMINASE [Wolinella succinogenes DSM 1740] emb CAE09453.1 SUCCINYLORNITHINE TRANSAMINASE [Wolinella succinogenes] sp Q7MAE6 ARGD_WOLSU Acetylornithine aminotransferase (ACOAT)			2.6.1.11
14953, 14954	34557931	75	2.00E-65	Wolinella succinogenes DSM 1740	PUTATIVE TRANSCRIPTION REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10646.1 PUTATIVE TRANSCRIPTION REGULATOR [Wolinella succinogenes]			2.1.1.63

14955, 14956	28210060	58	8.00E-30	Clostridium tetani E88	thymidine kinase [Clostridium tetani E88]				2.7.1.21
14959, 14960	32263380	44	1.00E-29	Helicobacter hepaticus ATCC 51449	thiamine monophosphate synthase [Helicobacter hepaticus ATCC 51449] ref NP_861359.1 thiamine monophosphate synthase [Helicobacter hepaticus ATCC 51449]				2.5.1.3
14961, 14962	15791002	37	1.00E-11	Halobacterium salinarum NRC-1	hypothetical protein VNG2170H [Halobacterium salinarum NRC-1] gb AAG20306.1 Vng2170h [Halobacterium sp. NRC-1] pir F84367 hypothetical protein Vng2170h [imported] - Halobacterium sp. NRC-1				
14965, 14966	50084270	34	3.00E-22	Acinetobacter sp. ADP1	cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAG67958.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAA86930.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] sp Q43989 COBQ_ACIAD Cobyrinic acid synthase				
14967, 14968	34557550	35	1.00E-16	Wolfinella succinogenes DSM 1740	hypothetical protein WS1180 [Wolfinella succinogenes DSM 1740] emb CAE10265.1 hypothetical protein [Wolfinella succinogenes]				
14975, 14976	57168891	39	2.00E-43	Campylobacter coli RM2228	conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56346.1 conserved hypothetical protein [Campylobacter coli RM2228]				
14979, 14980	34557672	44	1.00E-42	Wolfinella succinogenes DSM 1740	30S RIBOSOMAL PROTEIN S1 [Wolfinella succinogenes DSM 1740] emb CAE10387.1 30S RIBOSOMAL PROTEIN S1 [Wolfinella succinogenes]				
14981, 14982	57504658	49	5.00E-64	Campylobacter coli RM2228	methionyl-tRNA formyltransferase [Campylobacter coli RM2228] gb EAL56122.1 methionyl-tRNA formyltransferase [Campylobacter coli RM2228]				2.1.2.9
14983, 14984	29347846	45	5.00E-65	Bacteroides thetaiotaomicron VPI-5482	putative secreted tripeptidyl aminopeptidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77543.1 putative secreted tripeptidyl aminopeptidase [Bacteroides thetaiotaomicron VPI-5482]				
14985, 14986	48845271	42	7.00E-25	Geobacter metallireducens GS 15	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]				2.7.3.-
14989, 14990	34557665	44	1.00E-30	Wolfinella succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wolfinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolfinella succinogenes]				2.7.3.-
14991, 14992	29346503	23	2.00E-13	Bacteroides thetaiotaomicron VPI-5482	conserved hypothetical protein, putative TonB-dependent outer membrane receptor protein [Bacteroides thetaiotaomicron VPI-5482] conserved hypothetical protein, putative TonB-dependent outer membrane receptor protein [Bacteroides thetaiotaomicron VPI-5482]				
14995, 14996	57168163	46	2.00E-38	Campylobacter coli RM2228	probable periplasmic protein Cj0599 [Campylobacter coli RM2228] gb EAL57206.1 probable periplasmic protein Cj0599 [Campylobacter coli RM2228]				

14997, 14998	34396942	61	1.00E-31	Porphyromonas gingivalis W83	conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_905107.1 hypothetical protein PG0858 [Porphyromonas gingivalis W83]			
14999, 15000	34558164	30	9.00E-33	Wolinella succinogenes DSM 1740	CHEMOTAXIS PROTEIN CHEV-CheY like receiver domain [Wolinella succinogenes DSM 1740] emb CAE10879.1 CHEMOTAXIS PROTEIN CHEV-CheY like receiver domain [Wolinella succinogenes]			2.7.3.-
15, 16	46119894	30	3.00E-19	Crocospaera watsonii WH 8501	COG1106: Predicted ATPases [Crocospaera watsonii WH 8501] oxygen-independent coproporphyrinogen III oxidase, putative [Shewanella oneidensis MR-1] gb AAAN57484.1 oxygen-independent coproporphyrinogen III oxidase, putative [Shewanella oneidensis MR-1]			1.-.-.-
15007, 15008	24375997	46	3.00E-15	Shewanella oneidensis MR-1	glycogen synthase [Aquifex aeolicus VF5] gb AAC06894.1 glycogen synthase [Aquifex aeolicus VF5] pir C70363 glycogen synthase - Aquifex aeolicus sp O66935 GLGA_AQUAE Glycogen synthase (Starch [bacterial glycogen] synthase)			2.4.1.21
15009, 15010	15606118	47	2.00E-60	Aquifex aeolicus VF5	hypothetical protein BT3341 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78447.1 conserved hypothetical protein [Bacteroides thetaitaomicron VPI-5482]			
1501, 1502	29348750	33	3.00E-16	Bacteroides thetaitaomicron VPI-5482	COG0841: Cation/multidrug efflux pump [Cytophaga hutchinsonii]			
15011, 15012	48856922	38	9.00E-39	Cytophaga hutchinsonii	COG2202: FOG: PAS/PAC domain [Methanococcus burtonii DSM 6242] COG2265: SAM-dependent methyltransferases related to tRNA (uracil-5- γ) methyltransferase [Microbulifer degradans 2-40]			2.7.3.-
15013, 15014	46142049	45	2.00E-30	Methanococcus burtonii DSM 6242	ISPg3, transposase [Porphyromonas gingivalis W83] ref NP_905059.1 ISPg3, transposase [Porphyromonas gingivalis W83]			2.1.1.35
15015, 15016	48860700	53	6.00E-82	Microbulifer degradans 2-40	N-ACETYLGLUCOSAMINE TRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09473.1 N-ACETYLGLUCOSAMINE TRANSFERASE [Wolinella succinogenes]			2.4.1.-
15017, 15018	34396893	57	1.00E-57	Porphyromonas gingivalis W83	COG2303: Choline dehydrogenase and related flavoproteins [Crocospaera watsonii WH 8501]			1.-.-.-
15019, 15020	34556758	56	4.00E-60	Wolinella succinogenes DSM 1740	COG1600: Uncharacterized Fe-S protein [Cytophaga hutchinsonii] hypothetical membrane protein (BatD) [Desulfotalea psychrophila Lsv54] emb CAG35369.1 hypothetical membrane protein (BatD) [Desulfotalea psychrophila Lsv54]			
15025, 15026	53735985	29	5.00E-15	Crocospaera watsonii WH 8501	PUTATIVE HISTIDINOL PHOSPHATASE [Wolinella succinogenes DSM 1740] emb CAE09611.1 PUTATIVE HISTIDINOL PHOSPHATASE [Wolinella succinogenes]			3.1.3.15
15027, 15028	48855815	49	5.00E-36	Cytophaga hutchinsonii				
15031, 15032	51244492	28	1.00E-06	Desulfotalea psychrophila Lsv54				
15033, 15034	34556896	49	3.00E-36	Wolinella succinogenes DSM 1740				

15035, 15036	34558037	30	2.00E-34	Wolnella succinogenes DSM 1740	SENSOR/RESPONSE REGULATOR HYBRID [Wolnella succinogenes DSM 1740] emb CAE10752.1 SENSOR/RESPONSE REGULATOR HYBRID [Wolnella succinogenes]			2.7.3.-
15037, 15038	53713953	31	5.00E-15	Bacteroides fragilis YCH46	putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD49411.1 putative glycosyltransferase [Bacteroides fragilis YCH46]			2.7.8.6
15039, 15040	34558090	41	5.00E-50	Wolnella succinogenes DSM 1740	CINA-RELATED PROTEIN [Wolnella succinogenes DSM 1740] emb CAE10805.1 CINA-RELATED PROTEIN [Wolnella succinogenes]			
15041, 15042	34557573	40	7.00E-40	Wolnella succinogenes DSM 1740	SENSORY BOX/GGDEF FAMILY PROTEIN [Wolnella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolnella succinogenes]			2.7.3.-
15043, 15044	45521816	32	2.00E-34	Methylobacillus flagellatus KT	COG1305: Transglutaminase-like enzymes, putative cysteine proteases [Methylobacillus flagellatus KT]			
15047, 15048	34557665	25	2.00E-21	Wolnella succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wolnella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolnella succinogenes]			2.7.-
15049, 15050	34557050	54	1.00E-83	Wolnella succinogenes DSM 1740	FERREDOXIN DOMAIN INTEGRAL MEMBRANE [Wolnella succinogenes DSM 1740] emb CAE09765.1 FERREDOXIN DOMAIN INTEGRAL MEMBRANE [Wolnella succinogenes]			
1505, 1506	29610232	29	3.00E-08	Streptomyces avermitilis MA-4680	putative ATPase [Streptomyces avermitilis MA-4680] ref NP_827744.1 putative ATPase [Streptomyces avermitilis MA-4680]			2.7.1.-
15051, 15052	48846878	56	4.00E-95	Geobacter metallireducens GS- 15	COG0495: Leucyl-tRNA synthetase [Geobacter metallireducens GS-15] probable type IV pilus assembly protein (TapB) [Desulfotalea psychrophila LSv54] emb CAG36955.1 probable type IV pilus assembly protein (TapB) [Desulfotalea psychrophila LSv54]	Fusobacterium nucleatum subsp. nucleatum ATCC 25586, section 2 of 197 of the complete genome	83	7.00E-10 6.1.1.4
15053, 15054	51246078	44	1.00E-30	Desulfotalea psychrophila LSv54	COG2206: HD-GYP domain [Magnetococcus sp. MC-1]			
15055, 15056	48831584	42	3.00E-53	Magnetococcus sp. MC-1	hypothetical protein WS2057 [Wolnella succinogenes DSM 1740] emb CAE11057.1 hypothetical protein [Wolnella succinogenes]			
15063, 15064	34558342	36	3.00E-24	Wolnella succinogenes DSM 1740	sp Q7MQS0 HISZ_WOLSU ATP phosphoribosyltransferase regulatory subunit			

15069, 15070	45658014	25	5.00E-18	Leptospira interrogans serovar Copenhagen str. Flocruz L1-130	putative molybdenum cofactor biosynthesis protein [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130] ref NP_711798.1 Putative molybdopterin cofactor synthesis protein A [Leptospira interrogans serovar Lai str. 56601] gb AA048816.1 Putative molybdopterin cofactor synthesis protein A [Leptospira interrogans serovar lai str. 56601] gb AA070737.1 putative molybdenum cofactor biosynthesis protein [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130]			
1507, 1508	32472461	32	6.00E-19	Rhodopirellula baltica SH 1	conserved hypothetical protein-putative sodium:solute symporter [Rhodopirellula baltica SH 1] emb CAD73139.1 conserved hypothetical protein-putative sodium:solute symporter [Pirellula sp.]			
15071, 15072	57168968	40	3.00E-35	Campylobacter coli RM2228	hypothetical protein CCO1536 [Campylobacter coli gb EAL56323.1 hypothetical protein CCO1536 [Campylobacter coli RM2228]			
15075, 15076	32262242	38	1.00E-26	Helicobacter hepaticus ATCC 51449	tRNA (uracil-5-)-methyltransferase TmA [Helicobacter hepaticus ATCC 51449] ref NP_860224.1 tRNA (uracil-5-)-methyltransferase TmA [Helicobacter hepaticus ATCC 51449] sp Q7U326 Y693_HELHP Hypothetical RNA methyltransferase HH0693	2.1.1.35		
15077, 15078	46113312	40	2.00E-32	Exiguobacterium sp. 255-15	COG0324: RNA delta(2)-isopentenylpyrophosphate transferase [Exiguobacterium sp. 255-15]	2.5.1.8		
15079, 15080	29347555	64	5.00E-92	Bacteroides thetaiotaomicron VPI-5482	ribonucleoside-diphosphate reductase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AA077252.1 ribonucleoside-diphosphate reductase alpha chain [Bacteroides thetaiotaomicron VPI-5482] [NiFe] hydrogenase maturation protein HypF [Campylobacter lai RM2100] gb EAL54959.1 [NiFe] hydrogenase maturation protein HypF [Campylobacter lai RM2100]	1.17.4.1		
15081, 15082	57241263	50	7.00E-48	NiFe	rhodanese-like domain protein [Porphyromonas gingivalis W83] ref NP_905972.1 rhodanese-like domain protein [Porphyromonas gingivalis W83]	3.6.1.7		
15083, 15084	34397810	44	7.00E-50	Porphyromonas gingivalis W83				
15087, 15088	34558828	33	1.00E-31	Alvinella pompejana epibiont 7G3	KIAA1005 protein [Alvinella pompejana epibiont 7G3]			
15089, 15090	48856002	52	1.00E-83	Cytophaga hutchinsonii	hypothetical protein Chut02001232 [Cytophaga hutchinsonii] related to two-component system sensory/regulatory protein (Ntr family) [Desulfotalea psychrophila LSv54] emb CAG36654.1 related to two- component system sensory/regulatory protein (Ntr family) [Desulfotalea psychrophila LSv54]	2.7.3.-		
15097, 15098	51245777	45	1.00E-37	Desulfotalea psychrophila LSv54				

15099, 15100	42526444	35	2.00E-47	35405	Treponema denticola ATCC	adenylate/guanylate cyclase catalytic domain protein [Treponema denticola ATCC 35405] gb AA511423.1 adenylate/guanylate cyclase catalytic domain protein [Treponema denticola ATCC 35405]			4.6.1.1
15101, 15102	15894375	31	8.00E-21	ATCC 824	Clostridium acetobutylicum	5-formyltetrahydrofolate cyclo-ligase [Clostridium acetobutylicum ATCC 824] gb AAK79064.1 5-formyltetrahydrofolate cyclo-ligase [Clostridium acetobutylicum ATCC 824] pir E97034 5-formyltetrahydrofolate cyclo-ligase [imported] - Clostridium acetobutylicum			6.3.3.2
15103, 15104	34556710	36	7.00E-08	1740	Wolinella succinogenes DSM	LYTIC MUREIN TRANSGLYCOSYLASE [Wolinella succinogenes DSM 1740] emb CAE09425.1 LYTIC MUREIN TRANSGLYCOSYLASE [Wolinella succinogenes]			
15105, 15106	34556820	39	9.00E-44	1740	Wolinella succinogenes DSM	hypothetical protein WS0389 [Wolinella succinogenes DSM 1740] emb CAE09535.1 hypothetical protein [Wolinella succinogenes]			
15107, 15108	34556818	42	7.00E-39	1740	Wolinella succinogenes DSM	hypothetical protein WS0387 [Wolinella succinogenes DSM 1740] emb CAE09533.1 hypothetical protein [Wolinella succinogenes]			
15113, 15114	57233930	56	6.00E-58		Dehalococcoides ethenogenes 195	radical SAM/B12 binding domain protein [Dehalococcoides ethenogenes 195] gb AAW39435.1 radical SAM/B12 binding domain protein [Dehalococcoides ethenogenes 195]			
15115, 15116	57233930	49	2.00E-35		Dehalococcoides ethenogenes 195	radical SAM/B12 binding domain protein [Dehalococcoides ethenogenes 195] gb AAW39435.1 radical SAM/B12 binding domain protein [Dehalococcoides ethenogenes 195]			
15117, 15118	23015157	41	2.00E-51	MS-1	Magnetospirillum magnetotacticum	hypothetical protein Magn03009598 [Magnetospirillum magnetotacticum MS-1]			
15121, 15122	29349976	36	9.00E-27	VPI-5482	Bacteroides thetaiotaomicron	hypothetical protein BT4568 [Bacteroides thetaiotaomicron VPI-5482] gb AAC079673.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
15123, 15124	57167713	51	5.00E-29	RM2228	Campylobacter coli	probable proteinase Cj0701 [Campylobacter coli RM2228] gb EAL57499.1 probable proteinase Cj0701 [Campylobacter coli RM2228]			3.4.---
15125, 15126	16329982	43	3.00E-34	PCC 6803	Synechocystis sp.	short-chain alcohol dehydrogenase family [Synechocystis sp. PCC 6803] dbj BAA17390.1 short-chain alcohol dehydrogenase family [Synechocystis sp. PCC 6803] pir S77543 short-chain alcohol dehydrogenase-related protein, 72K - Synechocystis sp. (strain PCC 6803)			1.---
15129, 15130	20091293	31	9.00E-10	acetivorans C2A	Methanosarcina acetivorans C2A	glucosaminyltransferase [Methanosarcina acetivorans C2A] gb AAM05848.1 glucosaminyltransferase [Methanosarcina acetivorans str. C2A]			

15131,	34557246	29	1.00E-29	Wolonia succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolonia succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolonia succinogenes]				
15132				Wolonia succinogenes DSM 1740	TWO-COMPONENT HYBRID PROTEIN [Wolonia succinogenes DSM 1740] emb CAE10077.1 TWO-COMPONENT HYBRID PROTEIN [Wolonia succinogenes]				2.7.3.-
15137,	34557382	45	8.00E-22	Microbulifer degradans 2-40	COG1033: Predicted exporters of the RND superfamily [Microbulifer degradans 2-40]				
15138	48863979	29	4.00E-11	Campylobacter jejuni RM1221	DNA repair protein RecN [Campylobacter jejuni RM1221] gb AAW34538.1 DNA repair protein RecN [Campylobacter jejuni RM1221]				
15141,	57236955	44	5.00E-54	Clostridium thermocellum ATCC 27405	COG0500: SAM-dependent methyltransferases [Clostridium thermocellum ATCC 27405]				2.1.1.-
15143,	48859334	53	3.00E-61	Clostridium thermocellum ATCC 27405	COG1236: Predicted exonuclease of the beta-lactamase fold involved in RNA processing [Clostridium thermocellum ATCC 27405]				
15147,	48859380	43	7.00E-60	Francisella tularensis subsp. tularensis Schu 4	DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis Schu 4] emb CAG45292.1 DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis]				
15151,	56707780	58	1.00E-52	Methanosarcina acetivorans C2A	Integrase [Methanosarcina acetivorans C2A] gb AAM07145.1 Integrase [Methanosarcina acetivorans str. C2A]				
15152	20092590	35	1.00E-41	Pyrococcus furiosus DSM 3638	hypothetical protein PF1041 [Pyrococcus furiosus DSM 3638] gb AAL81165.1 hypothetical protein [Pyrococcus furiosus DSM 3638]				
15159,	18977413	32	2.00E-14	Xanthomonas campestris pv. campestris str. ATCC 33913	anticonodon nuclease [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM39782.1 anticonodon nuclease [Xanthomonas campestris pv. campestris str. ATCC 33913]				
15163,	21229941	57	7.00E-64	Bacteroides thetaiotaomicron VPI-5482	CDP-glucose 4,6-dehydratase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76457.1 CDP-glucose 4,6-dehydratase [Bacteroides thetaiotaomicron VPI-5482]				4.2.1.45
15164	29346760	66	3.00E-99	Wolonia succinogenes DSM 1740	DIGUANYLATE CYCLASE [Wolonia succinogenes DSM 1740] emb CAE10599.1 DIGUANYLATE CYCLASE [Wolonia succinogenes]				2.7.3.-
15167,	34557884	39	2.00E-49	Polaribacter filamentus	nicotinate-nucleotide adenyllyltransferase [Polaribacter filamentus] possible acetolactate synthase large subunit [Rhodopseudomonas palustris CGA009] emb CAE29495.1 possible acetolactate synthase large subunit [Rhodopseudomonas palustris CGA009]				2.7.7.18
15169,	36955846	46	2.00E-38	Rhodopseudomona s palustris CGA009					4.1.3.18
15170									
1517,	39937114	42	6.00E-40						
1518									

15173, 15174	49481576	26	7.00E-08	Bacillus thuringiensis serovar konkukian str. 97-27	oligopeptide ABC transporter, oligopeptide-binding protein [Bacillus thuringiensis serovar konkukian str. 97-27] gb AA163778.1 oligopeptide ABC transporter, oligopeptide-binding protein [Bacillus thuringiensis serovar konkukian str. 97-27]				
15177, 15178	29349965	25	1.00E-13	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT4557 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79662.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482]				
15181, 15182	34556853	53	9.00E-57	Wolinella succinogenes DSM 1740	TRIOSEPHOSPHATE ISOMERASE TIM [Wolinella succinogenes DSM 1740] emb CAE09568.1 TRIOSEPHOSPHATE ISOMERASE TIM [Wolinella succinogenes] sp Q7MA77 TPIS_WOLSU Triosephosphate isomerase (TIM) (Triose-phosphate isomerase)			5.3.1.1	
15185, 15186	51248430	47	1.00E-66	Desulfotalea psychrophila LSV54	hypothetical protein DP2578 [Desulfotalea psychrophila LSV54] emb CAG37307.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]				
15187, 15188	4234793	33	7.00E-35	Leptospira borgpetersenii	unknown [Leptospira borgpetersenii]				
1519, 1520	48894780	29	1.00E-29	Trichodesmium erythraeum IMS101	COG0006: Xaa-Pro aminopeptidase [Trichodesmium erythraeum IMS101] hypothetical protein PBPRB0708 [Photobacterium profundum SS9]			3.4.11.9	
15191, 15192	54302387	38	7.00E-33	Photobacterium profundum SS9	emb CAG22580.1 hypothetical protein [Photobacterium profundum] transcriptional regulator [Methanosarcina mazel Go1] gb AAM32650.1				
15193, 15194	21229056	37	6.00E-20	Methanosarcina mazel Go1	transcriptional regulator [Methanosarcina mazel Goe1]			2.7.3.-	
15195, 15196	48859134	29	1.00E-24	Clostridium thermocellum ATCC 27405	COG0507: ATP-dependent exoDNase (exonuclease V), alpha subunit - helicase superfamily I member [Clostridium thermocellum ATCC 27405]			3.1.11.5	
15197, 15198	28210082	27	1.00E-13	Clostridium tetani E88	exodeoxyribonuclease V alpha chain [Clostridium tetani E88] gb AAO34963.1 exodeoxyribonuclease V alpha chain [Clostridium tetani E88]			3.1.11.5	
15199, 15200	29349252	55	7.00E-73	Bacteroides thetaiotaomicron VPI-5482	ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gb AAO78949.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]			3.6.1.-	
15201, 15202	57505554	41	1.00E-44	Campylobacter upsaliensis RM3195	probable bax protein VC1430, putative [Campylobacter upsaliensis RM3195] gb EAL52888.1 probable bax protein VC1430, putative [Campylobacter upsaliensis RM3195]				
15203, 15204	21674888	49	9.00E-26	Chlorobium tepidum TLS	NADH oxidase, putative [Chlorobium tepidum TLS] gb AAM73295.1 NADH oxidase, putative [Chlorobium tepidum TLS]			1.6.-	
15205, 15206	52549060	42	3.00E-52	uncultured archaeon GZfos23H9	MinD superfamily P-loop ATPase [uncultured archaeon GZfos23H9]			1.6.4.-	

15207, 15208	57168617	52	3.00E-34	Campylobacter coli RM2228	HsdM [Campylobacter coli RM2228] gb EAL56578.1 HsdM [Campylobacter coli RM2228]			
15217, 15218	34556560	31	3.00E-24	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes] emb CAG36281.1 conserved hypothetical protein [Desulfotalea			
15219, 15220	51245404	37	1.00E-35	Desulfotalea psychrophila LSV54	emb CAG36281.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54] ATP-dependent RNA helicase DbpA [Vibrio cholerae O1 biovar eltor str.	Desc.T. thermophila Hc1 cDNA. Org: Tetrahymena thermophila	2.7.3.-	
15225, 15226	9657150	58	2.00E-63	Vibrio cholerae O1 biovar eltor str.	N16961 ref NP_232192.1 ATP-dependent RNA helicase DbpA [Vibrio cholerae O1 biovar eltor str. N16961] pir B82060 ATP-dependent RNA helicase DbpA VC2564 [Imported] - Vibrio cholerae (strain N16961 group O1)		97 8.00E-09 2.7.7.-	
15227, 15228	48855778	62	3.00E-32	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]		2.7.3.-	
15229, 15230	34396604	40	4.00E-32	Porphyromonas gingivalis W83	oxygen-independent coproporphyrinogen III oxidase, putative [Porphyromonas gingivalis W83] ref NP_904771.1 oxygen-independent coproporphyrinogen III oxidase, putative [Porphyromonas gingivalis W83]		1.-.-.-	
1523, 1524	15892850	62	5.00E-15	Rickettsia conorii str. Malish 7	hypothetical protein RC0927 [Rickettsia conorii str. Malish 7] gb AAL03465.1 unknown [Rickettsia conorii str. Malish 7] pir G97815 hypothetical protein RC0927 [Imported] - Rickettsia conorii (strain Malish 7)			
15231, 15232	29347290	39	6.00E-23	Bacteroides thetaiotaomicron VPI-5482	tetraacyldisaccharide 4'-kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76987.1 tetraacyldisaccharide 4'-kinase [Bacteroides thetaiotaomicron VPI-5482]			
15233, 15234	48894132	44	4.00E-38	Trichodesmium erythraeum IMS101	COG0616: Periplasmic serine proteases (ClpP class) [Trichodesmium erythraeum IMS101]		3.4.21.-	
15235, 15236	40062563	27	2.00E-10	uncultured bacterium 159	TonB-dependent receptor [uncultured bacterium 159]			
15237, 15238	29349779	35	7.00E-17	Bacteroides thetaiotaomicron VPI-5482	peptidyl-prolyl cis-trans isomerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79476.1 peptidyl-prolyl cis-trans isomerase [Bacteroides thetaiotaomicron VPI-5482]			
15239, 15240	53728999	27	8.00E-22	Actinobacillus pleuropneumoniae serovar 1 str. 4074	COG0419: ATPase involved in DNA repair [Actinobacillus pleuropneumoniae serovar 1 str. 4074]			
15241, 15242	48855414	47	6.00E-36	Cytophaga hutchinsonii	COG0483: Archaeal fructose-1,6-bisphosphatase and related enzymes of inositol monophosphatase family [Cytophaga hutchinsonii]		3.1.3.25	

15243, 15244	57241703	60	6.00E-85	Campylobacter lari RM2100	glutathionylspermidine synthase family protein [Campylobacter lari RM2100] gb EAL54373.1 glutathionylspermidine synthase family protein [Campylobacter lari RM2100]			6.3.1.8
15245, 15246	53712009	32	9.00E-19	Bacteroides fragilis YCH46	hypothetical protein BF0720 [Bacteroides fragilis YCH46] dbj BAD47467.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
15247, 15248	29347624	26	5.00E-10	Bacteroides thetataoamicon	hypothetical protein BT2214 [Bacteroides thetataoamicon VPI-5482] gb AAO77321.1 hypothetical protein [Bacteroides thetataoamicon VPI- 5482]			
15249, 15250	53757541	33	9.00E-23	Methylococcus capsulatus str. Bath	type I restriction-modification system, R subunit [Methylococcus capsulatus str. Bath] ref YP_114328.1 type I restriction-modification system, R subunit [Methylococcus capsulatus str. Bath]			
1525, 1526	22126310	31	2.00E-12	Yersinia pestis KIM	hypothetical protein y2426 [Yersinia pestis KIM] gb AAM85984.1			
15251, 15252	48834051	44	4.00E-55	Magnetococcus sp. MC-1	hypothetical [Yersinia pestis KIM]			3.5.2.6
15253, 15254	34557847	34	8.00E-20	Wolinella succinogenes DSM 1740	COG2602: Beta-lactamase class D [Magnetococcus sp. MC-1] ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes DSM 1740] emb CAE10562.1 ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes]			3.4.24.-
15255, 15256	29345965	63	4.00E-86	Bacteroides thetataoamicon VPI-5482	amidophosphoribosyltransferase [Bacteroides thetataoamicon VPI-5482] gb AAO75662.1 amidophosphoribosyltransferase [Bacteroides thetataoamicon VPI-5482]			2.4.2.14
15259, 15260	52144400	19	2.00E-15	Bacillus cereus ZK	hypothetical protein BCZK0824 [Bacillus cereus ZK] gb AAU19419.1 conserved hypothetical protein [Bacillus cereus ZK]			
15263, 15264	46581041	43	9.00E-34	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	HAMP domain protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS97109.1 HAMP domain protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			2.7.3.-
15265, 15266	48845647	43	1.00E-46	Geobacter metallireducens GS 15	hypothetical protein Gmet02001892 [Geobacter metallireducens GS-15]			
15267, 15268	53795087	35	8.00E-18	Chloroflexus aurantiacus	COG0110: Acetyltransferase (isoleucine patch superfamily) [Chloroflexus aurantiacus]			2.3.1.-
1527, 1528	6967633	41	1.00E-22	Campylobacter jejuni subsp. jejuni NCTC 11168	putative endonuclease [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81431 probable endonuclease Cj0139 [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281350.1 putative endonuclease [Campylobacter jejuni subsp. jejuni NCTC 11168]			
15273, 15274	57237474	55	1.00E-33	Campylobacter jejuni RM1221	HIT family protein [Campylobacter jejuni RM1221] gb AAW35057.1 HIT family protein [Campylobacter jejuni RM1221]			
15275, 15276	57241171	43	5.00E-18	Campylobacter lari RM2100	rhodanese family protein [Campylobacter lari RM2100] gb EAL54867.1 rhodanese family protein [Campylobacter lari RM2100]			

15277, 15278	16330590	42	8.00E-59	Synechocystis sp. PCC 6803	hybrid sensory kinase [Synechocystis sp. PCC 6803] dbj BAA17998.1 hybrid sensory kinase [Synechocystis sp. PCC 6803] pir S75136 sensory transduction histidine kinase slr2104 - Synechocystis sp. (strain PCC 6803)			2.7.3.-
15281, 15282	34556518	74	3.00E-53	Wolinella succinogenes DSM 1740	CYCLASE HISF [Wolinella succinogenes DSM 1740] emb CAE09233.1 CYCLASE HISF [Wolinella succinogenes] sp Q7MAS1 HIS6_WOLSU Imidazole glycerol phosphate synthase subunit hisF (IGP synthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthase subunit hisF) (IGPS subunit hisF)	Desc.N. gonorrhoeae nucleotide sequence SEQ ID 2425. Org:Neisseria gonorrhoeae	79	3.00E-07 4.1.3.-
15283, 15284	48854967	53	2.00E-27	Cytophaga hutchinsonii	COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii]			
15285, 15286	23130537	44	3.00E-29	Nostoc punctiforme PCC 73102	COG0778: Nitroreductase [Nostoc punctiforme PCC 73102]			
15287, 15288	24216675	34	2.00E-07	Leptospira interrogans serovar Lai str. 56601	putative globin-like protein [Leptospira interrogans serovar Lai str. 56601] gb AAAN51174.1 putative globin-like protein [Leptospira interrogans serovar lai str. 56601]			
15289, 15290	34557884	28	5.00E-24	Wolinella succinogenes DSM 1740	DIGUANYLATE CYCLASE [Wolinella succinogenes DSM 1740] emb CAE10599.1 DIGUANYLATE CYCLASE [Wolinella succinogenes] magnesium transporter, putative [Campylobacter lari RM2100] gb EAL55750.1 magnesium transporter, putative [Campylobacter lari RM2100]			
15291, 15292	57240636	34	4.00E-23	Campylobacter lari RM2100	putative potassium channel protein, putative [Campylobacter lari RM2100] gb EAL55554.1 putative potassium channel protein, putative [Campylobacter lari RM2100]			
15295, 15296	57240440	52	3.00E-63	Campylobacter lari RM2100	FERROCHELATASE LIKE PROTEIN, HemH [Wolinella succinogenes DSM 1740] emb CAE11151.1 FERROCHELATASE LIKE PROTEIN, HemH [Wolinella succinogenes] sp Q7M7P9 HEMZ_WOLSU Ferrochelatase (Protoheme ferro-lyase) (Heme synthetase)			4.99.1.1
15297, 15298	34558436	48	3.00E-66	Wolinella succinogenes DSM 1740	hypothetical protein MTH376 [Methanothermobacter thermoautotrophicus str. Delta H] gb AAB84882.1 conserved protein [Methanothermobacter thermoautotrophicus str. Delta H] pir F69148 hypothetical protein MTH376 - Methanobacterium thermoautotrophicum (strain Delta H)			2.4.1.-
15301, 15302	48845271	47	6.00E-54	Geobacter metallireducens GS-15	COG0842: Signal transduction histidine kinase [Geobacter metallireducens GS-15]			2.7.3.-

15303,	48855575	49	5.00E-39	Cytophaga hutchinsonii	COG0553: Superfamily II DNA/RNA helicases, SNF2 family [Cytophaga hutchinsonii]			3.6.1.3
15304					hypothetical protein CJE0806 [Campylobacter jejuni RM1221]			
15307,				Campylobacter jejuni RM1221	gb AAW34591.1 conserved hypothetical protein [Campylobacter jejuni RM1221]			
15308	57237008	43	2.00E-50	Wolinella succinogenes DSM 1740	PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10693.1 PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolinella succinogenes]			
15309,								
15310	34557978	48	6.00E-35	Myxococcus xanthus	mutant NtrC-like activator [Myxococcus xanthus]			2.7.-.-
1531,								
1532	34329419	37	1.00E-33	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]			
15311,								
15312	48856940	31	2.00E-11	Helicobacter hepaticus ATCC 51449	transcriptional regulator [Helicobacter hepaticus ATCC 51449] ref NP_860473.1 transcriptional regulator [Helicobacter hepaticus ATCC 51449]			
15313,								
15314	32262492	41	2.00E-21	Campylobacter coli RM2228	RNA methyltransferase, TrmH family, group 3 [Campylobacter coli RM2228] gb EAL56635.1 RNA methyltransferase, TrmH family, group 3 [Campylobacter coli RM2228]			2.1.1.-
15315,								
15316	57168674	53	4.00E-40	Wolinella succinogenes DSM 1740	hypothetical protein WS1513 [Wolinella succinogenes DSM 1740] emb CAE10561.1 conserved hypothetical protein [Wolinella succinogenes]			
15317,								
15318	34557846	44	1.00E-35	Helicobacter hepaticus ATCC 51449	carbamoylphosphate synthase small subunit [Helicobacter hepaticus ATCC 51449] ref NP_860419.1 carbamoylphosphate synthase small subunit [Helicobacter hepaticus ATCC 51449]			6.3.5.5
15319,								
15320	32262437	68	4.00E-77	Wolinella succinogenes DSM 1740	hypothetical protein WS2051 [Wolinella succinogenes DSM 1740] emb CAE11051.1 conserved hypothetical protein [Wolinella succinogenes]			
15321,								
15322	34558336	49	5.00E-45	Wolinella succinogenes DSM 1740	conserved hypothetical protein-DNA polymerase III delta subunit [Wolinella succinogenes DSM 1740] emb CAE10884.1 conserved hypothetical protein-DNA polymerase III delta subunit [Wolinella succinogenes]			
15325,								
15326	34558169	35	1.00E-38	Dechloromonas aromatica RCB	COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Dechloromonas aromatica RCB]			2.7.3.-
15327,								
15328	41725785	36	1.00E-29	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VPA1213 [Vibrio parahaemolyticus RIMD 2210633] db BAC62556.1 hypothetical protein [Vibrio parahaemolyticus]			
15333,								
15334	28901068	29	3.00E-16	Wolinella succinogenes DSM 1740	GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes DSM 1740] emb CAE09195.1			
15335,								
15336	34556480	62	6.00E-78	Wolinella succinogenes DSM 1740	GLUCOSAMINE-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE ISOMERIZING [Wolinella succinogenes]			2.6.1.16

15337, 15338	57241168	51	4.00E-28	Campylobacter lari RM2100	MiaB-like tRNA modifying enzyme [Campylobacter lari RM2100] gb EAL54864.1 MiaB-like tRNA modifying enzyme [Campylobacter lari RM2100]			1.8.-
15339, 15340	57242029	34	5.00E-08	Campylobacter upsaliensis RM3195	cell division protein (ftsH) [Campylobacter upsaliensis RM3195] gb EAL54002.1 cell division protein (ftsH) [Campylobacter upsaliensis RM3195]			3.4.24.-
15343, 15344	48833156	40	6.00E-29	Magnetococcus sp. MC-1	hypothetical protein Mmc102001351 [Magnetococcus sp. MC-1]			
15345, 15346	34557782	43	2.00E-45	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]			2.7.3.-
15347, 15348	34558185	83	1.00E-106	Wolinella succinogenes DSM 1740	RNA POLYMERASE SIGMA FACTOR [Wolinella succinogenes DSM 1740] emb CAE10900.1 RNA POLYMERASE SIGMA FACTOR [Wolinella succinogenes]	Campylobacter jejuni rpoD gene	82 8.00E-43	
15351, 15352	34558184	28	2.00E-08	Wolinella succinogenes DSM 1740	hypothetical protein WS1889 [Wolinella succinogenes DSM 1740] emb CAE10899.1 hypothetical protein [Wolinella succinogenes]			
15353, 15354	48854542	42	2.00E-58	Cytophaga hutchinsonii	COG1748: Saccharopine dehydrogenase and related proteins [Cytophaga hutchinsonii]			1.5.1.10
15355, 15356	34557593	39	4.00E-49	Wolinella succinogenes DSM 1740	hypothetical protein WS1227 [Wolinella succinogenes DSM 1740] emb CAE10308.1 hypothetical protein [Wolinella succinogenes] gb P59893 TRUD_WOLSU tRNA pseudouridine synthase D (Pseudouridylyl synthase) (Uracil hydrolyase)			
15359, 15360	53691857	54	2.00E-28	Desulfovibrio desulfuricans G20	COG1876: D-alanyl-D-alanine carboxypeptidase [Desulfovibrio desulfuricans G20]			
15361, 15362	32262224	51	4.00E-65	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860206.1 hypothetical protein HH0675 [Helicobacter hepaticus ATCC 51449]			2.7.7.22
15363, 15364	57238098	37	4.00E-22	Campylobacter jejuni RM1221	sensor histidine kinase [Campylobacter jejuni RM1221] gb AAW35681.1 sensor histidine kinase [Campylobacter jejuni RM1221] emb CAB73480.1 putative two-component sensor [Campylobacter jejuni subsp. jejuni NCTC 11168] pir D81329 probable two-component sensor Cj1226c [Imported] - 11168] ref NP_282373.1 putative two- component sensor [Campylobacter jejuni subsp. jejuni NCTC 11168]			2.7.3.-
15367, 15368	48863248	24	2.00E-13	Microbulifer degradans 2-40	hypothetical protein Mdeg02001322 [Microbulifer degradans 2-40]			
15369, 15370	21229061	40	5.00E-08	Methanosarcina mazel Go1	hypothetical protein MM2959 [Methanosarcina mazel Go1] gb AAM32655.1 hypothetical protein [Methanosarcina mazel Go1]			2.7.3.-
1537, 1538	48864231	29	8.00E-22	Microbulifer degradans 2-40	COG0577: ABC-type antimicrobial peptide transport system, permease component [Microbulifer degradans 2-40]			

15371, 15372	41724896	31	3.00E-20	Dechloromonas aromatica RCB	COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB]			2.7.3.-
15373, 15374	48859895	37	2.00E-55	Clostridium thermocellum ATCC 27405	COG1168: Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor activities [Clostridium thermocellum ATCC 27405]			2.6.1.-
15375, 15376	23495599	39	3.00E-19	Streptococcus oralis	L-cysteine desulfhydrase [Streptococcus oralis]			2.6.1.-
15377, 15378	48860720	59	4.00E-32	Microbulifer degradans 2-40	COG0019: Diaminopimelate decarboxylase [Microbulifer degradans 2-40]			4.1.1.-
15379, 15380	34397568	36	5.00E-32	Porphyromonas gingivalis W83	biotin--acetyl-CoA-carboxylase ligase [Porphyromonas gingivalis W83] ref NP_905731.1 biotin--acetyl-CoA-carboxylase ligase [Porphyromonas gingivalis W83]			6.3.4.15
15381, 15382	34557604	61	1.00E-56	Wolinella succinogenes DSM 1740	TRANSCRIPTION-REPAIR COUPLING FACTOR [Wolinella succinogenes DSM 1740] emb CAE10319.1 TRANSCRIPTION-REPAIR COUPLING FACTOR [Wolinella succinogenes]			
15387, 15388	48854182	53	4.00E-89	Cytophaga hutchinsonii	COG1472: Beta-glucosidase-related glycosidases [Cytophaga hutchinsonii]	Oceanobacillus lheyensis HTE831 genomic DNA, section 5/13	95	4.00E-08
1539, 1540	29346155	57	3.00E-32	Bacteroides thetaiotaomicron VPI-5482	3-deoxy-manno-octulosonate cytidyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75852.1 3-deoxy-manno-octulosonate cytidyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.7.7.38
15391, 15392	54032595	37	3.00E-28	Polaromonas sp. JS666	COG3177: Uncharacterized conserved protein [Polaromonas sp. JS666]			
15395, 15396	34557234	66	8.00E-77	Wolinella succinogenes DSM 1740	FDHD PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09949.1 FDHD PROTEIN [Wolinella succinogenes]			
15397, 15398	48855658	27	2.00E-18	Cytophaga hutchinsonii	hypothetical protein Chut02000849 [Cytophaga hutchinsonii] probable transcription regulator Cj0571 [Campylobacter lari RM2100] gb EAL55392.1 probable transcription regulator Cj0571 [Campylobacter lari RM2100]			
15403, 15404	57240278	27	3.00E-20	Campylobacter lari RM2100	COG1366: Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor) [Cytophaga hutchinsonii]			
15405, 15406	48856296	37	2.00E-14	Cytophaga hutchinsonii	hypothetical protein ACIAD2753 [Acinetobacter sp. ADP1] emb CAG69498.1 hypothetical protein [Acinetobacter sp. ADP1]			
15407, 15408	50085810	27	7.00E-12	Acinetobacter sp. ADP1	Beta-lactamase class C family protein [Idiomarina loihiensis L2TR] gb AAV80889.1 Beta-lactamase class C family protein [Idiomarina loihiensis L2TR]			3.5.2.6
1541, 1542	56459157	40	9.00E-34	Idiomarina loihiensis L2TR				

15413,	34558461	40	1.00E-43	Wolinella succinogenes DSM 1740	WBFR PROTEIN [Wolinella succinogenes DSM 1740] emb CAE11176.1 WBFR PROTEIN [Wolinella succinogenes]			6.3.5.4
15414								
15417,	48861826	27	2.00E-27	Microbulifer degradans 2-40	COG0842: Signal transduction histidine kinase [Microbulifer degradans 2-40]			
15418								
15421,								
15422	57240341	53	2.00E-37	Campylobacter lari RM2100	pyridoxal phosphate biosynthetic protein PdxJ [Campylobacter lari RM2100] gb EAL55455.1 pyridoxal phosphate biosynthetic protein PdxJ [Campylobacter lari RM2100]			
15423,								
15424	32262410	37	6.00E-28	Helicobacter hepaticus ATCC 51449	pyridoxal phosphate biosynthetic protein A [Helicobacter hepaticus ATCC 51449] ref NP_860392.1 pyridoxal phosphate biosynthetic protein A [Helicobacter hepaticus ATCC 51449]		1.1.1.26 2	
15425,	AAB4706	2						
15426		40	3.00E-56		Desc: Cold-active beta galactosidase. Org: Pseudoalteromonas haloplanktis		3.2.1.23	
15427,								
15428	48854136	27	8.00E-12	Cytophaga hutchinsonii	COG1566: Multidrug resistance efflux pump [Cytophaga hutchinsonii]			
1543,								
1544	29348691	42	3.00E-46	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3282 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78388.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
15431,								
15432	50591193	36	5.00E-43	Streptococcus suis 89/1591	COG0595: Predicted hydrolase of the metallo-beta-lactamase superfamily [Streptococcus suis 89/1591]		3.---	
15433,								
15434	16330553	26	4.00E-09	Synechocystis sp. PCC 6803	hypothetical protein sl0241 [Synechocystis sp. PCC 6803] dbj BAA17961.1 sl0241 [Synechocystis sp. PCC 6803] pir S75099 hypothetical protein sl0241 - Synechocystis sp. (strain PCC 6803)			
15435,								
15436	34556868	33	8.00E-43	Wolinella succinogenes DSM 1740	hypothetical protein WS0441 [Wolinella succinogenes DSM 1740] emb CAE09583.1 conserved hypothetical protein [Wolinella succinogenes]			
15439,								
15440	34556793	32	3.00E-19	Wolinella succinogenes DSM 1740	hypothetical protein WS0360 [Wolinella succinogenes DSM 1740] emb CAE09508.1 conserved hypothetical protein [Wolinella succinogenes]			
15441,								
15442	48853518	47	2.00E-60	Cytophaga hutchinsonii	COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii]			
15443,								
15444	48854173	25	9.00E-12	Cytophaga hutchinsonii	hypothetical protein Chut02002840 [Cytophaga hutchinsonii] putative abc transporter, ATP-binding protein [Helicobacter pylori J99] gb AAD06381.1 putative abc transporter, ATP-binding protein [Helicobacter pylori J99] pir H71886 probable ABC transporter, ATP-binding protein - Helicobacter pylori (strain J99)	Oceanobacillus ihayensis HTE831 genomic DNA, section 11/13	93 1.00E-08 1.8.---	
15445,								
15446	15611856	68	1.00E-113	Helicobacter pylori J99				
15447,								
15448	53712013	51	3.00E-35	Bacteroides fragilis YCH46	putative ATP/GTP hydrolase [Bacteroides fragilis YCH46] dbj BAD47471.1 putative ATP/GTP hydrolase [Bacteroides fragilis YCH46]			

15449, 15450	34557246	39	4.00E-35	Wolnella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolnella succinogenes DSM 1740] emb CAE09861.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolnella succinogenes]			2.7.3.-
1545, 1546	29348024	52	3.00E-52	Bacteroides thetaiotaomicron VPI-5482	putative mobilization protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO77721.1 putative mobilization protein [Bacteroides thetaiotaomicron VPI-5482]			
15453, 15454	15896153	52	7.00E-37	Clostridium acetobutylicum ATCC 824	Spore photoproduct lyase, SPL related protein [Clostridium acetobutylicum ATCC 824] gb AAK80842.1 Spore photoproduct lyase, SPL related protein [Clostridium acetobutylicum ATCC 824] pir G97256 spore photoproduct lyase, SPL related protein [Imported] - Clostridium acetobutylicum			4.1.99.-
15455, 15456	34557288	43	4.00E-43	Wolnella succinogenes DSM 1740	hypothetical protein WS0898 [Wolnella succinogenes DSM 1740] emb CAE10003.1 conserved hypothetical protein [Wolnella succinogenes]			
15457, 15458	53713589	51	1.00E-65	Bacteroides fragilis YCH46	putative phosphoserine phosphatase [Bacteroides fragilis YCH46] dbj BAD49047.1 putative phosphoserine phosphatase [Bacteroides fragilis YCH46]			3.1.3.3
15459, 15460	57241729	56	2.00E-52	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54399.1 conserved hypothetical protein [Campylobacter lari RM2100]			
15461, 15462	48846045	48	1.00E-17	Geobacter metallireducens GS	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15] general glycosylation pathway protein [Campylobacter lari RM2100] gb EAL54661.1 general glycosylation pathway protein [Campylobacter lari RM2100]			
15463, 15464	57241549	49	4.00E-60	Campylobacter lari RM2100	hypothetical protein bli7765 [Bradyrhizobium japonicum USDA 110] dbj BAC53030.1 bli7765 [Bradyrhizobium japonicum USDA 110]			
15465, 15466	27382876	47	2.00E-25	Bradyrhizobium japonicum USDA 110	HsdM protein [Staphylococcus aureus]			2.1.1.72
15469, 15470	49257053	33	3.00E-27	Staphylococcus aureus	Methionyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78039.1 Methionyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482]			6.1.1.10
1547, 1548	29348342	70	2.00E-77	Bacteroides thetaiotaomicron VPI-5482	thymidylate kinase [Clostridium tetani E88] gb AAO35554.1 thymidylate kinase [Clostridium tetani E88]			2.7.4.9
15471, 15472	28210673	41	2.00E-52	Clostridium tetani E88	hypothetical protein Chut02003004 [Cytophaga hutchinsonii]			
15473, 15474	48854333	34	1.00E-33	Cytophaga hutchinsonii	LysM domain protein [Shewanella oneidensis MR-1] gb AAN53120.1 LysM domain protein [Shewanella oneidensis MR-1]			
15475, 15476	24371633	35	9.00E-45	Shewanella oneidensis MR-1				

15479, 15480	29350128	35	9.00E-24	Bacteroides thetaiotaomicron VPI-5482	putative RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79825.1 putative RNA polymerase ECF- type sigma factor [Bacteroides thetaiotaomicron VPI-5482]				
15481, 15482	34557246	58	1.00E-86	Wolinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]	Leptospira interrogans serovar lai str. 56601 chromosome I, section 363 of 397 of the complete sequence	97	7.00E-07	2.7.3.-
15483, 15484	34557246	39	2.00E-51	Wolinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]				2.7.3.-
15485, 15486	34558230	42	4.00E-50	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT REGULATOR-CheY like receiver domain [Wolinella succinogenes DSM 1740] emb CAE10945.1 PUTATIVE TWO- COMPONENT REGULATOR-CheY like receiver domain [Wolinella succinogenes]				
15487, 15488	32261568	41	1.00E-10	Helicobacter hepaticus ATCC 51449	two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] ref NP_859552.1 two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449]				2.7.3.-
15489, 15490	27363715	37	1.00E-15	Vibrio vulnificus CMCP6	Predicted integral membrane protein [Vibrio vulnificus CMCP6] ref NP_933746.1 hypothetical protein VV0953 [Vibrio vulnificus YJ016] gb AAO08770.1 Predicted integral membrane protein [Vibrio vulnificus CMCP6] db BAC93717.1 conserved hypothetical protein [Vibrio vulnificus YJ016]				
15493, 15494	34556564	48	3.00E-74	Wolinella succinogenes DSM 1740	PUTATIVE OXIDOREDUCTASE [Wolinella succinogenes DSM 1740] emb CAE09279.1 PUTATIVE OXIDOREDUCTASE [Wolinella succinogenes]				1.-.-.-
15495, 15496	57241076	34	1.00E-25	Campylobacter lari RM2100	peptidase, M23/M37 family [Campylobacter lari RM2100] gb EAL54772.1 peptidase, M23/M37 family [Campylobacter lari RM2100]				
15499, 15500	29345941	56	5.00E-53	Bacteroides thetaiotaomicron VPI-5482	anthranilate synthase component II [Bacteroides thetaiotaomicron VPI-5482] gb AAO75638.1 anthranilate synthase component II [Bacteroides thetaiotaomicron VPI-5482]				4.1.3.27
155, 156	15678404	46	7.00E-45	Methanothermobac ter thermautotrophicus str. Delta H	hypothetical protein MTH376 [Methanothermobacter thermautotrophicus str. Delta H] gb AAB84882.1 conserved protein [Methanothermobacter thermautotrophicus str. Delta H] pir F69148 hypothetical protein MTH376 - Methanobacterium thermoautotrophicum (strain Delta H)				2.4.1.-

15505, 15506	42524949	30	5.00E-16	Bdellovibrio bacteriovorus HD100	hypothetical protein Bd3605 [Bdellovibrio bacteriovorus HD100] embjCAE80983.1 hypothetical protein predicted by Glimmer/Critica [Bdellovibrio bacteriovorus HD100]			
15507, 15508	45360231	33	1.00E-25	Pseudomonas aeruginosa	putative transposase [Pseudomonas aeruginosa]			
15511, 15512	48853348	29	1.00E-11	Cytophaga hutchinsonii	hypothetical protein Chut0200390.1 [Cytophaga hutchinsonii] serine/threonine protein kinase [Picrophilus torridus DSM 9790] gb AAAT42720.1 serine/threonine protein kinase [Picrophilus torridus DSM 9790]			2.7.1.37
15515, 15516	48477207	37	4.00E-22	Picrophilus torridus DSM 9790	probable periplasmic protein Cj0114 [Campylobacter coli RM2228] gb EAL56678.1 probable periplasmic protein Cj0114 [Campylobacter coli RM2228]			
15521, 15522	57168717	33	2.00E-15	Campylobacter coli RM2228	TagD protein [Mannheimia succiniciproducens MBEL55E] gb AAU37265.1 TagD protein [Mannheimia succiniciproducens MBEL55E]			2.7.7.39
15523, 15524	52424713	74	4.00E-51	Mannheimia succiniciproducens MBEL55E	Histidinol-phosphate aminotransferase/Tyrosine aminotransferase [Thermoanaerobacter tengcongensis MB4] gb AAM25302.1 Histidinol- phosphate aminotransferase/Tyrosine aminotransferase [Thermoanaerobacter tengcongensis MB4] sp Q8R5Q4 HIS8_THETN Histidinol-phosphate aminotransferase (Imidazole acetol-phosphate transaminase)			
15525, 15526	20808527	34	5.00E-36	Thermoanaerobact er tengcongensis MB4	hydrolase, HD family [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAT63786.1 hydrolase, HD family [Bacillus thuringiensis serovar konkukian str. 97-27]		Zea mays clone EL01N0430C11.c mRNA sequence 88	2.6.1.9
15529, 15530	49481584	50	7.00E-53	Bacillus thuringiensis serovar konkukian str. 97-27	hypothetical protein WS0003 [Wolnella succinogenes DSM 1740] embjCAE09177.1 conserved hypothetical protein [Wolnella succinogenes] hypothetical protein BF2483 [Bacteroides fragilis YCH46] dbj BAD49232.1 hypothetical protein [Bacteroides fragilis YCH46] COG0229: Conserved domain frequently associated with peptide methionine sulfoxide reductase [Cytophaga hutchinsonii]			
15531, 15532	34556462	71	6.00E-49	Wolnella succinogenes DSM 1740	COG2206: HD-GYP domain [Magnetococcus sp. MC-1]			
15533, 15534	53713774	29	3.00E-07	Bacteroides fragilis YCH46	COG2206: HD-GYP domain [Magnetococcus sp. MC-1]			
15535, 15536	48856175	67	7.00E-46	Cytophaga hutchinsonii	COG2206: HD-GYP domain [Magnetococcus sp. MC-1]			1.8.4.6
15537, 15538	48832299	43	2.00E-50	Magnetococcus sp. MC-1	COG2206: HD-GYP domain [Magnetococcus sp. MC-1]			
15539, 15540	48832299	47	2.00E-35	Magnetococcus sp. MC-1	COG2206: HD-GYP domain [Magnetococcus sp. MC-1]			3.1.4.17

15541, 15542 15543, 15544	15679233 38016731	29 43	1.00E-08 1.00E-30	Methanothermobacter thermautotrophicus str. Delta H Klebsiella pneumoniae	inosine-5'-monophosphate dehydrogenase related protein I [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85711.1 inosine-5'-monophosphate dehydrogenase related protein I [Methanothermobacter thermautotrophicus str. Delta H] pir C69030 MJ1225 protein homolog MTH1222 - Methanobacterium thermoautotrophicum (strain Delta H) unknown [Klebsiella pneumoniae] ref NP_943402.1 hypothetical protein LV233 [Klebsiella pneumoniae] DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Molinitella succinogenes DSM 1740] emb CAE09607.1 DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Molinitella succinogenes] spiQ7/MA56 RPBC_WOLSU Bifunctional DNA-directed RNA polymerase, beta and beta' chain [Includes: DNA-directed RNA polymerase beta chain (Transcriptase beta chain) (RNA polymerase beta subunit); DNA-directed RNA polymerase beta' chain (Transcriptase beta' chain) (RNA polymerase beta' subunit)]	Ehrlichia ruminantium RNA polymerase beta subunit (rpoB) gene, partial cds	88	4.00E-45	2.7.7.6	
15547, 15548	34556892	82	1.00E-139	Molinitella succinogenes DSM 1740	hypothetical protein WS1518 [Molinitella succinogenes DSM 1740] emb CAE10566.1 conserved hypothetical protein [Molinitella succinogenes] conserved hypothetical integral membrane protein [Campylobacter upsaliensis RM3195] gb EAL54000.1 conserved hypothetical integral membrane protein [Campylobacter upsaliensis RM3195]					
15549, 15550	34557851	31	2.00E-29	Molinitella succinogenes DSM 1740	anticonodon nuclease [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM39782.1 anticonodon nuclease [Xanthomonas campestris pv. campestris str. ATCC 33913]					
15551, 15552	57242027	49	7.00E-39	Xanthomonas campestris pv. campestris str. ATCC 33913	PUTATIVE AMINOTRANSFERASE PROTEIN [Molinitella succinogenes DSM 1740] emb CAE09898.1 PUTATIVE AMINOTRANSFERASE PROTEIN [Molinitella succinogenes] signal-transducing protein, histidine kinase [Campylobacter lari RM2100] gb EAL54233.1 signal-transducing protein, histidine kinase [Campylobacter lari RM2100]				2.6.1.1	
15553, 15554	21229941	62	4.00E-77	Molinitella succinogenes DSM 1740	COG2833: Uncharacterized protein conserved in bacteria [Thiobacillus denitrificans ATCC 25259] 3-demethylubiquinone-9 3-methyltransferase [Coxiella burnetii RSA 493] gb AAO89905.1 3-demethylubiquinone-9 3-methyltransferase [Coxiella burnetii RSA 493] sp Q820B5 UBIG_COXBU 3-demethylubiquinone-9 3- methyltransferase (3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase) (DHMB methyltransferase)				2.7.3.-	
15555, 15556	34557183	40	3.00E-50	Campylobacter lari RM2100						
15557, 15558	57241815	33	7.00E-22	Thiobacillus denitrificans ATCC 25259						
15559, 15560	52006638	39	8.00E-14							
15561, 15562	29653699	29	6.00E-10	Coxiella burnetii RSA 493						2.1.1.64

15563, 15564	34558827	44	6.00E-23	Alvinella pompejana epibiont 7G3	riboflavin biosynthesis protein [Alvinella pompejana epibiont 7G3]			3.5.4.26
15565, 15566	53715600	46	2.00E-36	Bacteroides fragilis YCH46	hypothetical protein BF4320 [Bacteroides fragilis YCH46] dbj BAD51058.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
15567, 15568	47222369	47	8.00E-27	Tetraodon nigroviridis	unnamed protein product [Tetraodon nigroviridis]			
15569, 15570	32262380	48	5.00E-44	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860362.1 hypothetical protein HH0831 [Helicobacter hepaticus ATCC 51449]			3.1.7.2
1557, 1558	45681187	35	5.00E-21	Mesorhizobium sp. BNC1	COG3734: 2-keto-3-deoxy-galactonokinase [Mesorhizobium sp. BNC1] TRIOSEPHOSPHATE ISOMERASE TIM [Wolnella succinogenes DSM 1740] emb CAE09568.1 TRIOSEPHOSPHATE ISOMERASE TIM [Wolnella succinogenes] sp Q7MA77 TPIS_WOLSU Triosephosphate isomerase (TIM) (Triose-phosphate isomerase)			2.7.1.58
15575, 15576	34556853	51	3.00E-63	Wolnella succinogenes DSM 1740	sensory box histidine kinase/response regulator [Shewanella oneidensis MR- 1] gbl AAN53935.1 sensory box histidine kinase/response regulator [Shewanella oneidensis MR-1]			5.3.1.1
15577, 15578	24372448	46	5.00E-47	Shewanella oneidensis MR-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			2.7.3.-
15579, 15580	48833325	27	9.00E-26	Magnetococcus sp. MC-1	hypothetical protein VVA1343 [Vibrio vulnificus YJ016] dbj BAC87369.1 conserved hypothetical protein [Vibrio vulnificus YJ016]			2.7.3.-
15581, 15582	37677003	22	5.00E-15	Vibrio vulnificus YJ016	Desc.H. pylori GHPO 881 protein. Org:Helicobacter pylori ABC-type multidrug transport system, ATPase component [Thermoanaerobacter tengcongensis MB4] gbl AAM25341.1 ABC-type multidrug transport system, ATPase component [Thermoanaerobacter tengcongensis MB4]			3.4.21.-
15585, 15586	AAW9831 1	33	2.00E-34	Thermoanaerobact er tengcongensis MB4	putative lipoprotein [Streptococcus equi]			1.8.4.6
15587, 15588	20808566	35	2.00E-29	Streptococcus equi MB4	COG0225: Peptide methionine sulfoxide reductase [Desulfotobacterium hafniense DCB-2]			91 2.00E-16 1.8.4.6
15589, 15590	23380366	41	1.00E-22	Desulfotobacterium hafniense DCB-2	hypothetical 23.6 kDa protein [Bacillus pseudofirmus]			
15591, 15592	53686114	59	6.00E-75	Bacillus pseudofirmus				
15593, 15594	15426420	28	1.00E-12					

15595, 15596	34558334	51	2.00E-34	Wollinella succinogenes DSM 1740	PENICILLIN-BINDING PROTEIN 1A PBP-1A [Wollinella succinogenes DSM 1740] emb CAE11049.1 PENICILLIN-BINDING PROTEIN 1A PBP-1A [Wollinella succinogenes]			2.4.2.-
15597, 15598	47526988	38	3.00E-15	Bacillus anthracis str. 'Ames Ancestor'	tpi/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] ref YP_027843.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne] ref NP_844138.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAP25624.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAT30812.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] gb AAT53894.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne]			
15599, 15600, 15603, 15604, 15607, 15608	56413961 48314770 48314770 48314770 4839711	34 32 32 46	5.00E-17 6.00E-34 9.00E-25	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150 Burkholderia cepacia R18194 Methanosarcina barkeri str. fusaro	putative membrane protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] gb AAV77724.1 putative membrane protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Burkholderia cepacia R18194] COG0732: Restriction endonuclease S subunits [Methanosarcina barkeri str. fusaro]			3.1.1.24 3.1.21.3
15609, 15610	48868930	36	9.00E-17	Haemophilus Influenzae 86- 028NP	COG1943: Transposase and inactivated derivatives [Haemophilus influenzae 86-028NP]			
1561, 1562	15896308	27	2.00E-16	Clostridium acetobutylicum ATCC 824	Glycosyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK80997.1 Glycosyltransferase [Clostridium acetobutylicum ATCC 824] pti B97276 glycosyltransferase [imported] - Clostridium acetobutylicum			
15611, 15612	34558283	72	9.00E-70	Wollinella succinogenes DSM 1740	1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE [Wollinella succinogenes DSM 1740] emb CAE10998.1 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE [Wollinella succinogenes] sp Q7M7Z0 DXS_WOLSU 1-deoxy-D-xylulose-5-phosphate synthase (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS)	Helicobacter hepaticus ATCC 51449 section 2 of 6 of the complete genome	92	3.00E-11 4.1.3.37
15615, 15616, 15617, 15618	34558493 48856844	58 31	1.00E-88 5.00E-31	Wollinella succinogenes DSM 1740 Cytophaga hutchinsonii	PUTATIVE ZINC PROTEASE [Wollinella succinogenes DSM 1740] emb CAE11208.1 PUTATIVE ZINC PROTEASE [Wollinella succinogenes] COG4775: Outer membrane protein/protective antigen OMA87 (Cytophaga hutchinsonii)			3.4.-
15619, 15620	42527469	28	1.00E-15	Treponema denticola ATCC 35405	Na/Pi cotransporter family protein [Treponema denticola ATCC 35405] gb AAS12478.1 Na/Pi cotransporter family protein [Treponema denticola ATCC 35405]			

15621, 15622	50745174	32	2.00E-24	Gallus gallus	PREDICTED: similar to L-gulon-gamma-lactone oxidase precursor [Gallus gallus]			1.1.3.8
15623, 15624	48833463	47	5.00E-26	Magnetococcus sp. MC-1	COG2202: FOG: PAS/PAC domain [Magnetococcus sp. MC-1]			2.7.3.-
15625, 15626	34558828	32	4.00E-19	Alvinella pompejana epibiont 7G3	KIAA1005 protein [Alvinella pompejana epibiont 7G3]			
15627, 15628	27366393	30	4.00E-22	Vibrio vulnificus CMCP6	Response regulator [Vibrio vulnificus CMCP6] gb AAO11448.1 Response regulator [Vibrio vulnificus CMCP6]			2.7.3.-
15629, 15630	34556560	33	2.00E-25	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]			
1563, 1564	28974569	49	5.00E-60	Pseudomonas sp. Y2	putative ring-oxydation complex protein 5 [Pseudomonas sp. Y2]			1.-.-.-
15631, 15632	34557905	54	6.00E-29	Wolinella succinogenes DSM 1740	PROLYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10620.1 PROLYL-TRNA SYNTHETASE [Wolinella succinogenes]			6.1.1.15
15633, 15634	32261568	29	2.00E-25	Helicobacter hepaticus ATCC 51449	two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] ref NP_859552.1 two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449]			2.7.3.-
15635, 15636	53712269	37	1.00E-34	Bacteroides fragilis YCH46	dipeptidyl peptidase IV [Bacteroides fragilis YCH46] dbj BAD47727.1 dipeptidyl peptidase IV [Bacteroides fragilis YCH46]			3.4.14.-
15637, 15638	34557444	47	6.00E-50	Wolinella succinogenes DSM 1740	hypothetical protein WS1061 [Wolinella succinogenes DSM 1740] emb CAE10159.1 conserved hypothetical protein [Wolinella succinogenes]			
15639, 15640	15643810	32	1.00E-08	Thermotoga maritima MSB8	comEA protein-related protein [Thermotoga maritima MSB8] gb AAD36129.1 comEA protein-related protein [Thermotoga maritima MSB8] pir F72301 comEA protein-related protein - Thermotoga maritima (strain MSB8)			
15641, 15642	34557665	50	7.00E-35	Wolinella succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes]			2.7.3.-
15643, 15644	27379227	29	5.00E-28	Bradyrhizobium japonicum USDA 110	hypothetical protein bir4116 [Bradyrhizobium japonicum USDA 110] dbj BAC49381.1 bir4116 [Bradyrhizobium japonicum USDA 110]			
15645, 15646	34557014	45	3.00E-42	Wolinella succinogenes DSM 1740	hypothetical protein WS0597 [Wolinella succinogenes DSM 1740] emb CAE09729.1 conserved hypothetical protein [Wolinella succinogenes]			
15647, 15648	39997537	37	6.00E-38	Geobacter sulfurreducens PCA	ReA/Spot domain protein [Geobacter sulfurreducens PCA] gb AAR35815.1 ReA/Spot domain protein [Geobacter sulfurreducens PCA]			

1565,	18266398	33	6.00E-22	Escherichia coli	putative galactosyltransferase WbgM [Escherichia coli]			2.4.1.52
1566,				Burkholderia				
15655,	48788830	35	8.00E-44	fungorum LB400	COG0845: Membrane-fusion protein [Burkholderia fungorum LB400]			
15656				Wolinnella	GLUTAMATE SYNTHASE SMALL CHAIN [Wolinnella succinogenes DSM 1740] emb CAE10285.1 GLUTAMATE SYNTHASE SMALL CHAIN			1.4.1.13
15657,	34557570	60	1.00E-97	succinogenes DSM 1740	[Wolinnella succinogenes]			
15658				Helicobacter	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449]			
15661,				hepaticus ATCC	ref NP_860422.1 hypothetical protein HH0891 [Helicobacter hepaticus ATCC 51449]			
15662	32262440	23	1.00E-11	51449	hemK protein [Enterococcus faecalis V583] gb AAO82265.1 hemK protein			
15663,	29377041	36	3.00E-07	Enterococcus	[Enterococcus faecalis V583]			
15664				faecalis V583	putative alpha-1,3-galactosyltransferase Cps9vG [Streptococcus pneumoniae]			
15665,	21552727	23	1.00E-06	Streptococcus				
15666				pneumoniae				
15667,	41726155	26	5.00E-08	Dechloromonas	COG0438: Glycosyltransferase [Dechloromonas aromatica RCB]			
15668				aromatica RCB				
15669,	48831520	29	5.00E-08	Magnetococcus sp.	hypothetical protein Mmc102002973 [Magnetococcus sp. MC-1]			
15670				MC-1				
1567,	24527254	28	1.00E-08	Escherichia coli	putative glycosyl transferase [Escherichia coli]			
1568				Geobacter				2.7.3.-
15671,				metallireducens GS-				
15672	48846045	37	3.00E-42	15	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]			
15675,				Rhodopirellula	hypothetical protein RB3944 [Rhodopirellula baltica SH 1] emb CAD73501.1			
15676	32472822	48	1.00E-21	baltica SH 1	conserved hypothetical protein [Pirellula sp.]			
15679,				Thermococcus	methylmalonyl-CoA decarboxylase, gamma subunit [Thermococcus kodakaraensis] ref YP_184037.1 methylmalonyl-CoA decarboxylase,			4.1.1.41
15680	57159883	38	7.00E-19	kodakaraensis	gamma subunit [Thermococcus kodakaraensis]			
15681,				Nostoc punctiforme	COG0732: Restriction endonuclease S subunits [Nostoc punctiforme PCC			3.1.21.3
15682	23130207	35	9.00E-19	PCC 73102	73102]			
15683,				Vibrio				
15684	28901068	27	2.00E-15	parahaemolyticus	hypothetical protein VPA1213 [Vibrio parahaemolyticus RIMD 2210633]			
				RIMD 2210633	dbj BAC62556.1 hypothetical protein [Vibrio parahaemolyticus]			
15685,	AAB5259				Wolinnella	succinogenes,		
15686	6	39	1.00E-39		complete genome;	segment 6/7	86	4.00E-20
15687,				Clostridium tetani	Desc:Helicobacter pylori bait polypeptide #114, Org:Helicobacter pylori			
15688	28210659	24	8.00E-09	E88	transcriptional regulator, merR family [Clostridium tetani E88]			

15691, 15692	52006879	30	3.00E-32	Thiobacillus denitrificans ATCC 25259	COG2199: FOG: GGDEF domain [Thiobacillus denitrificans ATCC 25259]			1.1.1.20 5
15695, 15696	53713382	39	4.00E-63	Bacteroides fragilis YCH46	outer membrane efflux protein [Bacteroides fragilis YCH46] dbj BAD48840.1 outer membrane efflux protein [Bacteroides fragilis YCH46]			
15697, 15698	48850440	61	3.00E-48	Novosphingobium aromaticivorans DSM 12444	COG0229: Conserved domain frequently associated with peptide methionine sulfoxide reductase [Novosphingobium aromaticivorans DSM 12444]			1.8.4.6
15699, 15700	34557204	28	5.00E-12	Wolinella succinogenes DSM 1740	hypothetical protein WS0806 [Wolinella succinogenes DSM 1740] emb CAE09919.1 conserved hypothetical protein [Wolinella succinogenes]			
15703, 15704	46202599	34	3.00E-22	Magnetospirillum magnetotacticum MS-1	hypothetical protein Magn03007449 [Magnetospirillum magnetotacticum MS- 1]			
15705, 15706	34558477	47	1.00E-14	Wolinella succinogenes DSM 1740	hypothetical protein WS2202 [Wolinella succinogenes DSM 1740] emb CAE11192.1 hypothetical protein [Wolinella succinogenes]			
15709, 15710	38637724	39	7.00E-41	Cupriavidus necator	putative integrase/recombinase [Cupriavidus necator] gb AAP85812.1 GTP-binding protein [Chlorobium tepidum TLS] gb AAM73005.1 GTP- binding protein [Chlorobium tepidum TLS] sp Q8KBK3 ENGA_CHLTE GTP- binding protein engA			
1571, 1572	21674598	44	4.00E-60	Chlorobium tepidum TLS	hypothetical protein PHG054 [Cupriavidus necator] gb AAP85807.1 hypothetical protein PHG054 [Ralstonia eutropha]			
15711, 15712	38637719	23	5.00E-11	Wolinella succinogenes DSM 1740	conserved hypothetical protein-PREDICTED PEMEASE [Wolinella succinogenes DSM 1740] emb CAE11076.1 conserved hypothetical protein- PREDICTED PEMEASE [Wolinella succinogenes]			
15713, 15714	34558361	30	8.00E-38	Campylobacter lari RM2100	HAD-superfamily hydrolase, subfamily IIA subfamily [Campylobacter lari RM2100] gb EAL54555.1 HAD-superfamily hydrolase, subfamily IIA subfamily [Campylobacter lari RM2100]			3.1.3.41
15717, 15718	47575513	49	5.00E-59	Rubrivivax gelatinosus PM1	COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Rubrivivax gelatinosus PM1]			3.4.21.-
15719, 15720	48862943	48	2.00E-70	Microbulbifer degradans 2-40	COG0845: Membrane-fusion protein [Microbulbifer degradans 2-40]			
15721, 15722	56315986	23	9.00E-14	Azoarcus sp. EbN1 Wolinella succinogenes DSM 1740	hypothetical protein [Azoarcus sp. EbN1]			
15723, 15724	34557291	28	3.00E-27	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]			

15725,	51573391	21	1.00E-08	Borrelia garinii PBI	hypothetical protein BG0579 [Borrelia garinii PBI] ref YP_073008.1			
15726					hypothetical protein BG0579 [Borrelia garinii PBI] COG0482: Predicted tRNA(5-methylaminomethyl-2-thiouridylylate)			
15727,	48853937	53	2.00E-63	Cytophaga hutchinsonii	methyltransferase, contains the PP-loop ATPase domain [Cytophaga hutchinsonii]			2.1.1.61
15729,	51209444	29	6.00E-07	Campylobacter coli	cpp12 [Campylobacter coli] gb AAR29496.1 cpp12 [Campylobacter coli] ref YP_063457.1 cpp12 [Campylobacter jejuni] gb AAR29546.1 cpp12 [Campylobacter jejuni]			
15731,	23015878	47	2.00E-60	Magnetospirillum magnetotacticum MS-1	COG2703: Hemerythrin [Magnetospirillum magnetotacticum MS-1]			
15732	28901068	30	2.00E-10	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VPA1213 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62556.1 hypothetical protein [Vibrio parahaemolyticus]			
15733,				Legionella pneumophila subsp. pneumophila	ATP-dependent DNA helicase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28619.1 ATP-dependent DNA helicase str. Philadelphia 1 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] probable outer membrane component of efflux system Cj1031			3.6.1.-
15737,	52842767	39	6.00E-38	Philadelphia 1	[Campylobacter upsaliensis RM3195] gb EAL53949.1 probable outer membrane component of efflux system Cj1031 [Campylobacter upsaliensis RM3195]			
15739,	57241976	33	2.00E-19	RM3195	alcohol dehydrogenase, zinc-containing [Bacillus cereus ATCC 10987] gb AAS39808.1 alcohol dehydrogenase, zinc-containing [Bacillus cereus ATCC 10987]			1.1.1.1
15741,	42779953	55	7.00E-49	Bacillus cereus ATCC 10987	hypothetical protein SO4465 [Shewanella oneidensis MR-1] gb AAN57430.1 conserved domain protein [Shewanella oneidensis MR-1]			
15742	24375943	56	4.00E-35	Shewanella oneidensis MR-1	sensory transduction histidine kinase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85323.1 sensory transduction histidine kinase [Methanothermobacter thermautotrophicus str. Delta H] pirl A69210 sensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain Delta H)			2.7.3.-
15747,	15678845	32	3.00E-19	str. Delta H	ferric uptake regulation protein, putative [Campylobacter coli RM2228] gb EAL57643.1 ferric uptake regulation protein, putative [Campylobacter coli RM2228]			
15748	57167857	36	2.00E-13	Campylobacter coli RM2228	COG4564: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-
15749,	48853443	26	3.00E-09	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			2.7.3.-
15750								
15751,	48831001	31	6.00E-27	Magnetococcus sp. MC-1				
15752								

15757, 15758	54031229	39	7.00E-33	Polaromonas sp. JS666	COG1032: Fe-S oxidoreductase [Polaromonas sp. JS666] hypothetical protein sil0624 [Synechocystis sp. PCC 6803] dbj BAA18682.1 sil0624 [Synechocystis sp. PCC 6803] pir S76770 hypothetical protein - Synechocystis sp. (strain PCC 6803)				
15759, 15760	16332142	36	6.00E-14	Synechocystis sp. PCC 6803	oligopeptide-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96557.1 oligopeptide-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinnella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinnella succinogenes]				2.7.3.-
15761, 15762	46580489	38	4.00E-50	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	long-chain-fatty-acid-CoA ligase (fadD-7) [Archaeoglobus fulgidus DSM 4304] gb AAB89478.1 long-chain-fatty-acid-CoA ligase (fadD-7) [Archaeoglobus fulgidus DSM 4304] pir C6947.1 probable fatty-acid-CoA ligase (EC 6.2.1.-) fadD7 - Archaeoglobus fulgidus				6.2.1.3
15763, 15764	34557573	34	1.00E-28	Archaeoglobus fulgidus DSM 4304	hypothetical protein MTH528 [Methanothermobacter thermotrophicus str. Delta H] gb AAB85034.1 unknown [Methanothermobacter thermotrophicus str. Delta H] pir F69169 conserved hypothetical protein MTH528 - Methanothermobacter thermotrophicus (strain Delta H) COG2360: LeuPhe-tRNA-protein transferase [Dechloromonas aromatica RCB]				2.3.2.6
1577, 1578	15678556	44	1.00E-18	Methanothermobac ter thermotrophicus str. Delta H	hypothetical protein BT1422 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76529.1 conserved hypothetical protein [Bacteroides thetaitaomicron VPI-5482] NAD dependent epimerase/dehydratase [Prochlorococcus marinus subsp. marinus str. CCMP1375] gb AAQ00326.1 NAD dependent epimerase/dehydratase [Prochlorococcus marinus subsp. marinus str. CCMP1375]				5.1.3.-
15771, 15772	46140415	55	1.00E-55	Dechloromonas aromatica RCB	NAD dependent epimerase/dehydratase [Prochlorococcus marinus subsp. marinus str. CCMP1375] Prochlorococcus marinus subsp. marinus str. CCMP1375				
15773, 15774	29346832	32	3.00E-12	Bacteroides thetaitaomicron VPI-5482	NAD dependent epimerase/dehydratase [Prochlorococcus marinus subsp. marinus str. CCMP1375] Prochlorococcus marinus subsp. marinus str. CCMP1375				
15777, 15778	33240731	21	4.00E-10	Prochlorococcus marinus subsp. marinus str. CCMP1375	POLYPHOSPHATE KINASE [Wolinnella succinogenes DSM 1740] emb CAE10955.1 POLYPHOSPHATE KINASE [Wolinnella succinogenes]				2.7.4.1
15779, 15780	33240731	26	9.00E-08	Prochlorococcus marinus subsp. marinus str. CCMP1375	amine oxidase, flavin-containing [Pseudomonas syringae pv. tomato str. DC3000] ref NP_790952.1 amine oxidase, flavin-containing [Pseudomonas syringae pv. tomato str. DC3000]				
15781, 15782	34558240	57	2.00E-64	Wolinnella succinogenes DSM 1740					
15783, 15784	28851570	43	5.00E-47	Pseudomonas syringae pv. tomato str. DC3000					

15785, 15786	34558264	50	8.00E-69	Wollinella succinogenes DSM 1740	TRNA DELTA-2-ISOPENTENYL PYROPHOSPHATE [Wollinella succinogenes DSM 1740] emb CAE10979.1 TRNA DELTA-2- ISOPENTENYL PYROPHOSPHATE [Wollinella succinogenes]			2.5.1.8
15787, 15788	39936981	49	9.00E-54	Rhodopseudomonas palustris CGA009	possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009] emb CAE29361.1 possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009]			2.7.-.-
15789, 15790	34762625	37	7.00E-17	Fusobacterium nucleatum subsp. vincentii ATCC 49256	hypothetical protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24781.1 hypothetical protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256]			
1579, 1580	29347556	44	6.00E-87	Bacteroides thetaiotaomicron VPI-5482	4-alpha-glucanotransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77253.1 4-alpha-glucanotransferase [Bacteroides thetaiotaomicron VPI-5482]	Desc: Genomic sequence of Lactococcus lactis IL1403. Org: Lactococcus lactis IL1403	90	2.00E-07 2.4.1.25
15793, 15794	2314704	35	8.00E-30	Helicobacter pylori 26695	H. pylori predicted coding region HP1519 [Helicobacter pylori 26695] pir G64709 hypothetical protein HP1519 - Helicobacter pylori (strain 26695) ref NP_208310.1 hypothetical protein HP1519 [Helicobacter pylori 26695]			
15803, 15804	34557709	39	3.00E-40	Wollinella succinogenes DSM 1740	AMINOPEPTIDASE [Wollinella succinogenes DSM 1740] emb CAE10424.1 AMINOPEPTIDASE [Wollinella succinogenes] sp Q7M8W6 AMPA_WOLSU Probable cytosol aminopeptidase (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase)			3.4.11.1
15805, 15806	34557341	49	6.00E-62	Wollinella succinogenes DSM 1740	hypothetical protein WS0953 [Wollinella succinogenes DSM 1740] emb CAE10056.1 conserved hypothetical protein [Wollinella succinogenes]			
1581, 1582	48892457	26	1.00E-09	Trichodesmium erythraeum IMS101	COG0438: Glycosyltransferase [Trichodesmium erythraeum IMS101] hypothetical protein DET0620 [Dehalococcoides ethenogenes 195]			
15811, 15812	57234561	26	8.00E-15	Dehalococcoides ethenogenes 195	gb AAW40066.1 conserved domain protein [Dehalococcoides ethenogenes 195]			
15819, 15820	34556768	70	1.00E-101	Wollinella succinogenes DSM 1740	DIAMINOPELMATE DECARBOXYLASE DAP DECARBOXYLASE [Wollinella succinogenes DSM 1740] emb CAE09483.1 DIAMINOPELMATE DECARBOXYLASE DAP DECARBOXYLASE [Wollinella succinogenes]			4.1.1.20
15821, 15822	53711856	41	2.00E-29	Bacteroides fragilis YCH46	5'-nucleotidase precursor [Bacteroides fragilis YCH46] db BAD47314.1 5'- nucleotidase precursor [Bacteroides fragilis YCH46]			3.1.3.5

15823, 15824	53757968	35	9.00E-14	Methylococcus capsulatus str. Bath	response regulator [Methylococcus capsulatus str. Bath] ref YP_113897.1 response regulator [Methylococcus capsulatus str. Bath]			2.7.3.-
15825, 15826	29346674	41	1.00E-40	Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76371.1 two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482]			2.7.3.-
15827, 15828	AAU0666 8	28	2.00E-08		Desc:Nisin T of Lactobacillus lactis. Org:Lactobacillus lactis			
1583, 1584	33862380	30	1.00E-09	Prochlorococcus marinus str. MIT 9313	hypothetical protein PMT0107 [Prochlorococcus marinus str. MIT 9313] emb CAE20282.1 conserved hypothetical protein [Prochlorococcus marinus str. MIT 9313]			
15833, 15834	48855091	38	4.00E-32	Cytophaga hutchinsonii	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii]			
15835, 15836	34557844	27	6.00E-26	Wolinella succinogenes DSM 1740	MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10559.1 MCP-SIGNAL TRANSDUCTION PROTEIN [Wolinella succinogenes]			
15837, 15838	48860427	50	1.00E-58	Clostridium thermocellum ATCC 27405	COG1052: Lactate dehydrogenase and related dehydrogenases [Clostridium thermocellum ATCC 27405]			1.1.1.95
15839, 15840	AAW7151 3	52	8.00E-55	Wolinella succinogenes DSM 1740	Desc:Helicobacter polypeptide GHPO 1378. Org:Helicobacter pylori TRANSCRIPTION ELONGATION FACTOR [Wolinella succinogenes DSM 1740] emb CAE10800.1 TRANSCRIPTION ELONGATION FACTOR [Wolinella succinogenes]			1.3.99.1
15843, 15844	34558085	49	2.00E-78	Cytophaga hutchinsonii	COG0845: Membrane-fusion protein [Cytophaga hutchinsonii]			
15847, 15848	48854902	35	3.00E-52	Methanosarcina acetivorans C2A	hypothetical protein MA4278 [Methanosarcina acetivorans C2A] gb AAM07622.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A]			3.2.1.8
1585, 1586	20093067	44	1.00E-21	Cytophaga hutchinsonii	COG0812: UDP-N-acetylmuramate dehydrogenase [Cytophaga hutchinsonii]			1.1.1.15
15851, 15852	48855478	45	2.00E-67		hypothetical protein PA1368 [Pseudomonas aeruginosa PAO1] pir E83474 hypothetical protein PA1368 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_250059.1 hypothetical protein PA1368 [Pseudomonas aeruginosa PAO1]			8
15853, 15854	9947311	34	8.00E-18	Pseudomonas aeruginosa PAO1	putative cystathionine beta-synthase [Streptomyces coelicolor A3(2)] ref NP_627297.1 putative cystathionine beta-synthase [Streptomyces coelicolor A3(2)]			4.2.1.22
15861, 15862	7672260	35	2.00E-42	Streptomyces coelicolor A3(2)				

15863, 15864	34557509	55	8.00E-79	Wolnella succinogenes DSM 1740	hypothetical protein WS1135 [Wolnella succinogenes DSM 1740] emb CAE10224.1 hypothetical protein [Wolnella succinogenes] 19718] emb CAD85036.1 AMP-dependent synthetase and ligase [Nitrosomonas europaea ATCC 19718]	Wolnella succinogenes, complete genome; segment 4/7	85	6.00E-10	
15865, 15866	30249114	31	2.00E-23	Nitrosomonas europaea ATCC 19718	hypothetical protein RB8789 [Rhodopirellula ballica SH 1] emb CAD75922.1 conserved hypothetical protein [Pirellula sp.]			6.2.1.3	
15867, 15868	32475551	41	4.00E-35	Rhodopirellula ballica SH 1	hypothetical protein RB8789 [Rhodopirellula ballica SH 1] emb CAD75922.1 conserved hypothetical protein [Pirellula sp.]				
15869, 15870	32475551	44	4.00E-15	Rhodopirellula ballica SH 1	DNA-binding response regulator [Campylobacter jejuni RM1221] gb AAW36097.1 DNA-binding response regulator [Campylobacter jejuni RM1221]			2.7.-	
15871, 15872	57238514	32	3.00E-27	Campylobacter jejuni RM1221	two-component sensor histidine kinase [Nostoc sp. PCC 7120] pir AE1966 two-component sensor histidine kinase all1280 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73237.1 two-component sensor histidine kinase [Nostoc sp. PCC 7120]			2.7.3.-	
15873, 15874	17228775	36	2.00E-21	Nostoc sp. PCC 7120	SIGNAL TRANSDUCTION REGULATORY PROTEIN-CheY like receiver domain [Wolnella succinogenes DSM 1740] emb CAE10959.1 SIGNAL TRANSDUCTION REGULATORY PROTEIN-CheY like receiver domain [Wolnella succinogenes]			2.7.3.-	
15875, 15876	34558244	30	2.00E-23	Wolnella succinogenes DSM 1740					
15877, 15878	2314136	57	6.00E-45	Helicobacter pylori 26695	H. pylori predicted coding region HP0994 [Helicobacter pylori 26695] pir B64644 hypothetical protein HP0994 - Helicobacter pylori (strain 26695) ref NP_207785.1 hypothetical protein HP0994 [Helicobacter pylori 26695]	Helicobacter pylori strain PeCan188 plasticity zone, containing type IV secretion system number three (tfs3) gene cluster, complete sequence	91	3.00E-07	
15879, 15880	53714586	26	1.00E-14	Bacteroides fragilis YCH46	hypothetical protein BF3300 [Bacteroides fragilis YCH46] dbj BAD50044.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
15881, 15882	15611103	40	2.00E-09	Helicobacter pylori J99	hypothetical protein jhp0032 [Helicobacter pylori J99] gb AAD05603.1 putative [Helicobacter pylori J99] pir F71983 hypothetical protein jhp0032 - Helicobacter pylori (strain J99)				
15883, 15884	23128114	34	1.00E-21	Nostoc punctiforme PCC 73102	hypothetical protein Npun02002480 [Nostoc punctiforme PCC 73102]				

15885, 15886	46142567	34	2.00E-37	Methanococcoides burtonii DSM 6242	COG0270: Site-specific DNA methylase [Methanococcoides burtonii DSM 6242]				2.1.1.73
15887, 15888	48853824	55	6.00E-80	Cytophaga hutchinsonii	COG0859: ADP-heptose:LPS heptosyltransferase [Cytophaga hutchinsonii]				
15889, 15890	48853824	56	9.00E-36	Cytophaga hutchinsonii	COG0859: ADP-heptose:LPS heptosyltransferase [Cytophaga hutchinsonii] ribonucleotide reductase (nrd) [Archaeoglobus fulgidus DSM 4304] gb AAB89584.1 ribonucleotide reductase (nrd) [Archaeoglobus fulgidus DSM 4304] pir G69457 ribonucleoside-diphosphate reductase (EC 1.17.4.1) large chain nrd - Archaeoglobus fulgidus			1.17.4.1	
1589, 1590	11499254	35	1.00E-30	Archaeoglobus fulgidus DSM 4304	ABC TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09403.1 ABC TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wolinella succinogenes]				1.8.-
15891, 15892	34556688	50	9.00E-26	Wolinella succinogenes DSM 1740	COG1011: Predicted hydrolase (HAD superfamily) [Cytophaga hutchinsonii] COG0542: ATPases with chaperone activity, ATP-binding subunit [Cytophaga hutchinsonii]				3.8.1.2
15893, 15894	48856129	39	5.00E-45	Cytophaga hutchinsonii	hypothetical protein [Streptomyces avermitilis MA-4680] ref NP_823856.1 hypothetical protein SAV2480 [Streptomyces avermitilis MA-4680]				
15895, 15896	48854713	53	2.00E-45	Cytophaga hutchinsonii	DNA polymerase I (polA) [Campylobacter coli RM2228] gb EAL56958.1 DNA polymerase I (polA) [Campylobacter coli RM2228] two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] dbj BAB81218.1 two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] PUTATIVE AMINOTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE10273.1 PUTATIVE AMINOTRANSFERASE [Wolinella succinogenes]			2.7.7.7	
15897, 15898	29606128	40	1.00E-15	Streptomyces avermitilis MA-4680	COG0642: Signal transduction histidine kinase [Crocosphaera watsonii WH 8501]				
15899, 15900	57168476	42	1.00E-56	Campylobacter coli RM2228	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] hypothetical protein DP1552 [Desulfotalea psychrophila LSV54] emb CAG36281.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]				
159, 160	18310494	31	1.00E-23	Clostridium perfringens str. 13 Wolinella	GGDEF DOMAIN PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09494.1 GGDEF DOMAIN PROTEIN [Wolinella succinogenes]				
15901, 15902	34557558	53	1.00E-54	Wolinella succinogenes DSM 1740					4.4.1.-
15903, 15904	53734795	39	6.00E-43	Crocosphaera watsonii WH 8501					2.7.3.-
15907, 15908	48853652	28	3.00E-18	Cytophaga hutchinsonii					
15911, 15912	51245404	36	4.00E-20	Desulfotalea psychrophila LSV54					
15913, 15914	34556779	35	4.00E-10	Wolinella succinogenes DSM 1740					

15915, 15916	AAW7148 1	46	3.00E-39		Desc:Helicobacter polypeptide GHPO 240. Org:Helicobacter pylori				
					putative acetyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] gb AAV79310.1 putative acetyltransferase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] ref NP_807484.1 putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhi Ty2] ref NP_462554.1 putative acetyltransferase [Salmonella typhimurium LT2] ref NP_458272.1 putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhi str. CT18] gb AAL22513.1 putative acetyltransferase [Salmonella typhimurium LT2] gb AAO71344.1 putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhi Ty2] emb CAD07975.1 putative acetyltransferase [Salmonella enterica subsp. enterica serovar Typhi] pir AC0981 probable acetyltransferase STY4148 [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)			2.3.1.-	
15917, 15918	56415547	48	3.00E-37	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150					
				Pseudomonas aeruginosa UCBPP-PA14	COG2199: FOG: GGDEF domain [Pseudomonas aeruginosa UCBPP-PA14]				2.7.3.-
15921, 15922	53727492	51	3.00E-16	Entamoeba histolytica HM-1:IMSS	Viral A-type inclusion protein repeat, putative [Entamoeba histolytica HM-1:IMSS]				
15923, 15924	56470397	27	3.00E-07			Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6	90	5.00E-12	1.11.1.5
15927, 15928	34557828	68	6.00E-46	Wolinella succinogenes DSM 1740	PUTATIVE CYTOCHROME C551 PEROXIDASE [Wolinella succinogenes DSM 1740] emb CAE10543.1 PUTATIVE CYTOCHROME C551 PEROXIDASE [Wolinella succinogenes]				
15929, 15930	19704976	37	5.00E-09	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Hypothetical cytosolic protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93770.1 Hypothetical cytosolic protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]				
1593, 1594	42525090	44	4.00E-49	Bdellovibrio bacteriovorus HD100	Adventurous gliding motility protein R [Bdellovibrio bacteriovorus HD100] emb CAE81124.1 Adventurous gliding motility protein R [Bdellovibrio bacteriovorus HD100]				3.6.3.16
15933, 15934	57236934	42	8.00E-28	Campylobacter jejuni RM1221	RNA pseudouridylylase synthase family protein [Campylobacter jejuni RM1221] gb AAW34517.1 RNA pseudouridylylase synthase family protein [Campylobacter jejuni RM1221]				4.2.1.70
15935, 15936	57505678	32	1.00E-07	Campylobacter upsaliensis RM3195	conserved hypothetical protein [Campylobacter upsaliensis RM3195] gb EAL52739.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195]				

15937, 15938 15939, 15940	20808519 42453422	42 33	1.00E-42 2.00E-22	Thermoanaerobacter tengcongensis MB4 Rickettsia rickettsii	Zn-dependent dipeptidase, microsomal dipeptidase homolog [Thermoanaerobacter tengcongensis MB4] COG223: Methionyl-tRNA formyltransferase [Rickettsia rickettsii]			3.4.13.1 9
15941, 15942 15943, 15944	15614411 32262087	32 22	3.00E-09 7.00E-10	Bacillus halodurans C-125 Helicobacter hepaticus ATCC 51449	hypothetical protein BH1848 [Bacillus halodurans C-125] dbj BAB05567.1 BH1848 [Bacillus halodurans C-125] pir H83880 hypothetical protein hypothetical protein HH0539 [Helicobacter hepaticus ATCC 51449] ref NP_860070.1 hypothetical protein HH0539 [Helicobacter hepaticus ATCC 51449]			2.1.2.9
15947, 15948 15949, 15950	57240977 57240598	63 27	1.00E-120 2.00E-09	Campylobacter lari RM2100 Campylobacter lari RM2100 Bacteroides thetaiotaomicron VPI-5482	DNA-directed RNA polymerase, beta subunit [Campylobacter lari RM2100] gb EAL55370.1 DNA-directed RNA polymerase, beta subunit [Campylobacter lari RM2100] probable periplasmic protein Cj0683 [Campylobacter lari RM2100] gb EAL55712.1 probable periplasmic protein Cj0683 [Campylobacter lari RM2100] hypothetical protein BT3341 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78447.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6	84	6.00E-32 2.7.7.6
15951, 15952 15955, 15956	57168666 53756870	55 35	1.00E-53 6.00E-24	Campylobacter coli RM2228 Methylococcus capsulatus str. Bath	molybdopterin cofactor biosynthesis protein A [Campylobacter coli RM2228] gb EAL56627.1 molybdopterin cofactor biosynthesis protein A [Campylobacter coli RM2228] hypothetical protein MCA2752 [Methylococcus capsulatus str. Bath] ref YP_115150.1 hypothetical protein MCA2752 [Methylococcus capsulatus str. Bath]			
15957, 15958 15959, 15960 15961, 15962	48859576 48859576 13472651	29 24 32	3.00E-22 2.00E-14 1.00E-11	Clostridium thermocellum ATCC 27405 Clostridium thermocellum ATCC 27405 Mesorhizobium loti MAFF303099	COG1078: HD superfamily phosphohydrolases [Clostridium thermocellum ATCC 27405] COG1078: HD superfamily phosphohydrolases [Clostridium thermocellum ATCC 27405] 5'-nucleotidase [Mesorhizobium loti MAFF303099] dbj BAB50004.1 5'-nucleotidase [Mesorhizobium loti MAFF303099]			3.1.3.5

15963, 15964	6968164	49	1.00E-67	Campylobacter jejuni subsp. jejuni NCTC 11168	3-deoxy-D-manno-octulosonic-acid transferase [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281879.1 3-deoxy-D-manno-octulosonic-acid transferase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir F81341.3- deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38) Cj0707 [similarity] - Campylobacter jejuni (strain NCTC 11168) HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] emb CAE80147.1 HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] phosphoenolpyruvate synthase [Bacteroides fragilis YCH46] dbj BAD50376.1 phosphoenolpyruvate synthase [Bacteroides fragilis YCH46]				2.4.99.-
15965, 15966	42523774	34	9.00E-23	Bdellovibrio bacteriovorus HD100					
15967, 15968	53714918	49	3.00E-48	Bacteroides fragilis YCH46					
15969, 15970	20808872	29	9.00E-33	Thermoanaerobact er tengcongensis MB4	transposase [Thermoanaerobacter tengcongensis MB4] ref NP_623662.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM25647.1 transposase [Thermoanaerobacter tengcongensis MB4] gb AAM25266.1 transposase [Thermoanaerobacter tengcongensis MB4]				
15971, 15972	48859784	41	1.00E-59	Clostridium thermocellum ATCC 27405	COG0771: UDP-N-acetylmuramoylalanine-D-glutamate ligase [Clostridium thermocellum ATCC 27405]				6.3.2.9
15973, 15974	42632042	39	5.00E-12	Haemophilus influenzae R2866	COG1708: Predicted nucleotidyltransferases [Haemophilus influenzae R2866]				
15975, 15976	27466960	40	2.00E-17	Staphylococcus epidermidis ATCC 12228	abortive phage resistance protein [Staphylococcus epidermidis ATCC 12228] gb AAO03639.1 abortive phage resistance protein [Staphylococcus epidermidis ATCC 12228] dbj BAC67555.1 hypothetical protein [Staphylococcus aureus] gb AAQ18167.1 abortive phage resistance protein [Staphylococcus aureus]				
15977, 15978	48858932	48	1.00E-38	Clostridium thermocellum ATCC 27405	COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405]				2.7.3.-
15979, 15980	34556843	39	1.00E-41	Wolfinella succinogenes DSM 1740	hypothetical protein WS0414 [Wolfinella succinogenes DSM 1740] emb CAE09558.1 conserved hypothetical protein [Wolfinella succinogenes] related to glycine cleavage system, T protein [Desulfotalea psychrophila LSv54] emb CAG35030.1 related to glycine cleavage system, T protein [Desulfotalea psychrophila LSv54]				2.7.3.-
15981, 15982	51244153	48	1.00E-42	Desulfotalea psychrophila LSv54					2.1.2.10
15983, 15984	51244152	65	5.00E-44	Desulfotalea psychrophila LSv54	probable glycine cleavage system, H protein [Desulfotalea psychrophila LSv54] emb CAG35029.1 probable glycine cleavage system, H protein [Desulfotalea psychrophila LSv54]	Desulfotalea psychrophila LSv54 chromosome	84	9.00E-08	

15985, 15986	51244716	26	1.00E-20	Desulfotalea psychrophila LSV54	hypothetical protein DP0864 [Desulfotalea psychrophila LSV54] emb CAG35593.1 unknown protein [Desulfotalea psychrophila LSV54]			
15989, 15990	29655303	40	2.00E-34	Coxiella burnetii RSA 493	hypothetical protein CBU2021 [Coxiella burnetii RSA 493] gb AAO91509.1 conserved hypothetical protein [Coxiella burnetii RSA 493]			
1599, 1600	39934587	21	7.00E-09	Rhodopseudomonas palustris CGA009	hypothetical protein RPA1515 [Rhodopseudomonas palustris CGA009] emb CAE26957.1 conserved unknown protein [Rhodopseudomonas palustris CGA009]			
15991, 15992	15606018	32	3.00E-29	Aquifex aeolicus VF5	hypothetical protein aq_563 [Aquifex aeolicus VF5] gb AAC06808.1 hypothetical protein [Aquifex aeolicus VF5] pir G70350 conserved hypothetical protein aq_563 - Aquifex aeolicus			
15993, 15994	17231331	25	2.00E-09	Nostoc sp. PCC 7120	hypothetical protein all3839 [Nostoc sp. PCC 7120] pir AH2285 hypothetical protein all3839 [imported] - Nostoc sp. (strain PCC 7120) db BAB75538.1 all3839 [Nostoc sp. PCC 7120]			
15995, 15996	48856125	54	1.00E-43	Cytophaga hutchinsonii	COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] guanylate kinase (GMP kinase) [Bacteroides thetaiotaomicron VPI-5482] gb AAO77116.1 guanylate kinase (GMP kinase) [Bacteroides thetaiotaomicron VPI-5482] sp Q8A677 KGUA_BACTN Guanylate kinase (GMP kinase)			2.7.4.8
15997, 15998	29347419	53	2.00E-46	Cytophaga hutchinsonii	COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Cytophaga hutchinsonii]			1.7.99.4
15999, 16000	48855088	39	2.00E-13	Bdellovibrio bacteriovorus HD100	sensor histidine kinase/response regulator [Bdellovibrio bacteriovorus HD100] emb CAE80630.1 sensor histidine kinase/response regulator [Bdellovibrio bacteriovorus HD100]			
16001, 16002	42524257	33	2.00E-07	Bacteroides fragilis YCH46	hypothetical protein BF0014 [Bacteroides fragilis YCH46] db BAD46763.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
16005, 16006	53711305	31	1.00E-20	Chlorobium tepidum TLS	CTP synthase [Chlorobium tepidum TLS] gb AAM71390.1 CTP synthase [Chlorobium tepidum TLS] sp P59040 PYRG_CHLTE CTP synthase (UTP- ammonia ligase) (CTP synthetase)			6.3.4.2
16007, 16008	21672983	58	3.00E-48	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861188.1 hypothetical protein HH1657 [Helicobacter hepaticus ATCC 51449]			2.7.3.-
16009, 16010	32263209	33	3.00E-28	Microbulbifer degradans 2-40	COG0657: Esterase/lipase [Microbulbifer degradans 2-40]			
1601, 1602	48863777	44	2.00E-14	Francisella tularensis subsp. tularensis Schu 4	dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis Schu 4] emb CAG46097.1 dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis] gb AAS60264.1 sugar dehydratase [Francisella tularensis subsp. tularensis]			4.2.1.-

16013, 16014	56708505	66	2.00E-94	Francisella tularensis subsp. tularensis Schu 4	dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis Schu 4] emb CAG46097.1 dTDP-glucose 4,6-dehydratase [Francisella tularensis subsp. tularensis] gb AAS60264.1 sugar dehydratase [Francisella tularensis subsp. tularensis]	Francisella tularensis subsp. tularensis insertion sequence ISFtu2 and O-antigen gene cluster, complete sequence	83	2.00E-09	4.2.1.-
16023, 16024	52550245	23	2.00E-07	uncultured archaeon GZfos37B2	hypothetical protein GZ37B2_1 [uncultured archaeon GZfos37B2]				
16025, 16026	1722856	24	1.00E-06		Structural maintenance of chromosome 2 (Chromosome-associated protein E) (Chromosome assembly protein XCAP-E) pir B55094 chromosomal protein XCAP-E - African clawed frog gb AA64680.1 XCAP-E				
16027, 16028	34556560	37	2.00E-36	Wollinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes]				2.7.3.-
16029, 16030	34556560	45	3.00E-68	Wollinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes]				
1603, 1604	48855850	30	2.00E-15	Cytophaga hutchinsonii	hypothetical protein Chut02001063 [Cytophaga hutchinsonii]				
16031, 16032	34557923	38	3.00E-25	Wollinella succinogenes DSM 1740	UROPOPHYRINOGEN III COSYNTHASE (HEMD) [Wollinella succinogenes DSM 1740] emb CAE10638.1 UROPOPHYRINOGEN III COSYNTHASE (HEMD) [Wollinella succinogenes]				4.2.1.75
16033, 16034	34557752	56	4.00E-14	Wollinella succinogenes DSM 1740	hypothetical protein WS1402 [Wollinella succinogenes DSM 1740] emb CAE10467.1 hypothetical protein [Wollinella succinogenes]				
16035, 16036	41722689	38	8.00E-36	Dechloromonas aromatica RCB	COG0426: Uncharacterized flavoproteins [Dechloromonas aromatica RCB]				
16037, 16038	28974233	53	2.00E-50	Campylobacter fetus	hypothetical protein C00333 [Campylobacter fetus]				
16039, 16040	28974233	43	4.00E-41	Campylobacter fetus	hypothetical protein C00333 [Campylobacter fetus]				
16041, 16042	34557958	44	2.00E-51	Wollinella succinogenes DSM 1740	FLAGELLAR BIOSYNTHESIS PROTEIN FLHF FLAGELLA ASSOCIATED GTP-BINDING PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10673.1 FLAGELLAR BIOSYNTHESIS PROTEIN FLHF FLAGELLA ASSOCIATED GTP-BINDING PROTEIN [Wollinella succinogenes]				

16045, 16046	48860009	50	3.00E-81	Clostridium thermocellum ATCC 27405	COG0696: Phosphoglyceromutase [Clostridium thermocellum ATCC 27405]	Desc: Mycoplasma genitalium genome. Org: Mycoplasma genitalium	93	8.00E-07	5.4.2.1
16047, 16048	2128139	33	7.00E-10		hypothetical protein MJ0126 - Methanococcus jannaschii				2.7.7.-
16049, 16050	20090160	30	1.00E-11	Methanosarcina acetivorans C2A	hypothetical protein MA1296 [Methanosarcina acetivorans C2A] gb AA04715.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] sp Q8TR85 YC96_METAC Hypothetical UPF0331 protein MA1296				2.7.7.-
1605, 1606	48855574	37	2.00E-16	Cytophaga hutchinsonii	COG0782: Transcription elongation factor [Cytophaga hutchinsonii]				
16051, 16052	34557570	54	2.00E-87	Wolinella succinogenes DSM 1740	GLUTAMATE SYNTHASE SMALL CHAIN [Wolinella succinogenes DSM 1740] emb CAE10285.1 GLUTAMATE SYNTHASE SMALL CHAIN [Wolinella succinogenes]				1.4.1.13
16053, 16054	29346178	37	4.00E-15	Bacteroides thetaiotaomicron VPI-5482	putative para-aminobenzoate synthase component I [Bacteroides thetaiotaomicron VPI-5482] gb AAO75875.1 putative para-aminobenzoate synthase component I [Bacteroides thetaiotaomicron VPI-5482]				4.---
16055, 16056	34557268	65	5.00E-49	Wolinella succinogenes DSM 1740	TRANSCRIPTIONAL REGULATOR (LYSR FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09983.1 TRANSCRIPTIONAL REGULATOR (LYSR FAMILY) [Wolinella succinogenes]				
16057, 16058	26991094	42	3.00E-56	Pseudomonas putida KT2440	sensory box protein [Pseudomonas putida KT2440] gb AA069983.1 sensory box protein [Pseudomonas putida KT2440]				2.7.3.-
16059, 16060	23129412	26	2.00E-18	Nostoc punctiforme PCC 73102	COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102]				2.7.3.-
16061, 16062	48860427	49	2.00E-38	Clostridium thermocellum ATCC 27405	COG1052: Lactate dehydrogenase and related dehydrogenases [Clostridium thermocellum ATCC 27405]				1.1.1.95
16067, 16068	50084270	75	1.00E-56	Acinetobacter sp. ADP1	cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAG67958.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAA86930.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] sp Q43989 COBQ_ACIAD Cobyrinic acid synthase				3.---
16069, 16070	57241466	67	7.00E-40	Campylobacter lari RM2100	beta-ketoacyl-acc synthase III [Campylobacter lari RM2100] gb EAL54578.1 beta-ketoacyl-acc synthase III [Campylobacter lari RM2100]				2.3.1.41
16071, 16072	29349736	50	1.00E-38	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT4328 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79433.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				

16073, 16074	48861626	28	1.00E-32	Microbulbifer degradans 2-40	COG0642: Signal transduction histidine kinase [Microbulbifer degradans 2-40]			2.7.3.-
16075, 16076	13516917	26	1.00E-19	Myxococcus xanthus	hybrid sensor [Myxococcus xanthus]			
16077, 16078	34398055	73	8.00E-50	Porphyromonas gingivalis W83	glycyl-tRNA synthetase [Porphyromonas gingivalis W83] ref[NP_906216.1]			
16079, 16080	29349019	71	1.00E-87	Bacteroides thetaiotaomicron VPI-5482	glycyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78716.1 glycyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482]	Myroides odoratimimus metallo-beta- lactamase (MUS-1) gene, complete cds	88 2.00E-30	6.1.1.14
16081, 16082	32262994	42	3.00E-41	Helicobacter hepaticus ATCC 51449	putative endonuclease [Helicobacter hepaticus ATCC 51449] ref[NP_860974.1] putative endonuclease [Helicobacter hepaticus ATCC 51449]			6.1.1.14
16083, 16084	34557543	36	8.00E-50	Wolinella succinogenes DSM 1740	PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10258.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes] emb CAD5552.1 NapL protein [Wolinella succinogenes]			
16085, 16086	34556868	28	3.00E-17	Wolinella succinogenes DSM 1740	hypothetical protein WS0441 [Wolinella succinogenes DSM 1740] emb CAE09583.1 conserved hypothetical protein [Wolinella succinogenes]			
16089, 16090	53728999	29	1.00E-15	Actinobacillus pleuropneumoniae serovar 1 str. 4074	COG0419: ATPase involved in DNA repair [Actinobacillus pleuropneumoniae serovar 1 str. 4074]			
16093, 16094	54308776	33	4.00E-07	Photobacterium profundum SS9	hypothetical protein PBPRA1583 [Photobacterium profundum SS9] emb CAG19994.1 hypothetical protein [Photobacterium profundum]			
16095, 16096	29346283	41	2.00E-58	Bacteroides thetaiotaomicron VPI-5482	putative sulfatase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75980.1 putative sulfatase [Bacteroides thetaiotaomicron VPI-5482]			
16101, 16102	27365538	27	1.00E-22	Vibrio vulnificus CMCP6	hypothetical protein VV12211 [Vibrio vulnificus CMCP6] gb AAO10593.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6]			2.7.3.-
16103, 16104	39996209	44	1.00E-33	Geobacter sulfurreducens PCA	conserved hypothetical protein TIGR00296 [Geobacter sulfurreducens PCA] gb AAR34433.1 conserved hypothetical protein TIGR00296 [Geobacter sulfurreducens PCA]			
16109, 16110	34558474	42	5.00E-63	Wolinella succinogenes DSM 1740	hypothetical protein WS2199 [Wolinella succinogenes DSM 1740] emb CAE11189.1 conserved hypothetical protein [Wolinella succinogenes]			

1611, 1612	48854837	37	2.00E-31	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]				
16115, 16116	34556483	63	1.00E-112	Wolinella succinogenes DSM 1740	PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wolinella succinogenes DSM 1740] embjCAE09198.1 PUTATIVE UDP- GLUCURONIC ACID EPIMERASE [Wolinella succinogenes]	B.thuringiensis PK1 & cap genes, putative	85	3.00E-18	5.1.3.-
16117, 16118	16332176	26	4.00E-08	Synechocystis sp. PCC 6803	hypothetical protein sir1575 [Synechocystis sp. PCC 6803] dbj BAA18716.1 sir1575 [Synechocystis sp. PCC 6803] pir S76804 hypothetical protein - Synchocystis sp. (strain PCC 6803)				
16121, 16122	16263569	36	5.00E-24	Sinorhizobium meliloti 1021	probable oxidoreductase [Sinorhizobium meliloti 1021] gb AAK65774.1 probable oxidoreductase [Sinorhizobium meliloti 1021] pir D95401 probable oxidoreductase Sma2041 [Imported] - Sinorhizobium meliloti (strain 1021)				1.2.99.2
16125, 16126	39997114	52	8.00E-55	Geobacter sulfurreducens PCA	magaplasmid pSymA sensory box/GGDEF family protein [Geobacter sulfurreducens PCA] gb AAR35392.1 sensory box/GGDEF family protein [Geobacter sulfurreducens PCA]				2.7.3.-
16127, 16128	37677003	24	8.00E-15	Vibrio vulnificus YJ016	hypothetical protein VVA1343 [Vibrio vulnificus YJ016] dbj BAC97369.1 conserved hypothetical protein [Vibrio vulnificus YJ016]				
16129, 16130	AAB5259 6	28	5.00E-18	Thermotoga maritima MSB8	Desc:Helicobacter pylori bait polypeptide #114. Org:Helicobacter pylori				
1613, 1614	15644379	38	1.00E-09	Thermoanaerobact er tengcongensis MB4	hypothetical protein TM1631 [Thermotoga maritima MSB8] gb AAD36698.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir G72229 conserved hypothetical protein - Thermotoga maritima (strain MSB8)				3.1.11.5
16133, 16134	20806994	33	2.00E-26	Leptospira interrogans serovar Lai str. 56601	ATP-dependent exoDNase (exonuclease V), alpha subunit - helicase superfamily I member [Thermoanaerobacter tengcongensis MB4] gb AAM23769.1 ATP-dependent exoDNase (exonuclease V), alpha subunit helicase superfamily I member [Thermoanaerobacter tengcongensis MB4]				
16135, 16136	24214122	37	4.00E-30	Leptospira interrogans serovar Lai str. 56601	Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601]				
16137, 16138	57240902	50	1.00E-26	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55295.1 conserved hypothetical protein [Campylobacter lari RM2100]				

16139, 16140	21228703	28	4.00E-18	[Methanosarcina mazel Go1]	Zinc metalloprotease [Methanosarcina mazel Go1] gb AAM32297.1 Zinc metalloprotease [Methanosarcina mazel Go1]			3.4.24.-
16141, 16142	23098814	55	2.00E-26	Oceanobacillus theyensis HTE831	truncated nitrogen fixation positive activator [Oceanobacillus theyensis HTE831] dbj BAC13315.1 nitrogen fixation positive activator (partial)			
16145, 16146	21885306	44	6.00E-18	Vibrio cholerae	unknown [Vibrio cholerae]			3.1.21.-
16149, 16150	34556927	59	1.00E-69	Wolinella succinogenes DSM 1740	PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09642.1 PUTATIVE GTP-BINDING PROTEIN [Wolinella succinogenes]			
1615, 1616	48854579	38	2.00E-12	Cytophaga hutchinsonii	hypothetical protein Chut0202781 [Cytophaga hutchinsonii]			
16151, 16152	30249180	51	1.00E-22	Nitrosomonas europaea ATCC 19718	ATPase component ABC-type nitrate transport system [Nitrosomonas europaea ATCC 19718] emb CAD85106.1 ATPase component ABC-type nitrate transport system [Nitrosomonas europaea ATCC 19718]			
16153, 16154	29347576	45	4.00E-61	Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77273.1 two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482]			2.7.3.-
16155, 16156	34558820	57	3.00E-53	Alvinella pompejana epibiont 7G3	NAD(P)H-flavin oxidoreductase [Alvinella pompejana epibiont 7G3]			1.-.-.-
16157, 16158	46142136	37	2.00E-23	Methanococcoides burtonii DSM 6242	COG5002: Signal transduction histidine kinase [Methanococcoides burtonii DSM 6242]			2.7.3.-
16163, 16164	24373111	92	1.00E-46	Shewanella oneidensis MR-1	isocitrate dehydrogenase, NAD-dependent [Shewanella oneidensis MR-1] gb AAN54598.1 isocitrate dehydrogenase, NAD-dependent [Shewanella oneidensis MR-1]	Shewanella oneidensis MR-1 section 148 of 457 of the complete genome	80 1.00E-27	1.1.1.41
16165, 16166	48854568	31	9.00E-19	Cytophaga hutchinsonii	COG0849: Actin-like ATPase involved in cell division [Cytophaga hutchinsonii]			
16167, 16168	53715653	37	2.00E-21	Bacteroides fragilis YCH46	hypothetical protein BF4373 [Bacteroides fragilis YCH46] dbj BAD51111.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
1617, 1618	48853807	43	3.00E-60	Cytophaga hutchinsonii	COG0793: Periplasmic protease [Cytophaga hutchinsonii]			3.4.21.-
16171, 16172	51244492	27	4.00E-08	Desulfotalea psychrophila LSv54	hypothetical membrane protein (BatD) [Desulfotalea psychrophila LSv54] emb CAG35369.1 hypothetical membrane protein (BatD) [Desulfotalea psychrophila LSv54]			
16175, 16176	48861337	33	3.00E-07	Microbulbifer degradans 2-40	hypothetical protein Mdeg02003513 [Microbulbifer degradans 2-40]			

16177, 16178	38482512	44	1.00E-27	Photorhabdus luminescens	putative toxin transporter [Photorhabdus luminescens] hypothetical protein aq_563 [Aquifex aeolicus VF5] gb AAC06808.1 hypothetical protein [Aquifex aeolicus VF5] pir G70350 conserved hypothetical protein aq_563 - Aquifex aeolicus				2.7.3.-	
16179, 16180	15606018	34	1.00E-47	Aquifex aeolicus VF5						
16187, 16188	48845132	44	2.00E-39	Geobacter metallireducens GS-15	COG0643: Chemotaxis protein histidine kinase and related kinases [Geobacter metallireducens GS-15]					2.7.3.-
16189, 16190	34557884	52	1.00E-16	Wolinella succinogenes DSM 1740	DIGUANYLATE CYCLASE [Wolinella succinogenes DSM 1740] emb CAE10599.1 DIGUANYLATE CYCLASE [Wolinella succinogenes] putative selenide,water dikinase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir D81297 probable selenide, water dikinase (EC 2.7.9.3) Cj1504c [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282641.1 putative selenide,water dikinase [Campylobacter jejuni subsp. jejuni NCTC 11168]				2.7.9.3	
16191, 16192	6968929	41	1.00E-52	Campylobacter jejuni subsp. jejuni NCTC 11168						
16197, 16198	48730848	48	1.00E-24	Pseudomonas fluorescens PFO-1	hypothetical protein Pflu02002728 [Pseudomonas fluorescens PFO-1]					
16199, 16200	47527379	25	1.00E-09	Bacillus anthracis str. 'Ames Ancestor'	acetyltransferase, gnat family [Bacillus anthracis str. 'Ames Ancestor'] ref YP_028202.1 acetyltransferase, GNAT family [Bacillus anthracis str. Sterne] ref NP_844486.1 acetyltransferase, GNAT family [Bacillus anthracis str. Ames] ref NP_655942.1 Acetyltransf. Acetyltransferase (GNAT) family [Bacillus anthracis str. A2012] gb AAP25972.1 acetyltransferase, GNAT family [Bacillus anthracis str. Ames] gb AAT31203.1 acetyltransferase, GNAT family [Bacillus anthracis str. 'Ames Ancestor'] gb AAT54253.1 acetyltransferase, GNAT family [Bacillus anthracis str. Sterne]					2.7.3.-
16201, 16202	53730018	44	2.00E-52	Dechloromonas aromatica RCB	COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB]					
16203, 16204	29347584	45	8.00E-49	Bacteroides thetaiotaomicron VPI-5482	ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI- 5482] gb AAO77281.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482]					1.8.-
16205, 16206	51246820	65	9.00E-92	Desulfotalea psychrophila Lsv54	probable 2-isopropylmalate synthase [Desulfotalea psychrophila Lsv54] emb CAG37497.1 probable 2-isopropylmalate synthase [Desulfotalea psychrophila Lsv54]	Desulfotalea psychrophila Lsv54 chromosome	94	2.00E-19	4.1.3.12	
16207, 16208	46201501	33	8.00E-19	Magnetospirillum magnetotacticum MS-1	COG2208: Serine phosphatase RsbU, regulator of sigma subunit [Magnetospirillum magnetotacticum MS-1]					
1621, 1622	48854610	39	1.00E-18	Cytophaga hutchinsonii	COG0438: Glycosyltransferase [Cytophaga hutchinsonii]					

16211, 16212	39997484	31	1.00E-19	Geobacter sulfurreducens PCA	ABC transporter, periplasmic substrate-binding protein, putative [Geobacter sulfurreducens PCA] gblAAR35762.1 ABC transporter, periplasmic substrate-binding protein, putative [Geobacter sulfurreducens PCA]				
16215, 16216	48846045	39	3.00E-15	Geobacter metallireducens GS-15	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]				2.7.3.-
16219, 16220	42526809	32	4.00E-34	Treponema denticola ATCC 35405	DNA repair protein RecN [Treponema denticola ATCC 35405] gblAAS11818.1 DNA repair protein RecN [Treponema denticola ATCC 35405]				
16223, 16224	34558828	23	8.00E-18	Alvinella pompejana epibiont 7G3	KIAA1005 protein [Alvinella pompejana epibiont 7G3]				
16225, 16226	34558828	28	3.00E-17	Alvinella pompejana epibiont 7G3	KIAA1005 protein [Alvinella pompejana epibiont 7G3]				
16227, 16228	15643985	44	3.00E-69	Thermotoga maritima MSB8	hypothetical protein TM1229 [Thermotoga maritima MSB8] gblAAD36304.1 conserved hypothetical protein [Thermotoga maritima MSB8] p1r[F72278 conserved hypothetical protein - Thermotoga maritima (strain MSB8)]				
16229, 16230	56460387	49	5.00E-67	Idiomarina loihlensis L2TR	NAD-specific glutamate dehydrogenase [Idiomarina loihlensis L2TR] gblAAV82119.1 NAD-specific glutamate dehydrogenase [Idiomarina loihlensis L2TR]				1.4.1.2
1623, 1624	40556689	27	1.00E-09	Bacillus cereus Wolfinella succinogenes DSM 1740	putative peptide synthetase/polyketide synthase [Bacillus cereus] PUTATIVE TWO-COMPONENT SENSOR [Wolfinella succinogenes DSM 1740] emb[CAE09456.1] PUTATIVE TWO-COMPONENT SENSOR [Wolfinella succinogenes]				
16231, 16232	34556741	45	2.00E-67	Mimivirus	DNA mismatch repair ATPase MutS [Mimivirus] gblAAV50628.1 DNA mismatch repair ATPase MutS [Mimivirus]				2.7.3.-
16235, 16236	55819234	26	9.00E-28	Bacteroides thetaiotaomicron VPI-5482	putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] gblAAO78738.1 putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482]				
16237, 16238	29349041	30	3.00E-10	Bacteroides thetaiotaomicron VPI-5482	primosomal protein N' (replication factor Y) [Bacteroides thetaiotaomicron VPI-5482] gblAAO77858.1 primosomal protein N' (replication factor Y) [Bacteroides thetaiotaomicron VPI-5482]				
16239, 16240	29348161	47	9.00E-21	Photobacterium luminescens subsp. laumondii TTO1	Transposase, IS30 family [Photobacterium luminescens subsp. laumondii TTO1] emb[CAE15390.1] Transposase, IS30 family [Photobacterium luminescens subsp. laumondii TTO1]				
16241, 16242	37526904	51	6.00E-27						

16243, 16244	57241555	35	2.00E-38	Campylobacter lari RM2100	lipopolysaccharide heptosyltransferase-1 (rfac) [Campylobacter lari RM2100] gb EAL54667.1 lipopolysaccharide heptosyltransferase-1 (rfacC)			2.4.1.-
16247, 16248	57237448	56	2.00E-95	Campylobacter jejuni RM1221	malate:quinone oxidoreductase, putative [Campylobacter jejuni RM1221] gb AAW35031.1 malate:quinone oxidoreductase, putative [Campylobacter jejuni RM1221]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6	86 1.00E-146	1.1.99.1
16249, 16250	53713571	29	3.00E-22	Bacteroides fragilis YCH46	putative outer membrane protein [Bacteroides fragilis YCH46] db BAD49029.1 putative outer membrane protein [Bacteroides fragilis YCH46]			
1625, 1626	48853082	31	2.00E-14	Ferroplasma acidarmanus	COG0417: DNA polymerase elongation subunit (family B) [Ferroplasma acidarmanus]			2.7.7.7
16251, 16252	53714415	69	3.00E-93	Bacteroides fragilis YCH46	dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] db BAD49873.1 dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46]			2.4.1.83
16253, 16254	53756578	38	4.00E-39	Methylococcus capsulatus str. Bath	conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_115444.1 hypothetical protein MCA3057 [Methylococcus capsulatus str. Bath]			
16257, 16258	34557072	34	5.00E-10	Wolinella succinogenes DSM 1740	TWO COMPONENT RESPONSE REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09787.1 TWO COMPONENT RESPONSE REGULATOR [Wolinella succinogenes]			
16263, 16264	53713669	33	2.00E-10	Bacteroides fragilis YCH46	hypothetical protein BF2378 [Bacteroides fragilis YCH46] db BAD49127.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
16265, 16266	29348287	61	1.00E-30	Bacteroides thetaiotaomicron VPI-5482	putative translation initiation factor SU11 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78984.1 putative translation initiation factor SU11 [Bacteroides thetaiotaomicron VPI-5482]			
16267, 16268	53713299	58	5.00E-61	Bacteroides fragilis YCH46	putative aminopeptidase C [Bacteroides fragilis YCH46] db BAD48757.1 putative aminopeptidase C [Bacteroides fragilis YCH46]			3.4.22.-
16269, 16270	48856607	57	1.00E-49	Cytophaga hutchinsonii	COG1321: Mn-dependent transcriptional regulator [Cytophaga hutchinsonii]			
1627, 1628				Geobacter sulfurreducens PCA	bacterial signal domain protein [Geobacter sulfurreducens PCA] gb AAR34925.1 bacterial signal domain protein [Geobacter sulfurreducens PCA]			3.1.3.16
16271, 16272	28974235	41	3.00E-46	Campylobacter fetus	putative putative two-component sensor Cf0035 [Campylobacter fetus]			2.7.3.-

16275, 16276	45657982	46	9.00E-21	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	sugar transferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_711831.1 hemolysin hemolytic protein hlpA [Leptospira interrogans serovar Lai str. 56601] gb AA048849.1 hemolysin hemolytic protein hlpA [Leptospira interrogans serovar lai str. 56601] gb AAK19900.1 unknown [Leptospira interrogans] gb AAD52178.1 unknown [Leptospira interrogans] gb AAS70705.1 sugar transferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			
16277, 16278	46580432	28	2.00E-24	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	hypothetical protein DVU2025 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96500.1 conserved hypothetical protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			
16279, 16280	41720084	50	4.00E-54	Methanococcoides burtonii DSM 6242	COG2865: Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen [Methanococcoides burtonii DSM 6242]			
16281, 16282	15826957	32	2.00E-17	Mycobacterium leprae TN	hypothetical protein ML0126 [Mycobacterium leprae TN] emb CAC29634.1 hypothetical protein [Mycobacterium leprae] pir F86924 hypothetical protein [imported] - Mycobacterium leprae			
16283, 16284	22298538	36	1.00E-09	Thermosynechococcus elongatus BP-1	putative glycosyl transferase [Thermosynechococcus elongatus BP-1] db BAC08547.1 gi0995 [Thermosynechococcus elongatus BP-1]			
1629, 1630	48861626	46	2.00E-38	Microbulbifer degradans 2-40	COG0642: Signal transduction histidine kinase [Microbulbifer degradans 2-40]			
16295, 16296	24461248	54	4.00E-22	Lactobacillus sakei	HsdS [Lactobacillus sakei] ref NP_862273.1 HsdS [Lactobacillus sakei]			3.1.21.3
16299, 16300	34557975	49	9.00E-61	Wolinella succinogenes DSM 1740	AAA FAMILY ATPASE [Wolinella succinogenes DSM 1740] emb CAE10690.1 AAA FAMILY ATPASE [Wolinella succinogenes]			
16301, 16302	40063094	48	6.00E-77	uncultured bacterium 561	Polyphosphate kinase [uncultured bacterium 561]			2.7.4.1
16303, 16304	29346970	57	5.00E-71	Bacteroides thetaiotaomicron VPI-5482	nicotinate-nucleotide pyrophosphorylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76667.1 nicotinate-nucleotide pyrophosphorylase [Bacteroides thetaiotaomicron VPI-5482]			2.4.2.19
16305, 16306	34556546	53	2.00E-80	Wolinella succinogenes DSM 1740	LIN1802 PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09261.1 LIN1802 PROTEIN [Wolinella succinogenes]			
16307, 16308	41725785	40	1.00E-29	Dechloromonas aromatica RCB	COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Dechloromonas aromatica RCB]			2.7.3.-

16308, 16310	29349346	35	1.00E-28	Bacteroides thetaiotaomicron VPI-5482	ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gb AAO79043.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]				
1631, 1632	48733660	51	9.00E-57	Pseudomonas fluorescens PFO-1	COG1638: TRAP-type C4-dicarboxylate transport system, periplasmic component [Pseudomonas fluorescens PFO-1]				
16311, 16312	15602874	64	4.00E-53	Pasteurella multocida subsp. multocida str. Pm70	WbJD [Pasteurella multocida subsp. multocida str. Pm70] gb AAK03093.1 WbJD [Pasteurella multocida subsp. multocida str. Pm70]				5.1.3.14
16313, 16314	AAAY4377 4	56	2.00E-22		Desc: Amino acid sequence of eps8 of Streptococcus thermophilus Sfi39. Org: Streptococcus thermophilus				2.---
16315, 16316	34557638	65	3.00E-84	Wolinella succinogenes DSM 1740	QUINOLINATE SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10353.1 QUINOLINATE SYNTHETASE [Wolinella succinogenes]				
16317, 16318	42526943	35	1.00E-41	Treponema denticola ATCC 35405	hypothetical protein TDE1435 [Treponema denticola ATCC 35405] gb AAS11952.1 hypothetical protein TDE1435 [Treponema denticola ATCC 35405]				
16319, 16320	53712204	71	6.00E-81	Bacteroides fragilis YCH46	putative phosphoribosylformylglycinamide cyclo-ligase [Bacteroides fragilis YCH46] dbj BAD47662.1 putative phosphoribosylformylglycinamide cyclo-ligase [Bacteroides fragilis YCH46]				6.3.3.1
16321, 16322	48733100	27	1.00E-30	Pseudomonas fluorescens PFO-1	COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Pseudomonas fluorescens PFO-1]				
16323, 16324	53711799	40	1.00E-37	Bacteroides fragilis YCH46	putative protoporphyrinogen oxidase [Bacteroides fragilis YCH46] dbj BAD47257.1 putative protoporphyrinogen oxidase [Bacteroides fragilis YCH46]				2.1.1.-
16327, 16328	57168512	52	3.00E-54	Campylobacter coli RM2228	phosphoglycerate dehydrogenase [Campylobacter coli RM2228] gb EAL56694.1 phosphoglycerate dehydrogenase [Campylobacter coli RM2228]				1.1.1.95
16331, 16332	51246430	58	3.00E-73	Desulfotalea psychrophila LSV54	hypothetical protein DP2578 [Desulfotalea psychrophila LSV54] emb CAG37307.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]				1.6.5.3
16335, 16336	57241512	31	3.00E-22	Campylobacter lari RM2100	probable periplasmic protein Cj1289 [Campylobacter lari RM2100] gb EAL54624.1 probable periplasmic protein Cj1289 [Campylobacter lari RM2100]				
16337, 16338	33862569	36	7.00E-10	Prochlorococcus marinus str. MIT 9313	TPR repeat [Prochlorococcus marinus str. MIT 9313] emb CAE20471.1 TPR repeat [Prochlorococcus marinus str. MIT 9313]				
16341, 16342	57241555	38	8.00E-55	Campylobacter lari RM2100	lipopolysaccharide heptosyltransferase-1 (rfuC) [Campylobacter lari RM2100] gb EAL54667.1 lipopolysaccharide heptosyltransferase-1 (rfuC) [Campylobacter lari RM2100]				2.4.1.-

16343, 16344	24216023	42	1.00E-13	Leptospira interrogans serovar Lai str. 56601	Leucine-rich repeat containing protein [Leptospira interrogans serovar Lai str. 56601] [Leptospira interrogans serovar lai str. 56601]				
16347, 16348	34556857	65	3.00E-68	Wolinella succinogenes DSM 1740	DNA POLYMERASE I [Wolinella succinogenes DSM 1740] emb CAE09572.1 DNA POLYMERASE I [Wolinella succinogenes]			2.7.7.7	
1635, 1636	53711474	43	2.00E-32	Bacteroides fragilis YCH46	hypothetical protein BF0183 [Bacteroides fragilis YCH46] dbj BAD46932.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
16351, 16352	54293057	47	1.00E-49	Legionella pneumophila str. Lens	hypothetical protein lp10094 [Legionella pneumophila str. Lens] emb CAH14324.1 hypothetical protein [Legionella pneumophila str. Lens]			3.1.3.5	
16353, 16354	34557014	43	6.00E-57	Wolinella succinogenes DSM 1740	hypothetical protein WS0597 [Wolinella succinogenes DSM 1740] emb CAE09729.1 conserved hypothetical protein [Wolinella succinogenes] conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_902615.1 hypothetical protein CV2945 [Chromobacterium violaceum ATCC 12472]				
16355, 16356	34104254	37	2.00E-56	Rhodopirellula baltica SH 1	putative Na(+)-linked D-alanine glycine permease [Rhodopirellula baltica SH 1] emb CAD76934.1 putative Na(+)-linked D-alanine glycine permease [Pirellula sp.]				
16357, 16358	32476567	61	6.00E-53	Bacteroides fragilis YCH46	hypothetical protein BF0448 [Bacteroides fragilis YCH46] dbj BAD47197.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
16359, 16360	53711739	24	1.00E-06	Actinobacillus pleuropneumoniae serovar 1 str. 4074	COG1123: ATPase components of various ABC-type transport systems, contain duplicated ATPase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]			1.8.-.-	
16363, 16364	32033790	33	5.00E-26	Thiocapsa roseopersicina	HoxY [Thiocapsa roseopersicina]			1.12.-.-	
16365, 16366	37787354	48	2.00E-42	Clostridium acetobutylicum ATCC 824	FerriC uptake regulator (FUR family), YGAG B. subtilis ortholog [Clostridium acetobutylicum ATCC 824] gb AAK80581.1 FerriC uptake regulator (FUR family), YGAG B. subtilis ortholog [Clostridium acetobutylicum ATCC 824] pir B97224 ferriC uptake regulator (FUR family), YGAG B. subtilis ortholog [Imported] - Clostridium acetobutylicum				
16367, 16368	15895892	39	3.00E-17	Pseudomonas putida KT2440	hypothetical protein PP1921 [Pseudomonas putida KT2440] gb AAAN67538.1 hypothetical protein [Pseudomonas putida KT2440]				
16371, 16372	26988649	31	1.00E-13						

16375, 16376	34558196	36	1.00E-32	Wollinella succinogenes DSM 1740	DNA PRIMASE PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wollinella succinogenes]			2.7.7.-
16377, 16378	45358661	69	1.00E-35	Methanococcus maripaludis S2	phosphate ABC transporter, ATP-binding protein [Methanococcus maripaludis S2] emb CAF30654.1 phosphate ABC transporter, ATP-binding protein [Methanococcus maripaludis S2]	Staphylococcus aureus subsp. aureus strain MRSA252, complete genome	85 4.00E-12	1.8.-
16379, 16380	57286071	25	1.00E-07	Staphylococcus aureus subsp. aureus COL	phosphate transport system protein PhoU, putative [Staphylococcus aureus subsp. aureus COL] ref YP_043448.1 putative phosphate transport system protein [Staphylococcus aureus subsp. aureus MSSA476] ref NP_646090.1 hypothetical protein MW1273 [Staphylococcus aureus subsp. aureus MW2] ref NP_374498.1 hypothetical protein SA1217 [Staphylococcus aureus subsp. aureus N315] emb CAG43102.1 putative phosphate transport system protein [Staphylococcus aureus subsp. aureus MSSA476] dbj BAB57547.1 similar to negative regulator PhoU [Staphylococcus aureus subsp. aureus Mu50] dbj BAB95138.1 MW1273 [Staphylococcus aureus subsp. aureus MW2] dbj BAB42477.1 SA1217 [Staphylococcus aureus subsp. aureus N315] pir JAB9915 hypothetical protein SA1217 [imported] - Staphylococcus aureus (strain N315) ref NP_371909.1 similar to negative regulator PhoU [Staphylococcus aureus subsp. aureus Mu50] ref YP_186272.1 phosphate transport system protein PhoU, putative [Staphylococcus aureus subsp. aureus COL]			
16381, 16382	34557665	50	1.00E-38	Wollinella succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wollinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wollinella succinogenes]			2.7.3.-
16383, 16384	51244082	42	1.00E-36	Desulfotalea psychrophila L Sv54	hypothetical protein DP0230 [Desulfotalea psychrophila L Sv54] emb CAG34959.1 hypothetical protein [Desulfotalea psychrophila L Sv54]			2.7.3.-
16387, 16388	57241681	58	3.00E-81	Campylobacter lari RM2100	DNA gyrase, B subunit [Campylobacter lari RM2100] gb EAL54351.1 DNA gyrase, B subunit [Campylobacter lari RM2100]	Desc:Staphylococ- us epidermidis ORF nucleic acid sequence SEQ ID NO:2390. Org:Staphylococcus epidermidis	92 6.00E-16	5.99.1.3
16389, 16390	27366980	22	5.00E-12	Vibrio vulnificus CMCP6	Predicted signal transduction protein [Vibrio vulnificus CMCP6] gb AAO07497.1 Predicted signal transduction protein [Vibrio vulnificus CMCP6]			

16395, 16396	21232019	30	8.00E-15	Xanthomonas campestris pv. campestris str. ATCC 33913	lipoprotein [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AA41860.1 lipoprotein [Xanthomonas campestris pv. campestris str. ATCC 33913]				
16397, 16398	46581041	26	3.00E-28	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	HAMP domain protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS97109.1 HAMP domain protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]				2.7.3.-
16399, 16400	34556884	56	3.00E-80	Wolnella succinogenes DSM 1740	hypothetical protein WS0457 [Wolnella succinogenes DSM 1740] emb CAE09599.1 conserved hypothetical protein [Wolnella succinogenes]				1.-.-.-
16401, 16402	20808732	39	2.00E-18	Thermoanaerobact er tengcongensis MB4	8-pyruvoyl-tetrahydropterin synthase [Thermoanaerobacter tengcongensis MB4] gb AAM25507.1 6-pyruvoyl-tetrahydropterin synthase [Thermoanaerobacter tengcongensis MB4]				4.6.1.10
16403, 16404	48833156	46	2.00E-44	Magnetococcus sp. MC-1	hypothetical protein Mmc102001351 [Magnetococcus sp. MC-1] putative periplasmic protein [Campylobacter jejuni subsp. jejuni NCTC 11168] pir B81399 probable periplasmic protein Cj0530 [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281714.1 putative periplasmic protein [Campylobacter jejuni subsp. jejuni NCTC 11168]				
16405, 16406	6967998	24	1.00E-08	Campylobacter jejuni subsp. jejuni NCTC 11168	alanine racemase, putative [Campylobacter upsaliensis RM3195] gb EAL53686.1 alanine racemase, putative [Campylobacter upsaliensis RM3195]				5.1.1.1
16407, 16408	57242224	42	8.00E-22	Bacteriophage Aeh1	NudE nudix hydrolase [Bacteriophage Aeh1] ref NP_942229.1 NudE nudix hydrolase [Bacteriophage Aeh1]				
16409, 16410	33414958	36	2.00E-12	Photothabdus luminescens subsp. laumondii TTO1	adenosylmethionine-8-amino-7-oxononanoate transaminase (DAPA aminotransferase) [Photothabdus luminescens subsp. laumondii TTO1] emb CAE13777.1 adenosylmethionine-8-amino-7-oxononanoate transaminase (DAPA aminotransferase) [Photothabdus luminescens subsp. laumondii TTO1]				2.6.1.62
16413, 16414	37525435	51	7.00E-58	Cytophaga hutchinsonii	COG0438: Glycosyltransferase [Cytophaga hutchinsonii]				
16419, 16420	48853840	27	2.00E-18	Cytophaga hutchinsonii	COG0206: Cell division GTPase [Cytophaga hutchinsonii]				3.4.24.-
16421, 16422	48854567	36	8.00E-42	Clostridium acetobutylicum ATCC 824	O-acetylhomoserine sulphydrylase [Clostridium acetobutylicum ATCC 824] gb AAK78087.1 O-acetylhomoserine sulphydrylase [Clostridium acetobutylicum ATCC 824] pir D96912 O-acetylhomoserine sulphydrylase [imported] - Clostridium acetobutylicum				4.2.99.1 0
16423, 16424	15893398	34	9.00E-36	Vibrio parahaemolyticus RIMD 2210633	DPS family protein [Vibrio parahaemolyticus RIMD 2210633] db BAC61906.1 DPS family protein [Vibrio parahaemolyticus]				
16425, 16426	28900418	56	1.00E-32						

1643, 1644	32262346	35	3.00E-30	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860328.1 hypothetical protein HH0797 [Helicobacter hepaticus ATCC 51449]			2.7.7.-
16431, 16432	48855803	62	6.00E-73	Cytophaga hutchinsonii	COG0042: tRNA-dihydrouridine synthase [Cytophaga hutchinsonii]			
16435, 16436	57505258	44	1.00E-34	Campylobacter upsallensis RM3195	conserved hypothetical protein [Campylobacter upsallensis gb EAL53179.1 conserved hypothetical protein [Campylobacter upsallensis RM3195]			
16437, 16438	29346214	56	1.00E-97	Bacteroides thetaiotaomicron VPI-5482	putative carbon-nitrogen hydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75911.1 putative carbon-nitrogen hydrolase [Bacteroides thetaiotaomicron VPI-5482]			
16439, 16440	34557033	59	5.00E-64	Wolinella succinogenes DSM 1740	GLUTAMINE AMIDOTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09748.1 GLUTAMINE AMIDOTRANSFERASE [Wolinella succinogenes] sp Q7M9X0 HIS5_WOLSU Imidazole glycerol phosphate synthase subunit hisH (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (ImGP synthase subunit hisH) (IGPS subunit hisH)		2.4.2.-	
16441, 16442	17231520	39	3.00E-12	Nostoc sp. PCC 7120	hypothetical protein air4028 [Nostoc sp. PCC 7120] pir AE2309 hypothetical protein air4028 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75727.1 air4028 [Nostoc sp. PCC 7120]			
16443, 16444	34557685	34	3.00E-43	Wolinella succinogenes DSM 1740	HYPOTHETICAL INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10400.1 HYPOTHETICAL INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes]			
16445, 16446	29346628	38	2.00E-34	Bacteroides thetaiotaomicron VPI-5482	conserved hypothetical protein, with conserved domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76325.1 conserved hypothetical protein, with conserved domain [Bacteroides thetaiotaomicron VPI-5482]			
16447, 16448	56478721	30	3.00E-12	Azoarcus sp. EbN1	transposase, is4 family [Azoarcus sp. EbN1] ref YP_160303.1 transposase (IS4) [Azoarcus sp. EbN1] ref YP_159286.1 transposase (IS4) [Azoarcus sp. EbN1] ref YP_157078.1 transposase (IS4) [Azoarcus sp. EbN1] ref YP_157069.1 transposase (IS4) [Azoarcus sp. EbN1] emb CAI09409.1 transposase, is4 family [Azoarcus sp. EbN1] emb CAI09402.1 Transposase (IS4) [Azoarcus sp. EbN1] emb CAI08385.1 Transposase (IS4) [Azoarcus sp. EbN1] emb CAI06177.1 Transposase (IS4) [Azoarcus sp. EbN1] emb CAI06168.1 Transposase (IS4) [Azoarcus sp. EbN1]			
16449, 16450	53690822	47	5.00E-67	Desulfovibrio desulfuricans G20	COG0380: Trehalose-6-phosphate synthase [Desulfovibrio desulfuricans G20]			2.4.1.15
1645, 1646	55978212	29	6.00E-10	Thermus thermophilus HB8	hypothetical protein TTHB029 [Thermus thermophilus HB8] dbj BAD71825.1 conserved hypothetical protein [Thermus thermophilus HB8]			

16451, 16452, 16453, 16454, 16455, 16456	48864235 48863907 51893967	29 26 32	7.00E-31 5.00E-07 7.00E-20	Microbulbifer degradans 2-40 Microbulbifer degradans 2-40 Symbiobacterium thermophilum IAM 14863	COG0642: Signal transduction histidine kinase [Microbulbifer degradans 2-40] COG5651: PPE-repeat proteins [Microbulbifer degradans 2-40] hypothetical protein STH2829 [Symbiobacterium thermophilum IAM 14863] dbj BAD41814.1 conserved hypothetical protein [Symbiobacterium thermophilum IAM 14863]				
16457, 16458	45658050	50	9.00E-23	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	mannose-1-phosphate guanylyltransferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] guanylyltransferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				2.7.7.13
16461, 16462	28896971	80	7.00E-49	Vibrio parahaemolyticus RIMD 2210633	putative capsular polysaccharide biosynthesis protein D [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58460.1 putative capsular polysaccharide biosynthesis protein D [Vibrio parahaemolyticus]	Vibrio parahaemolyticus DNA, chromosome 1, complete sequence	84	1.00E-15	
16463, 16464	45658032	28	4.00E-07	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	hypothetical protein LIC12183 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711780.1 hypothetical protein LA1599 [Leptospira interrogans serovar Lai str. 56601] gb AA48798.1 hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AA50755.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				
16467, 16468, 16469, 16470	46143757 48834423	31 38	5.00E-13 9.00E-40	Actinobacillus pleuropneumoniae serovar 1 str. 4074 Magnetococcus sp. MC-1	COG1305: Transglutaminase-like enzymes, putative cysteine proteases [Actinobacillus pleuropneumoniae serovar 1 str. 4074] COG0535: Predicted Fe-S oxidoreductases [Magnetococcus sp. MC-1]				1.97.1.4
16477, 16478	48856329	62	2.00E-92	Cytophaga hutchinsonii	COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii] cell division protein FtsX [Helicobacter hepaticus ATCC 51449] ref NP_860318.1 cell division protein FtsX [Helicobacter hepaticus ATCC 51449]				1.8.-.-
16481, 16482	32262336	24	5.00E-22	Helicobacter hepaticus ATCC 51449	PUTATIVE FIBRONECTIN DOMAIN-CONTAINING LIPOPROTEIN [Wolnella succinogenes DSM 1740] emb CAE09307.1 PUTATIVE FIBRONECTIN DOMAIN-CONTAINING LIPOPROTEIN [Wolnella succinogenes]				
16483, 16484	34556592	35	3.00E-44	Wolnella succinogenes DSM 1740					

16485,					Wollinella	hypothetical protein WS2166 [Wollinella succinogenes DSM 1740]				
16486	34558443	36	2.00E-13		succinogenes DSM 1740	emb CAE11158.1 hypothetical protein [Wollinella succinogenes]				
16487,	ABB9146					Desc:Herbicide active polypeptide SEQ ID NO 672. Org:Arabidopsis thaliana				3.4.21.-
16488	1	44	7.00E-32							
16489,					Magnetococcus sp.					
16490	48831039	56	3.00E-33		MC-1	COG0686: Alanine dehydrogenase [Magnetococcus sp. MC-1]				1.4.1.1
16491,					Plasmodium					
16492	23508398	26	2.00E-08		falciparum 3D7	hypothetical protein PF11_0207 [Plasmodium falciparum 3D7]				
16493,					Burkholderia					
16494	53721220	24	6.00E-10		pseudomallei K96243	gb AAN35791.1 hypothetical protein [Plasmodium falciparum 3D7]				
16495,					Microbulbifer					
16496	48862581	31	1.00E-18		degradans 2-40	hypothetical protein BPSS0184 [Burkholderia pseudomallei K96243]				
16497,					Thermus					
16498	55981423	47	7.00E-75		thermophilus HB8	emb CAH37629.1 hypothetical protein [Burkholderia pseudomallei K96243]				
16499,						COG0642: Signal transduction histidine kinase [Microbulbifer degradans 2-40]				
16500	56478683	38	1.00E-15		Azoarcus sp. Ebn1	emb CAI09371.1 Two-component system response regulator [Azoarcus sp. Ebn1]				1.3.99.1
16501,					Cytophaga					
16502	48854579	38	2.00E-12		hutchinsonii	hypothetical protein Chut0202781 [Cytophaga hutchinsonii]				2.7.-
16503,	48856514	45	7.00E-52		Cytophaga	COG2148: Sugar transferases involved in lipopolysaccharide synthesis [Cytophaga hutchinsonii]				2.-
16504	940147	42	3.00E-19							2.7.3.-
16505,					Wollinella					
16506	34557407	36	3.00E-49		succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wollinella succinogenes DSM 1740] emb CAE10122.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wollinella succinogenes]				2.7.3.-
16507,					Helicobacter					
16508	32263159	42	2.00E-26		hepaticus ATCC 51449	two-component system histidine kinase [Helicobacter hepaticus ATCC 51449] ref NP_861138.1 two-component system histidine kinase [Helicobacter hepaticus ATCC 51449]				2.7.3.-
16509,										
16510	558571	58	1.00E-95		Escherichia coli	site-specific DNA-methyltransferase (cytosine-specific) [Escherichia coli] sp P50196 MTE8_ECOLI Modification methylase Eco47II (Cytosine-specific methyltransferase Eco47II) (M.Eco47II) prf 2115269B methyltransferase Eco47IIM				94 2.00E-10 2.1.1.73
16511,					Cytophaga					
1652	48854286	45	1.00E-56		hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]				

16511,	42527140	37	3.00E-32	Treponema denticola ATCC 35405	citrate lyase, beta subunit [Treponema denticola ATCC 35405]			4.1.3.6
16512					gb AAS12149.1 citrate lyase, beta subunit [Treponema denticola ATCC 35405]			
16513,	28212137	53	3.00E-54	Clostridium tetani E88	citrate lyase alpha chain [Clostridium tetani E88]			2.8.3.10
16514					lyase alpha chain [Clostridium tetani E88]			
16515,				Clostridium thermocellum ATCC 27405	COG4191: Signal transduction histidine kinase regulating C4-dicarboxylate transport system [Clostridium thermocellum ATCC 27405]			2.7.3.-
16516	48859709	29	2.00E-15					
16517,				Campylobacter jejuni RM1221	UDP-N-acetylpyruvoylglucosamine reductase [Campylobacter jejuni RM1221]			1.1.1.15
16518	57238687	41	2.00E-22		reductase [Campylobacter jejuni RM1221]			8
16521,				Helicobacter hepaticus ATCC 51449	dimethyladenosine transferase (rRNA methylation) [Helicobacter hepaticus ATCC 51449] ref NP_860705.1 dimethyladenosine transferase (rRNA methylation) [Helicobacter hepaticus ATCC 51449]			2.1.1.-
16522	32262724	40	5.00E-20		aspartokinase [Chlorobium tepidum TLS] gb AAM71343.1 aspartokinase			
16523,	21672936	33	6.00E-33	Chlorobium tepidum TLS	[Chlorobium tepidum TLS]			2.7.2.4
16524				Dechloromonas aromatica RCB				
16525,	46140339	37	4.00E-15		COG2863: Cytochrome c553 [Dechloromonas aromatica RCB]			
16526								
16527,				Wollinella succinogenes DSM 1740	SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wollinella succinogenes DSM 1740] emb CAE10864.1			
16528	34558149	24	1.00E-07		SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wollinella succinogenes]			
16529,				Ustilago maydis 521	hypothetical protein UM00177.1 [Ustilago maydis 521] ref XP_397792.1			
16530	46096329	52	4.00E-57		hypothetical protein UM00177.1 [Ustilago maydis 521]			
16535,				Acinetobacter sp. ADP1	hypothetical protein ACIAD0599 [Acinetobacter sp. ADP1]			
16536	50083834	32	6.00E-32		emb CAG67522.1 conserved hypothetical protein [Acinetobacter sp. ADP1]			
16537,				Leifsonia xyl i subsp. xyl i str. CTCB07	glycosyltransferase [Leifsonia xyl i subsp. xyl i str. CTCB07] gb AAT89751.1			
16538	50955568	39	3.00E-17		glycosyltransferase [Leifsonia xyl i subsp. xyl i str. CTCB07]			
16539,				Xanthomonas axonopodis pv. citri str. 306	transcriptional regulator [Xanthomonas axonopodis pv. citri str. 306]			2.7.3.-
16540	21243215	37	3.00E-47		gb AAM37333.1 transcriptional regulator [Xanthomonas axonopodis pv. citri str. 306]			
16541,				Methanococcoides burtonii DSM 6242	COG3769: Predicted hydrolase (HAD superfamily) [Methanococcoides burtonii DSM 6242]			
16542	46142672	41	5.00E-21					

16543, 16544	52550565	32	7.00E-19	uncultured archaeon GZfos9E5	mannosyl-3-phosphoglycerate phosphatase [uncultured archaeon GZfos9E5]				
16545, 16546	34557665	44	3.00E-30	Wolinella succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes]				2.7.3.-
16547, 16548	34556943	43	1.00E-57	Wolinella succinogenes DSM 1740	PUTATIVE TONB-INDEPENDENT PROTEIN-UTAKE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09658.1 PUTATIVE TONB- INDEPENDENT PROTEIN-UTAKE PROTEIN [Wolinella succinogenes]				
1655, 1656	57233885	25	6.00E-20	Dehalococcoides ethenogenes 195	GGDEF domain/HD domain protein [Dehalococcoides ethenogenes 195] gb AAW39390.1 GGDEF domain/HD domain protein [Dehalococcoides ethenogenes 195]				2.7.3.-
16551, 16552	57505920	32	2.00E-08	Campylobacter upsaliensis RM3195	conserved hypothetical protein [Campylobacter upsaliensis RM3195] gb EAL52510.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195]				
16553, 16554	48854031	55	8.00E-94	Cytophaga hutchinsonii	COG0445: NAD/FAD-utilizing enzyme apparently involved in cell division [Cytophaga hutchinsonii]	Desc:Mycoplasma genitalium genome. Org:Mycoplasma genitalium	86	1.00E-11	
16557, 16558	ABP2948 1	39	2.00E-15	Clostridium tetani E88	Desc:Streptococcus pyogenes polypeptide SEQ ID NO 8138. Org:Streptococcus pyogenes				
16559, 16560	28210192	29	3.00E-07		hypothetical protein CTC00439 [Clostridium tetani E88] gb AAO35073.1 conserved protein [Clostridium tetani E88]				
16561, 16562	46142687	37	2.00E-21	Methanococcoides burtonii DSM 6242	COG0726: Predicted xylanase/chitin deacetylase [Methanococcoides burtonii DSM 6242]				
16563, 16564	34557975	46	9.00E-83	Wolinella succinogenes DSM 1740	AAA FAMILY ATPASE [Wolinella succinogenes DSM 1740] emb CAE10690.1 AAA FAMILY ATPASE [Wolinella succinogenes]				
16565, 16566	34557975	70	3.00E-79	Wolinella succinogenes DSM 1740	AAA FAMILY ATPASE [Wolinella succinogenes DSM 1740] emb CAE10690.1 AAA FAMILY ATPASE [Wolinella succinogenes]				3.4.24.-
16567, 16568	34556615	67	9.00E-42	Wolinella succinogenes DSM 1740	conserved hypothetical protein CJO172C [Wolinella succinogenes DSM 1740] emb CAE09330.1 conserved hypothetical protein CJO172C [Wolinella succinogenes]				1.1.1.-
16569, 16570	47572668	23	5.00E-12	Rubrivivax gelatinosus PM1	COG0270: Site-specific DNA methylase [Rubrivivax gelatinosus PM1] Desc:C glutamicum protein fragment SEQ ID NO: 6894.				2.1.1.73
16571, 16572	AAG9314 0	28	2.00E-15		Org:Corynebacterium glutamicum				

16573, 16574	53715006	52	1.00E-54	Bacteroides fragilis YCH46	cation efflux system protein [Bacteroides fragilis YCH46] dbj BAD50464.1 cation efflux system protein [Bacteroides fragilis YCH46]			
16575, 16576	48860160	37	1.00E-21	Clostridium thermocellum ATCC 27405	COG0111: Phosphoglycerate dehydrogenase and related dehydrogenases [Clostridium thermocellum ATCC 27405]			
16577, 16578	57240770	37	9.00E-46	Campylobacter lari RM2100	flagellar motor switch protein FlmM [Campylobacter lari gb EAL55163.1 flagellar motor switch protein FlmM [Campylobacter lari RM2100]			
16579, 16580	29347938	30	2.00E-36	Bacteroides thetaiotaomicron VPI-5482	putative Na+-dependent phosphate transporter [Bacteroides thetaiotaomicron VPI-5482] gb AAO77635.1 putative Na+-dependent phosphate transporter [Bacteroides thetaiotaomicron VPI-5482]			
16581, 16582	46446644	47	3.00E-70	Parachlamydia sp. UWE25	hypothetical protein pc1010 [Parachlamydia sp. UWE25] emb CAF23734.1 conserved hypothetical protein [Parachlamydia sp. UWE25]			
16585, 16586	57236909	63	3.00E-40	Campylobacter jejuni RM1221	GTP cyclohydrolase I family protein [Campylobacter jejuni RM1221] gb AAW34492.1 GTP cyclohydrolase I family protein [Campylobacter jejuni RM1221]			
16587, 16588	48862944	43	7.00E-31	Microbulifer degradans 2-40	COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Microbulifer degradans 2-40]			
16589, 16590	4838141	29	6.00E-24	Bacteroides fragilis	BatD [Bacteroides fragilis]			
16591, 16592	48853811	51	9.00E-80	Cytophaga hutchinsonii	COG0587: DNA polymerase III, alpha subunit [Cytophaga hutchinsonii] hypothetical protein aq_429 [Aquifex aeolicus VF5] gb AAC06701.1 putative protein [Aquifex aeolicus VF5] pir C70339 hypothetical protein aq_429 - Aquifex aeolicus	2.7.7.7		
16593, 16594	15605926	24	6.00E-07	Aquifex aeolicus VF5				
16595, 16596	34556462	70	4.00E-47	Wolinella succinogenes DSM 1740	hypothetical protein WS0003 [Wolinella succinogenes DSM 1740] emb CAE09177.1 conserved hypothetical protein [Wolinella succinogenes] hypothetical protein LIC12325 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711602.1 hypothetical protein LA1421			
16597, 16598	45658173	32	9.00E-14	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	[Leptospira interrogans serovar Lai str. 56601] gb AAN48620.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS70896.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			

16599, 16600	45658174	38	2.00E-18	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	hypothetical protein LIC12326 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70897.1] conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			
16601, 16602	48730848	47	1.00E-23	Pseudomonas fluorescens PfO-1	hypothetical protein PflU02002728 [Pseudomonas fluorescens PfO-1]			
16603, 16604	56419029	35	2.00E-11	Geobacillus kaustophilus HTA426	transcriptional repressor of PBSX genes [Geobacillus kaustophilus HTA426] dbj BAD74779.1] transcriptional repressor of PBSX genes [Geobacillus kaustophilus HTA426]			
16605, 16606	16127072	32	2.00E-15	Caulobacter crescentus CB15	hypothetical protein CC2840 [Caulobacter crescentus CB15]			
16607, 16608	48854772	42	3.00E-47	Cytophaga hutchinsonii	gb AAK24804.1] hypothetical protein [Caulobacter crescentus CB15] pir H87600 hypothetical protein CC2840 [imported] - Caulobacter crescentus			
16609, 16610	48832299	48	1.00E-43	Magnetococcus sp. MC-1	COG2234: Predicted aminopeptidases [Cytophaga hutchinsonii]			3.4.11.-
16611, 16612	50841972	43	4.00E-16	Propionibacterium acnes KPA171202	COG2206: HD-GYP domain [Magnetococcus sp. MC-1]			3.1.4.17
16613, 16614	23475955	44	2.00E-24	Desulfovibrio desulfuricans G20	UTP-glucose-1-phosphate uridylyltransferase [Propionibacterium acnes KPA171202] KPA171202] gb AAT82241.1] UTP-glucose-1-phosphate uridylyltransferase [Propionibacterium acnes KPA171202]			2.7.7.9
16617, 16618	48846045	38	2.00E-24	Geobacter metallireducens GS	COG4284: UDP-glucose pyrophosphorylase [Desulfovibrio desulfuricans G20]			2.7.7.9
					COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]			2.7.3.-
16621, 16622	17935724	34	7.00E-20	Agrobacterium tumefaciens str. C58	mutT like protein [Agrobacterium tumefaciens str. C58] gb AAL42830.1] mutT like protein [Agrobacterium tumefaciens str. C58] gb AAK87603.1] AGR_C_3368p [Agrobacterium tumefaciens str. C58] pir AH2801 mutT like protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir B97581 hypothetical protein AGR_C_3368 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) ref NP_354818.1] hypothetical protein AGR_C_3368 [Agrobacterium tumefaciens str. C58]			3.6.1.-
16623, 16624	34558202	40	9.00E-22	Wolinella succinogenes DSM 1740	LIPID A BIOSYNTHESIS ACYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE10917.1] LIPID A BIOSYNTHESIS ACYLTRANSFERASE [Wolinella succinogenes]			2.3.1.-
16625, 16626	48832666	45	1.00E-56	Magnetococcus sp. MC-1	COG3959: Transketolase, N-terminal subunit [Magnetococcus sp. MC-1]			2.2.1.1
16629, 16630	48854899	56	2.00E-26	Cytophaga hutchinsonii	COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii]			2.1.1.-

1663, 1664	18976925	46	1.00E-27	Pyrococcus furiosus DSM 3638	arsenate reductase [Pyrococcus furiosus DSM 3638] gb AAL80677.1 arsenate reductase: (arsC) [Pyrococcus furiosus DSM 3638]				1.97.1.5
16631, 16632	48853718	35	6.00E-44	Cytophaga hutchinsonii	COG2120: Uncharacterized proteins, LmbE homologs [Cytophaga hutchinsonii]				
16633, 16634	34558265	53	3.00E-34	Wolinella succinogenes DSM 1740	PUTATIVE HEMOLYSIN [Wolinella succinogenes DSM 1740] emb CAE10980.1 PUTATIVE HEMOLYSIN [Wolinella succinogenes]				
16635, 16636	32262573	44	2.00E-38	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860554.1 hypothetical protein HH1023 [Helicobacter hepaticus ATCC 51449]				
16637, 16638	57241759	35	3.00E-07	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54429.1 conserved hypothetical protein [Campylobacter lari RM2100]				
16639, 16640	21673017	36	8.00E-32	Chlorobium tepidum TLS	penicillin-binding protein 1 [Chlorobium tepidum TLS] gb AAM71424.1 penicillin-binding protein 1 [Chlorobium tepidum TLS]				2.4.2.-
16641, 16642	32263042	23	4.00E-10	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861022.1 hypothetical protein HH1491 [Helicobacter hepaticus ATCC 51449]				
16643, 16644	48856580	47	2.00E-20	Cytophaga hutchinsonii	hypothetical protein Chut02000314 [Cytophaga hutchinsonii]				
16645, 16646	29346299	46	2.00E-36	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0889 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75996.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
16647, 16648	53687530	65	2.00E-37	Nostoc punctiforme PCC 73102	hypothetical protein Npun02005570 [Nostoc punctiforme PCC 73102]				
16649, 16650	53713319	49	6.00E-76	Bacteroides fragilis YCH46	putative TonB-dependent outer membrane receptor protein [Bacteroides fragilis YCH46] db BAD48777.1 putative TonB-dependent outer membrane receptor protein [Bacteroides fragilis YCH46]				
16651, 16652	37811998	29	4.00E-07	Aeromonas hydrophila	putative cil protein [Aeromonas hydrophila]				
16655, 16656	34558493	58	3.00E-82	Wolinella succinogenes DSM 1740	PUTATIVE ZINC PROTEASE [Wolinella succinogenes DSM 1740] emb CAE11208.1 PUTATIVE ZINC PROTEASE [Wolinella succinogenes]				3.4.-.-
16657, 16658	34556560	46	4.00E-66	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]				
16659, 16660	34558171	28	4.00E-26	Wolinella succinogenes DSM 1740	hypothetical protein WS1876 [Wolinella succinogenes DSM 1740] emb CAE10886.1 conserved hypothetical protein [Wolinella succinogenes]				

16661, 16662	34557356	37	3.00E-55	Wolinnella succinogenes DSM 1740	NRFI PROTEIN [Wolinnella succinogenes DSM 1740] emb CAE10071.1 NRFI PROTEIN [Wolinnella succinogenes] emb CAB53161.1 Nrfi protein [Wolinnella succinogenes] sp Q9S1E4 NRFI_WOLSU Nrfi protein			
16663, 16664	57207873	23	1.00E-14	Staphylococcus aureus	hypothetical protein [Staphylococcus aureus]			
16665, 16666	34557782	35	4.00E-33	Wolinnella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinnella succinogenes DSM 1740] emb CAE10487.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinnella succinogenes]	2.7.3.-		
16667, 16668	31195231	60	2.00E-71	Anopheles gambiae	ENSANGP00000001058 [Anopheles gambiae] gb EAA02216.1 ENSANGP00000001058 [Anopheles gambiae str. PEST] ref XP_561308.1 ENSANGP00000001058 [Anopheles gambiae str. PEST]	1.1.1.34		
16669, 16670	48855423	26	2.00E-20	Cytophaga hutchinsonii	COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii]	5.2.1.8		
1667, 1668	53713909	33	3.00E-16	Bacteroides fragilis YCH46	hypothetical protein BF2617 [Bacteroides fragilis YCH46] dbj BAD49367.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
16671, 16672	34558447	54	4.00E-78	Wolinnella succinogenes DSM 1740	PUTATIVE CATION-TRANSPORTING ATPASE [Wolinnella succinogenes DSM 1740] emb CAE11162.1 PUTATIVE CATION-TRANSPORTING ATPASE [Wolinnella succinogenes]	3.6.1.-		
16673, 16674	53684563	38	2.00E-37	Desulfitobacterium hafniense DCB-2	COG1373: Predicted ATPase (AAA+ superfamily) [Desulfitobacterium hafniense DCB-2]			
16677, 16678	20806705	37	8.00E-29	Thermoanaerobact er tengcongensis MB4	hypothetical protein TTE0179 [Thermoanaerobacter tengcongensis MB4] gb AAM23480.1 conserved hypothetical protein [Thermoanaerobacter tengcongensis MB4]			
16679, 16680	34397903	53	1.00E-40	Porphyromonas gingivalis W83	excinuclease ABC, C subunit [Porphyromonas gingivalis W83] ref NP_906065.1 excinuclease ABC, C subunit [Porphyromonas gingivalis W83]			
16681, 16682	34396304	38	6.00E-46	Porphyromonas gingivalis W83	mannosyltransferase [Porphyromonas gingivalis W83] ref NP_904472.1 mannosyltransferase [Porphyromonas gingivalis W83]	2.4.1.-		
16689, 16690	57168872	56	2.00E-54	Campylobacter coli RM2228	MiaB-like tRNA modifying enzyme [Campylobacter coli RM2228] gb EAL56394.1 MiaB-like tRNA modifying enzyme [Campylobacter coli RM2228]	89 4.00E-07 1.8.-		
1669, 1670	48854786	40	1.00E-41	Cytophaga hutchinsonii	COG0584: Glycerophosphoryl diester phosphodiesterase [Cytophaga hutchinsonii]	3.1.4.46		

16691, 16692	57168872	56	1.00E-41	Campylobacter coli RM2228	MiaB-like tRNA modifying enzyme [Campylobacter coli RM2228] gb EAL56394.1 MiaB-like tRNA modifying enzyme [Campylobacter coli RM2228]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6	89	3.00E-07	1.8.-.-
16693, 16694	28211918	24	2.00E-09	Clostridium tetani E88	sensory transduction protein kinase [Clostridium tetani E88] gb AAO36799.1 sensory transduction protein kinase [Clostridium tetani E88]				
16695, 16696	45915115	42	5.00E-18	Mesorhizobium sp. BNC1	COG0489: ATPases involved in chromosome partitioning [Mesorhizobium sp. BNC1]				
16697, 16698	5739402	51	3.00E-60	Flavobacterium johnsoniae	TruB [Flavobacterium johnsoniae] sp Q9RB36 TRUB_CYTJO tRNA pseudouridine synthase B (tRNA pseudouridine 55 synthase) (Psi55 synthase) (Pseudouridylylase synthase) (Uracil hydrolyase)			4.2.1.70	
16699, 16700	52548848	27	6.00E-18	archaeon GZfos19A5	transposase [uncultured archaeon GZfos19A5]				
167, 168	48853766	33	6.00E-26	Cytophaga hutchinsonii	COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii]			2.7.3.-	
16703, 16704	48767890	52	1.00E-30	Ralstonia metallidurans CH34	COG0796: Glutamate racemase [Ralstonia metallidurans CH34]			5.1.1.3	
16705, 16706	53715260	54	8.00E-30	Bacteroides fragilis YCH46	putative transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD50718.1 putative transcriptional regulator [Bacteroides fragilis YCH46]				
16707, 16708	AAO2094	8	3.00E-25		Desc:Protein of the Bpm1 M1 methylase gene (Bpm1M1). Org:Baillus pumilus			2.1.1.72	
16709, 16710	48833968	41	4.00E-63	Magnetococcus sp. MC-1	COG0673: Predicted dehydrogenases and related proteins [Magnetococcus sp. MC-1]			1.-.-.-	
1671, 1672	48853961	37	4.00E-19	Cytophaga hutchinsonii	COG1995: Pyridoxal phosphate biosynthesis protein [Cytophaga hutchinsonii]			1.1.1.26	2
16711, 16712	48863156	34	1.00E-14	Microbulifer degradans 2-40	COG4067: Uncharacterized protein conserved in archaea [Microbulifer degradans 2-40]				

16723, 16724	48847450	39	3.00E-15	15	Geobacter metallireducens GS-15	COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00301665.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00301374.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00300257.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00300170.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00298468.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00298384.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15]				
16725, 16726	34397615	33	7.00E-22		Porphyromonas gingivalis W83	ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ66097.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65881.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65455.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65413.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_905778.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_905198.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904782.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904556.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904514.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAD38020.1 transposase [Porphyromonas gingivalis]				
16729, 16730	34556563	46	6.00E-66	1740	Wolinella succinogenes DSM 1740	PANTOATE-BETA-ALANINE LIGASE [Wolinella succinogenes DSM 1740] emb CAE09278.1 PANTOATE-BETA-ALANINE LIGASE [Wolinella succinogenes]				6.3.2.1
16731, 16732	34556563	53	2.00E-38	1740	Wolinella succinogenes DSM 1740	PANTOATE-BETA-ALANINE LIGASE [Wolinella succinogenes DSM 1740] emb CAE09278.1 PANTOATE-BETA-ALANINE LIGASE [Wolinella succinogenes]				6.3.2.1
16733, 16734	57242486	32	8.00E-19		Campylobacter upsaliensis RM3195	methyl-accepting chemotaxis protein (tpa) [Campylobacter upsaliensis RM3195] gb EAL53554.1 methyl-accepting chemotaxis protein (tpa) [Campylobacter upsaliensis RM3195]				
16735, 16736	48855820	44	3.00E-35		Cytophaga hutchinsonii	COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii]				
16737, 16738	23478426	21	1.00E-09		Plasmodium yoelii yoelii	hypothetical protein [Plasmodium yoelii yoelii]				3.1.11.-
16741, 16742	AA33437	3	3.00E-25			Desc:Porphyromonas gingivalis protein PG4. Org:Porphyromonas gingivalis COG0726: Predicted xylanase/chitin deacetylase [Microbulifer degradans 2- 40]				
16743, 16744	48861641	36	1.00E-26		Microbulifer degradans 2-40					

16745, 16746	15606040	40	6.00E-21	Aquifex aeolicus VF5	hypothetical protein aq_598 [Aquifex aeolicus VF5] gb AAC06817.1 putative protein [Aquifex aeolicus VF5] pir E70353 hypothetical protein aq_598 - Aquifex aeolicus			
16747, 16748				Vibrio parahaemolyticus RIMD 2210633	tail-specific protease [Vibrio parahaemolyticus RIMD 2210633] dbj BAC59869.1 tail-specific protease [Vibrio parahaemolyticus] tail-specific protease [Xanthomonas axonopodis pv. citri str. 306] gb AAM35558.1 tail-specific protease [Xanthomonas axonopodis pv. citri str. 306]			3.4.21.-
16749, 16750	21241440	48	5.00E-76	Xanthomonas axonopodis pv. citri str. 306				3.4.21.-
1675, 1676	48856102	51	5.00E-42	Cytophaga hutchinsonii	COG2353: Uncharacterized conserved protein [Cytophaga hutchinsonii] putative integrase/recombinase [Cupriavidus necator] gb AAP65797.1 putative integrase/recombinase [Ralstonia eutropha]			
16753, 16754	38637709	30	2.00E-12	Cupriavidus necator	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]			
16757, 16758	34557419	35	9.00E-11	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10495.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes]			2.7.3.-
16759, 16760	34557780	38	2.00E-40	Wolinella succinogenes DSM 1740	Desc:Chondroitinase AC. Org:Flavobacterium heparinum			
16761, 16762	AAR8914 5	30	7.00E-09		putative glycosyl transferase [Thermosynechococcus elongatus BP-1] dbj BAC08547.1 tli0995 [Thermosynechococcus elongatus BP-1] DNA repair protein Rada [Campylobacter lari RM2100] gb EAL55738.1 DNA repair protein Rada [Campylobacter lari RM2100]			2.4.1.-
16763, 16764	22298538	41	5.00E-25	Thermosynechococ cus elongatus BP-1	COG0006: Xaa-Pro aminopeptidase [Trichodesmium erythraeum IMS101] putative ABC transporter ATP-binding protein yhiH [Azoarcus sp. Ebn1] emb CAI09981.1 putative ABC transporter ATP-binding protein yhiH [Azoarcus sp. Ebn1]			
16769, 16770	57240624	64	2.00E-61	Campylobacter lari RM2100	hypothetical protein PBPR80710 [Photobacterium profundum SS9] emb CAG22582.1 hypothetical protein [Photobacterium profundum]			1.8.-
1677, 1678	48894780	31	2.00E-29	Trichodesmium erythraeum IMS101	SIROHEME SYNTHASE [Wolinella succinogenes DSM 1740] emb CAE10105.1 SIROHEME SYNTHASE [Wolinella succinogenes] Desc:High growth methanotrophic bacterial strain polypeptide #26. Org:Methylobacter 16a			2.1.1.10 7
16771, 16772	58479293	50	5.00E-19	Azoarcus sp. Ebn1				
16773, 16774	54302389	54	1.00E-23	Photobacterium profundum SS9				
16775, 16776	34557390	40	7.00E-49	Wolinella succinogenes DSM 1740				
16777, 16778	ABG6157 6	35	5.00E-41					1.7.99.4

16779, 16780	28209890	31	5.00E-19	E88	Clostridium tetani	acyl-acyl carrier protein thioesterase [Clostridium tetani E88] gb AAO34771.1 acyl-acyl carrier protein thioesterase [Clostridium tetani E88]			
16781, 16782	17233315	39	4.00E-08	7120	Nostoc sp. PCC	hypothetical protein alr7299 [Nostoc sp. PCC 7120] dbj BAB78383.1 alr7299 [Nostoc sp. PCC 7120] pir AC2515 hypothetical protein alr7299 [Imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha			
16785, 16786	27127146	46	1.00E-60	NRCPB-10	Agrobacterium sp.	phosphoenol pyruvate carboxylase [Agrobacterium sp. NRCPB-10]			4.1.1.49
16787, 16788	17940320	23	6.00E-13	PBC5	Sinorhizobium melloti phage	putative DNA methylase [Sinorhizobium melloti phage PBC5] ref NP_542283.1 putative DNA methylase [Sinorhizobium melloti phage PBC5]			
16789, 16790	20807875	48	9.00E-18	MB4	Thermoanaerobacter tengcongensis	CheY-like receiver domains [Thermoanaerobacter tengcongensis MB4] gb AAM24650.1 CheY-like receiver domains [Thermoanaerobacter tengcongensis MB4]			3.1.1.61
16791, 16792	53729414	38	1.00E-30	aromatica RCB	Dechloromonas	COG0515: Serine/threonine protein kinase [Dechloromonas aromatica RCB]			2.7.1.37
16793, 16794	33284889	39	2.00E-21	Danio rerio	Danio rerio	novel protein similar to human telomerase-associated protein 1 (TEP1) [Danio rerio]			
16795, 16796	24372449	46	2.00E-19	Shewanella oneidensis MR-1	Shewanella oneidensis MR-1	response regulator [Shewanella oneidensis MR-1] gb AAN53936.1 response regulator [Shewanella oneidensis MR-1]			
16799, 16800	53715569	37	4.00E-35	YCH46	Bacteroides fragilis	hypothetical protein BF4287 [Bacteroides fragilis YCH46] dbj BAD51027.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
16801, 16802	17232096	47	1.00E-62	7120	Nostoc sp. PCC	type I site-specific deoxyribonuclease chain R [Nostoc sp. PCC 7120] dbj BAB76303.1 type I site-specific deoxyribonuclease chain R [Nostoc sp. PCC 7120] pir AD2381 type I site-specific deoxyribonuclease chain R [Imported] - Nostoc sp. (strain PCC 7120)			3.1.21.3
16805, 16806	57241016	28	4.00E-26	RM2100	Campylobacter lari	methyl-accepting chemotaxis protein (tipB), putative [Campylobacter lari RM2100] gb EAL54712.1 methyl-accepting chemotaxis protein (tipB), putative [Campylobacter lari RM2100]			
16807, 16808	20089643	30	9.00E-23	acetivorans C2A	Methanosarcina acetivorans C2A	sensory transduction histidine kinase [Methanosarcina acetivorans C2A] gb AAM04198.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A]			2.7.3.-
16811, 16812	57242712	29	2.00E-09	RM3195	Campylobacter upsallensis	probable transmembrane protein Cj0352 [Campylobacter upsallensis RM3195] gb EAL53425.1 probable transmembrane protein Cj0352 [Campylobacter upsallensis RM3195]			
16815, 16816	53735986	36	5.00E-42	WH 8501	Crocospaera watsonii WH 8501	COG3347: Uncharacterized conserved protein [Crocospaera watsonii WH 8501]			1.-.-.-

16817, 16818	34557562	38	3.00E-22	1740	Wollinella succinogenes DSM 1740	PUTATIVE TRANSCRIPTIONAL REGULATOR [Wollinella succinogenes DSM 1740] emb CAE10277.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wollinella succinogenes]				
16821, 16822	20806576	37	3.00E-26	MB4	Thermoanaerobact er tengcongensis MB4	Response regulators consisting of a CheY-like receiver domain and an HD- GYP domain [Thermoanaerobacter tengcongensis MB4] gb AAM23351.1 Response regulators consisting of a CheY-like receiver domain and an HD- GYP domain [Thermoanaerobacter tengcongensis MB4]			2.7.3.-	
16823, 16824	21229428	24	3.00E-09	mazei Go1	Methanosarcina mazei Go1	aldehyde ferredoxin oxidoreductase [Methanosarcina mazei Go1] gb AAM33022.1 aldehyde ferredoxin oxidoreductase [Methanosarcina mazei Go1]			1.2.7.-	
16825, 16826	48860413	57	6.00E-50	ATCC 27405	Clostridium thermocellum ATCC 27405	COG1331: Highly conserved protein containing a thioredoxin domain [Clostridium thermocellum ATCC 27405]			84 7.00E-12 2.7.4.9	
16827, 16828	20807051	41	6.00E-14	MB4	Thermoanaerobact er tengcongensis MB4	NtrC family Transcriptional regulator, ATPase domain [Thermoanaerobacter tengcongensis MB4] gb AAM23826.1 NtrC family Transcriptional regulator, ATPase domain [Thermoanaerobacter tengcongensis MB4]				
1683, 1684	51891955	43	3.00E-54	14863	Symbiobacterium thermophilum IAM 14863	hypothetical protein STH817 [Symbiobacterium thermophilum IAM 14863] dbj BAD39802.1 conserved hypothetical protein [Symbiobacterium thermophilum IAM 14863]			2.8.1.6	
16833, 16834	29349667	46	2.00E-72	VPI-5482	Bacteroides thetaiotaomicron VPI-5482	carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79364.1 carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482]			3.4.21.-	
16837, 16838	15644333	32	3.00E-37	maritima MSB8	Thermotoga maritima MSB8	glycerate kinase, putative [Thermotoga maritima MSB8] gb AAD36652.1 glycerate kinase, putative [Thermotoga maritima MSB8] pir A72236 hypothetical protein TM1585 - Thermotoga maritima (strain MSB8)			1.1.1.81	
16839, 16840	29347128	35	2.00E-38	VPI-5482	Bacteroides thetaiotaomicron VPI-5482	putative 2-aminoethylphosphonate pyruvate aminotransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76825.1 putative 2- aminoethylphosphonate pyruvate aminotransferase [Bacteroides thetaiotaomicron VPI-5482]			2.6.1.-	
16841, 16842	29346727	70	8.00E-21	VPI-5482	Bacteroides thetaiotaomicron VPI-5482	riboflavin synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76424.1 riboflavin synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482]			2.5.1.9	

16843,	57167730	71	1.00E-114	Campylobacter coli RM2228	DNA polymerase III, alpha subunit [Campylobacter coli RM2228] gb EAL57516.1 DNA polymerase III, alpha subunit [Campylobacter coli RM2228]	Clostridium tetani E88, section 9 of 10 of the complete genome	84	5.00E-11	2.7.7.7
16844,	13123741	42	1.00E-47	Campylobacter jejuni	WaaF [Campylobacter jejuni]				
16848,	56677131	32	3.00E-14	Silicibacter pomeroi DSS-3	SSSpo8, transposase [Silicibacter pomeroi DSS-3] ref YP_165742.1 SSSpo8, transposase [Silicibacter pomeroi DSS-3]				
16850,	18312445	44	1.00E-33	Pyrobaculum aerophilum str. IM2	hypothetical protein PAE1163 [Pyrobaculum aerophilum str. IM2] gb AAL63294.1 conserved hypothetical protein [Pyrobaculum aerophilum str. IM2]				
16851,	48857812	48	4.00E-38	Clostridium thermocellum ATCC 27405	COG0324: tRNA delta(2)-isopentenylpyrophosphate transferase [Clostridium thermocellum ATCC 27405]				2.5.1.8
16853,	48856515	42	4.00E-24	Cytophaga hutchinsonii	COG2518: Protein-L-isoaspartate carboxylmethyltransferase [Cytophaga hutchinsonii]				2.1.1.77
16854,	21674157	34	2.00E-13	Chlorobium tepidum TLS	hypothetical protein CT1335 [Chlorobium tepidum TLS] gb AAM72564.1 hypothetical protein [Chlorobium tepidum TLS]				
16855,				Wolinella succinogenes DSM 1740	hypothetical protein WS2098 [Wolinella succinogenes DSM 1740] emb CAE11096.1 hypothetical protein [Wolinella succinogenes]				
16856,	34558381	46	3.00E-26	Microbulbifer degradans 2-40	COG0308: Aminopeptidase N [Microbulbifer degradans 2-40] DNA polymerase III delta prime subunit (hoB) [Campylobacter coli RM2228] gb EAL57223.1 DNA polymerase III delta prime subunit (hoB) [Campylobacter coli RM2228]			3.4.11.2	
16861,	48862107	47	8.00E-31	Campylobacter coli RM2228					2.7.7.7
16862,	57168180	48	1.00E-16	Wolinella succinogenes DSM 1740	hypothetical protein WS1730 [Wolinella succinogenes DSM 1740] emb CAE10755.1 conserved hypothetical protein [Wolinella succinogenes] probable periplasmic protein Cj0530 [Campylobacter upsaliensis RM3195] gb EAL53524.1 probable periplasmic protein Cj0530 [Campylobacter upsaliensis RM3195]				
16863,	34558040	44	4.00E-42	Campylobacter upsaliensis RM3195	cell division protein FtsA [Methylococcus capsulatus str. Bath] ref YP_114838.1 cell division protein FtsA [Methylococcus capsulatus str. Bath]				
16864,	57242456	27	2.00E-26	Methylococcus capsulatus str. Bath					
16865,	53757202	38	2.00E-33	Nostoc punctiforme PCC 73102	COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] hypothetical protein TTC1571 [Thermus thermophilus HB27] gb AAS81913.1 hypothetical conserved protein [Thermus thermophilus HB27]			2.7.3.-	
16866,	23128539	30	6.00E-14	Thermus thermophilus HB27					
16867,	46199873	31	2.00E-13						

16875, 16876	34558498	60	5.00E-51	Wolinella succinogenes DSM 1740	hypothetical protein WS2225 [Wolinella succinogenes DSM 1740] emb CAE11213.1 conserved hypothetical protein [Wolinella succinogenes]			2.7.3.-
16877, 16878	57240555	37	6.00E-27	Campylobacter lari RM2100	transformation system protein [Campylobacter lari RM2100] gb EAL55669.1 transformation system protein [Campylobacter lari RM2100]			
16879, 16880	34397664	35	3.00E-46	Porphyromonas gingivalis W83	ABC transporter, ATP-binding protein, MsbA family [Porphyromonas gingivalis W83] ref NP_905827.1 ABC transporter, ATP-binding protein, MsbA family [Porphyromonas gingivalis W83]			
16881, 16882	49524759	27	5.00E-13	Candida glabrata CBS138	unnamed protein product [Candida glabrata CBS138] ref XP_445454.1 unnamed protein product [Candida glabrata]			3.1.3.3
16883, 16884	57238095	46	3.00E-49	Campylobacter jejuni RM1221	DNA-binding response regulator [Campylobacter jejuni RM1221] gb AAW35678.1 DNA-binding response regulator [Campylobacter jejuni RM1221] emb CAB73477.1 putative two-component regulator [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282370.1 putative two-component regulator [Campylobacter jejuni subsp. jejuni NCTC 11168] pir A81329 probable two-component regulator Cj1223c [imported] - Campylobacter jejuni (strain NCTC 11168)	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 4/6	87 8.00E-12	2.7.3.-
16885, 16886	AAW9831	32	3.00E-16		Desc.H. pylori GHPO 881 protein. Org:Helicobacter pylori			
16887, 16888	48856048	37	4.00E-11	Cytophaga hutchinsonii	COG1597: Sphingosine kinase and enzymes related to eukaryotic diacylglycerol kinase [Cytophaga hutchinsonii]			
16889, 16890	34557780	37	4.00E-21	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10495.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes]			2.7.3.-
16891, 16892	51244370	42	6.00E-25	Desulfotalea psychrophila LSv54	hypothetical protein DP0518 [Desulfotalea psychrophila LSv54] emb CAG35247.1 conserved hypothetical protein [Desulfotalea psychrophila LSv54]			
16893, 16894	54028700	22	2.00E-10	Polaromonas sp. JS666	COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Polaromonas sp. JS666]			
16895, 16896	45656429	33	1.00E-16	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	tetraacyldisaccharide 4'-kinase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS69152.1 tetraacyldisaccharide 4'- kinase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			2.7.1.13 0
16899, 16900	23130537	38	5.00E-44	Nostoc punctiforme PCC 73102	COG0778: Nitroreductase [Nostoc punctiforme PCC 73102]			

169,170	3282095	45	7.00E-30	Thermotoga neapolitana	hypothetical protein [Thermotoga neapolitana] sp O86953 PANC_THENE Pantoate-beta-alanine ligase (Pantothenate synthetase) (Pantoate activating enzyme)				6.3.2.1
16901,16902	34557978	40	1.00E-53	Wolinella succinogenes DSM 1740	PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10693.1 PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolinella succinogenes]				2.3.2.-
16905,16906	57242230	53	1.00E-70	Campylobacter upsaliensis RM3195	ribosomal protein S1, putative [Campylobacter upsaliensis RM3195] gb EAL53692.1 ribosomal protein S1, putative [Campylobacter upsaliensis RM3195]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6	90	6.00E-07	
16907,16908	48854003	41	1.00E-40	Cytophaga hutchinsonii	hypothetical protein Chut02003091 [Cytophaga hutchinsonii] collagenase precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO78178.1 collagenase precursor [Bacteroides thetaiotaomicron VPI-5482]				
16909,16910	29348481	62	2.00E-88	Bacteroides thetaiotaomicron VPI-5482	COG3604: Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains [Cytophaga hutchinsonii]				3.4.-
16911,16912	48856412	41	7.00E-22	Cytophaga hutchinsonii	hypothetical protein BT1057 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76164.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
16915,16916	29346467	31	5.00E-15	Plasmodium falciparum 3D7	hypothetical protein PF14_0667 [Plasmodium falciparum 3D7] gb AAN37280.1 hypothetical protein [Plasmodium falciparum 3D7]				
16919,16920	23509889	26	3.00E-07	Wolinella succinogenes DSM 1740	RIBONUCLEASE [Wolinella succinogenes DSM 1740] emb CAE10885.1 RIBONUCLEASE [Wolinella succinogenes]				3.1.-
16921,16922	34558170	42	9.00E-41	Alvinella pompejana epibiont	DNA-binding response regulator RprY [Alvinella pompejana epibiont 6C6] ARGINYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE09347.1 ARGINYL-TRNA SYNTHETASE [Wolinella succinogenes]				2.7.3.-
16925,16926	34558806	36	8.00E-35	Wolinella succinogenes DSM 1740	COG1555: DNA uptake protein and related DNA-binding proteins [Moorella thermoacetica ATCC 39073]				6.1.1.19
16929,16930	34556632	59	5.00E-92	Moorella thermoacetica ATCC 39073	mannosyltransferase A (mtfA) [Archaeoglobus fulgidus DSM 4304] gb AAB91182.1 mannosyltransferase A (mtfA) [Archaeoglobus fulgidus DSM 4304] pir E69255 mannosyltransferase A (mtfA) homolog - Archaeoglobus fulgidus				2.4.1.-
1693,1694	49235971	54	6.00E-14	Archaeoglobus fulgidus DSM 4304					
16931,16932	11497665	28	1.00E-12	Archaeoglobus fulgidus DSM 4304					

16933, 16934, 16937, 16938, 16939, 16940, 16941, 16942, 16943, 16944, 16945, 16946, 16947, 16948, 1695, 1696, 16951, 16952, 16953, 16954, 16955, 16956, 16957, 16958, 16959, 16960, 16961, 16962	34556520 48854887 48854887 32261577 48844818 38503877 48853770 57240288 5123897 21283478 16125586 46580489 57240920 34558414 20090834	65 31 31 40 34 35 59 50 42 28 42 41 52 57 34	3.00E-98 6.00E-13 6.00E-13 1.00E-16 7.00E-10 3.00E-07 8.00E-93 2.00E-32 4.00E-24 4.00E-11 8.00E-28 3.00E-22 1.00E-33 5.00E-31 2.00E-24	Wollinella succinogenes DSM 1740 Cytophaga hutchinsonii Helicobacter hepaticus ATCC 51449 Geobacter metallireducens GS 15 Synechocystis sp. PCC 6803 Cytophaga hutchinsonii Campylobacter lari RM2100 Streptomyces coelicolor A3(2) Staphylococcus aureus subsp. aureus MW2 Caulobacter crescentus CB15 Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough Campylobacter lari RM2100 Wollinella succinogenes DSM 1740 Methanosarcina acetivorans C2A	hypothetical protein WS0066 [Wollinella succinogenes DSM 1740] emb CAE09235.1 conserved hypothetical protein [Wollinella succinogenes] COG0538: isocitrate dehydrogenases [Cytophaga hutchinsonii] conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_859561.1 hypothetical protein HH0030 [Helicobacter hepaticus ATCC 51449] COG0500: SAM-dependent methyltransferases [Geobacter metallireducens GS-15] hypothetical protein [Synechocystis sp. PCC 6803] db EAD02109.1 sl 6052 [Synechocystis sp. PCC 6803] COG0046: Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Cytophaga hutchinsonii] conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55402.1 conserved hypothetical protein [Campylobacter lari RM2100] putative aminotransferase [Streptomyces coelicolor A3(2)] ref NP_627817.1 putative aminotransferase [Streptomyces coelicolor A3(2)] pir T35390 probable aminotransferase - Streptomyces coelicolor hypothetical protein MW1749 [Staphylococcus aureus subsp. aureus MW2] db BAB95614.1 hypothetical protein [Staphylococcus aureus subsp. aureus MW2] peptidyl-prolyl cis-trans isomerase A [Caulobacter crescentus CB15] gb AAK23318.1 peptidyl-prolyl cis-trans isomerase A [Caulobacter crescentus CB15] pir B87415 peptidyl-prolyl cis-trans isomerase A [imported] - Caulobacter crescentus oligopeptide-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96557.1 oligopeptide-binding protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] hydrolase, haloacid dehalogenase-like family, putative [Campylobacter lari RM2100] gb EAL55313.1 hydrolase, haloacid dehalogenase-like family, putative [Campylobacter lari RM2100] PYRUVATE:FERREDOXIN OXIDOREDUCTASE GAMMA SUBUNIT [Wollinella succinogenes DSM 1740] emb CAE11129.1 PYRUVATE:FERREDOXIN OXIDOREDUCTASE GAMMA SUBUNIT [Wollinella succinogenes] transposase [Methanosarcina acetivorans C2A] gb AAM05389.1 transposase [Methanosarcina acetivorans str. C2A]	3.1.3.18 2.6.1.1 5.2.1.8 3.1.3.18 1.2.7.1
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16965, 16966	24375997	42	2.00E-08	Shewanella oneidensis MR-1	oxygen-independent coproporphyrinogen III oxidase, putative [Shewanella oneidensis MR-1] gb AA57484.1 oxygen-independent coproporphyrinogen III oxidase, putative [Shewanella oneidensis MR-1]			
16969, 16970 1697, 1698 16971, 16972	27807025 46131192	50 24	3.00E-38 1.00E-09	ubiquinone Ralstonia eutropha JMP134	NADH dehydrogenase flavoprotein 2 (24kD) [ubiquinone] [NADH-ubiquinone reductase 24 kDa mitochondrial] [Bos taurus] sp P04394 NUHM_BOVIN NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial precursor (Polypeptide II) pir B30113 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) 24K chain precursor - bovine gb AAA87358.1 NADH-ubiquinone reductase 24 kDa subunit [Bos taurus] COG0859: ADP-heptose:LPS heptosyltransferase [Ralstonia eutropha JMP134]		1.6.5.3	
16973, 16974	48854899 34558362	56 43	2.00E-26 1.00E-31	Cytophaga hutchinsonii Wolinella succinogenes DSM 1740	COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] PEPTIDYL-TRNA HYDROLASE [Wolinella succinogenes DSM 1740] emb CAE11077.1 PEPTIDYL-TRNA HYDROLASE [Wolinella succinogenes] sp Q7M7U8 PTH_WOLSU Peptidyl-tRNA hydrolase (PTH)		2.1.1.-	3.1.1.29
16975, 16976	57169449	33	2.00E-33	Campylobacter coli RM2228	probable integral membrane protein Cj0313 [Campylobacter coli RM2228] gb EAL56931.1 probable integral membrane protein Cj0313 [Campylobacter coli RM2228]			
16979, 16980	34557405	25	7.00E-07	Wolinella succinogenes DSM 1740	hypothetical protein WS1018 [Wolinella succinogenes DSM 1740] emb CAE10120.1 hypothetical protein [Wolinella succinogenes]			
16981, 16982	34558264	55	2.00E-36	Wolinella succinogenes DSM 1740	TRNA DELTA-2-ISOPENTENYL PYROPHOSPHATE [Wolinella succinogenes DSM 1740] emb CAE10979.1 TRNA DELTA-2-ISOPENTENYL PYROPHOSPHATE [Wolinella succinogenes]		2.5.1.8	
16985, 16986	48846313	45	3.00E-37	Geobacter metallireducens GS-15	COG1450: Type II secretory pathway, component Puid [Geobacter metallireducens GS-15]			
16989, 16990	34556574	23	3.00E-15	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09289.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]			
1699, 1700	21226642	31	1.00E-11	Methanosarcina mazel Go1	hypothetical protein MM0540 [Methanosarcina mazel Go1] gb AAM30236.1 conserved protein [Methanosarcina mazel Go1]			
16991, 16992	57169076	28	1.00E-13	Campylobacter coli RM2228	signal-transducing histidine kinase, putative [Campylobacter coli RM2228] gb EAL56225.1 signal-transducing histidine kinase, putative [Campylobacter coli RM2228]		2.7.3.-	
16993, 16994	13475786	38	9.00E-09	Mesorhizobium loti MAFF303099	hypothetical protein ml6953 [Mesorhizobium loti MAFF303099] db BAB53139.1 ml6953 [Mesorhizobium loti MAFF303099]			

16995,	5120987	33	2.00E-09	Gracilaria tenuistipitata var. liui	sec-independent protein translocase-like protein [Gracilaria tenuistipitata var. liui] gb AA779706.1 sec-independent protein translocase-like protein		
16996				Bacteroides fragilis	aminopeptidase C [Bacteroides fragilis YCH46] dbj BAD50108.1		
16999,	53714650	26	3.00E-20	YCH46	aminopeptidase C [Bacteroides fragilis YCH46]		
17000							
17001,				Pyrococcus	hypothetical protein PH0872 [Pyrococcus horikoshii OT3] dbj BAA29966.1		
17002	14590731	32	2.00E-12	horikoshii OT3	500aa long hypothetical protein [Pyrococcus horikoshii OT3] pir H71075		
17003,				Campylobacter coli	hypothetical protein PH0872 - Pyrococcus horikoshii		
17004	57167790	28	3.00E-11	RM2228	tRNA nucleotidyltransferase [Campylobacter coli RM2228] gb EAL57576.1		
17005,				Desulfotribro	tRNA nucleotidyltransferase [Campylobacter coli RM2228]		
17006	23474422	34	3.00E-34	desulfuricans G20	COG0640: Methyl-accepting chemotaxis protein [Desulfotribro desulfuricans G20]		2.7.7.25
17009,							
17010	49089808	57	3.00E-51	Helicobacter pylori	peptide deformylase [Helicobacter pylori]		3.5.1.88
1701,				Magnetococcus sp.	COG0673: Predicted dehydrogenases and related proteins [Magnetococcus sp. MC-1]		
1702	48833968	47	3.00E-56	MC-1			1.1.1.18
17011,				Campylobacter lari	Mg chelatase-related protein [Campylobacter lari RM2100] gb EAL54444.1		
17012	57241774	49	1.00E-30	RM2100	Mg chelatase-related protein [Campylobacter lari RM2100]		
17015,				Cytophaga			
17016	48853625	49	1.00E-55	hutchinsonii	COG4122: Predicted O-methyltransferase [Cytophaga hutchinsonii]		2.1.1.-
17017,					pxo1-96 [Bacillus anthracis] gb AAD32400.1 pXO1-96 [Bacillus anthracis]		
17018					gb AAA74029.1 ORFB [Bacillus anthracis] gb AAA74027.1 ORFB [Bacillus anthracis] pir H59102 hypothetical protein pXO1-96 - Bacillus anthracis virulence plasmid pXO1		
17019,	10956343	41	2.00E-29	Bacillus anthracis	Desc:Helicobacter pylori cellular proliferation protein #241. Org:Helicobacter pylori		4.6.1.4
17020	AAU3592	62	6.00E-46		putative RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD48085.1 putative RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46]		
17021,				Bacteroides fragilis	hypothetical protein glr0227 [Gloeobacter violaceus PCC 7421] dbj BAC88168.1 glr0227 [Gloeobacter violaceus PCC 7421]		
17022	53712627	38	9.00E-13	YCH46	REGULATORY PROTEIN DNIR [Wolinella succinogenes DSM 1740] embi CAE11071.1 REGULATORY PROTEIN DNIR [Wolinella succinogenes]		
17023,				Gloeobacter			
17024	37519796	28	2.00E-11	violaceus PCC			
17025,				Wolinella			
17026	34558356	45	7.00E-26	succinogenes DSM 1740			3.2.1.-
17027,				Geobacter	penicillin-binding protein, 1A family [Geobacter sulfurreducens PCA]		
17028	39998223	48	5.00E-18	sulfurreducens	gb AAR36524.1 penicillin-binding protein, 1A family [Geobacter sulfurreducens PCA]		2.4.2.-

17029, 17030	27377226	45	8.00E-31	110	Bradyrhizobium japonicum USDA	hypothetical protein b1r2115 [Bradyrhizobium japonicum USDA 110] dbj BAC47380.1 b1r2115 [Bradyrhizobium japonicum USDA 110]				
17033, 17034	34558237	39	2.00E-43	1740	Wolonia succinogenes DSM	hypothetical protein WS1946 [Wolonia succinogenes DSM 1740] emb CAE10952.1 hypothetical protein [Wolonia succinogenes]				
17035, 17036	52008197	30	4.00E-18	25259	Thiobacillus denitrificans ATCC	COG3528: Uncharacterized protein conserved in bacteria [Thiobacillus denitrificans ATCC 25259]				
17037, 17038	53712193	32	7.00E-14	YCH46	Bacteroides fragilis	hypothetical protein BF0900 [Bacteroides fragilis YCH46] hypothetical protein [Bacteroides fragilis YCH46]				2.7.3.-
17039, 17040	15838587	25	2.00E-10	9a5c	Xylella fastidiosa	hypothetical protein XF1993 [Xylella fastidiosa 9a5c] gb AAF84795.1 hypothetical protein XF1993 [Xylella fastidiosa 9a5c] pir C82611 hypothetical protein XF1993 [imported] - Xylella fastidiosa (strain 9a5c)				
17041, 17042	21673056	46	2.00E-68	Chlorobium tepidum TLS	Chlorobium	ABC transporter, ATP-binding protein [Chlorobium tepidum TLS] gb AAM71463.1 ABC transporter, ATP-binding protein [Chlorobium tepidum TLS]				3.4.21.-
17043, 17044	15643327	42	2.00E-46	maritima MSB8	Thermotoga	divalent cation transport-related protein [Thermotoga maritima MSB8] gb AAD35646.1 divalent cation transport-related protein [Thermotoga maritima MSB8] pir H72360 divalent cation transport-related protein - Thermotoga maritima (strain MSB8)				
17047, 17048	52140234	35	3.00E-34	Bacillus cereus ZK	Bacillus cereus ZK	modification methylase, HemK family [Bacillus cereus ZK] gb AAU15253.1 modification methylase, HemK family [Bacillus cereus ZK]				2.1.1.-
17051, 17052	20808143	45	2.00E-21	MB4	Thermoanaerobacter tengcongensis	Thiol-disulfide isomerase and thioredoxins [Thermoanaerobacter tengcongensis MB4] gb AAM24918.1 Thiol-disulfide isomerase and thioredoxins [Thermoanaerobacter tengcongensis MB4]				
17053, 17054	21673718	29	7.00E-23	Chlorobium tepidum TLS	Chlorobium	methyltransferase, putative [Chlorobium tepidum TLS] gb AAM72125.1 methyltransferase, putative [Chlorobium tepidum TLS]				1.-.-
17057, 17058	57242467	29	3.00E-24	RM3195	Campylobacter upsaliensis	restriction and modification enzyme CjeI [Campylobacter upsaliensis RM3195] gb EAL53535.1 restriction and modification enzyme CjeI [Campylobacter upsaliensis RM3195]				3.1.21.3
17059, 17060	48853400	52	1.00E-39	hutchinsonii	Cytophaga	COG0732: Restriction endonuclease S subunits [Cytophaga hutchinsonii]				3.1.21.3
17061, 17062	53613391	31	2.00E-29	vinelandii	Azotobacter	COG1357: Uncharacterized low-complexity proteins [Azotobacter vinelandii]				
17065, 17066	34556739	32	3.00E-34	1740	Wolonia succinogenes DSM	hypothetical protein WS0303 [Wolonia succinogenes DSM 1740] emb CAE09454.1 hypothetical protein [Wolonia succinogenes]				

17067, 17068	12517728	42	2.00E-28	Escherichia coli O157:H7	putative tagatose 6-phosphate kinase 2 [Escherichia coli ref NP_289703.1 putative tagatose 6-phosphate kinase 2 [Escherichia coli O157:H7 EDL933] pir B85975 probable tagatose 6-phosphate kinase 2 agaZ [imported] - Escherichia coli (strain O157:H7, substrain EDL933)			2.7.1.14 4
17069, 17070	15643576	27	1.00E-17	Thermotoga maritima MSB8	hypothetical protein TM0813 [Thermotoga maritima MSB8] gb AAD35895.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir F72331 conserved hypothetical protein - Thermotoga maritima (strain MSB8)			2.6.1.16
17071, 17072	51246243	43	2.00E-35	Desulfotalea psychrophila LSV54	probable two-component system sensory/regulatory protein (Ntr family) [Desulfotalea psychrophila LSV54] emb CAG37120.1 probable two- component system sensory/regulatory protein (Ntr family) [Desulfotalea psychrophila LSV54]			2.7.3.-
17075, 17076	48865290	36	3.00E-37	Oenococcus oeni PSU-1	COG1609: Transcriptional regulators [Oenococcus oeni PSU-1] nucleotidyltransferase PLUS glutamate rich protein GrpB PLUS ribosomal protein alanine acetyltransferase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27174.1 nucleotidyltransferase PLUS glutamate rich protein GrpB PLUS ribosomal protein alanine acetyltransferase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			2.3.1.12 8
17079, 17080	30250106	35	3.00E-09	Nitrosomonas europaea ATCC 19718	SAM (and some other nucleotide) binding motif [Nitrosomonas europaea ATCC 19718] emb CAD86083.1 SAM (and some other nucleotide) binding motif [Nitrosomonas europaea ATCC 19718] dTDP-4-dehydrothiamine reductase [Bacillus clausii KSM-K16] db BAD66221.1 dTDP-4-dehydrothiamine reductase [Bacillus clausii KSM- K16]			1.1.1.13 3
17081, 17082	56965450	30	1.00E-14	Bacillus clausii KSM-K16	COG0438: Glycosyltransferase [Cytophaga hutchinsonii]			
17083, 17084	48853395	46	4.00E-26	Cytophaga hutchinsonii	glycosyltransferase WbaZ [Escherichia coli] transposase, similar to IS240 [Methanocaldococcus jannaschii DSM 2661] gb AAB99474.1 transposase, similar to IS240 [Methanocaldococcus jannaschii DSM 2661] pir A64483 hypothetical protein MJ1466 - Methanococcus jannaschii sp Q58861 YE66_METJA Hypothetical protein MJ1466			2.4.1.-
17085, 17086	4512014	51	4.00E-77	Escherichia coli	COG0768: Cell division protein FtsI/penicillin-binding protein 2 [Cytophaga hutchinsonii]			
1709, 1710	15668657	34	7.00E-21	Methanocaldococ- us jannaschii DSM 2661				
17091, 17092	48853585	35	4.00E-30	Cytophaga hutchinsonii				

17093, 17094	34557033	59	1.00E-64	Wolinella succinogenes DSM 1740	GLUTAMINE AMIDOTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09748.1 GLUTAMINE AMIDOTRANSFERASE [Wolinella succinogenes] sp Q7M9X0 HIS5_WOLS5 lmidazole glycerol phosphate synthase subunit hisH (IGP synthase glutamine amidotransferase subunit) (IGP synthase subunit hisH) (mGP synthase subunit hisH) (IGPS subunit hisH)				2.4.2.-
17095, 17096	15896194	26	1.00E-08	Clostridium acetobutylicum ATCC 824	HAD superfamily hydrolase [Clostridium acetobutylicum ATCC 824] gb AAK80883.1 HAD superfamily hydrolase [Clostridium acetobutylicum ATCC 824] pir H97261 HAD superfamily hydrolase [imported] - Clostridium acetobutylicum				
17097, 17098	57240961	63	3.00E-64	Campylobacter lari RM2100	conserved hypothetical protein TIGR00423 [Campylobacter lari RM2100] gb EAL55354.1 conserved hypothetical protein TIGR00423 [Campylobacter lari RM2100]				2.8.1.6
17099, 17100	48854814	79	1.00E-108	Cytophaga hutchinsonii	COG0396: ABC-type transport system involved in Fe-S cluster assembly, ATPase component [Cytophaga hutchinsonii]	Desc:Enterococcus faecalis contig sequence #929. Org:Enterococcus faecalis	81	6.00E-07	1.8.-
171, 172	48855001	31	1.00E-14	Cytophaga hutchinsonii	COG2849: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				2.7.1.68
17105, 17106	48856573	41	2.00E-61	Cytophaga hutchinsonii	COG2207: AraC-type DNA-binding domain-containing proteins [Cytophaga hutchinsonii]				
17109, 17110	34556843	40	8.00E-44	Wolinella succinogenes DSM 1740	hypothetical protein WS0414 [Wolinella succinogenes DSM 1740] emb CAE09558.1 conserved hypothetical protein [Wolinella succinogenes] putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79084.1 putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-
1711, 1712	29349387	50	1.00E-28	Bacteroides thetaitaomicron VPI-5482	rod shape-determining protein (mreC), putative [Campylobacter coli RM2228] gb EAL56879.1 rod shape-determining protein (mreC), putative [Campylobacter coli RM2228]				2.1.1.-
17111, 17112	57168397	31	3.00E-23	Campylobacter coli RM2228	phenylalanyl-tRNA synthetase, beta subunit [Thermotoga maritima MSB8] gb AAD35904.1 phenylalanyl-tRNA synthetase, beta subunit [Thermotoga maritima MSB8] pir A72330 phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - Thermotoga maritima (strain MSB8) sp Q9WZS9 SYFB_THEMEA Phenylalanyl-tRNA synthetase beta chain (Phenylalanine-tRNA ligase beta chain) (PheRS)				
17113, 17114	15843585	44	1.00E-54	Thermotoga maritima MSB8	hypothetical NosD, Nitrous oxidase accessory protein [Photobacterium profundum SS9] emb CAG22720.1 hypothetical NosD, Nitrous oxidase accessory protein [Photobacterium profundum]	Photobacterium profundum SS9 chromosome 2; segment 3/7	79	3.00E-08	6.1.1.20
17115, 17116	54302527	73	6.00E-86	Photobacterium profundum SS9					

17119, 17120 17127, 17128	15644023 46131517	68 36	2.00E-48 8.00E-13	Thermotoga maritima MSB8 Ralstonia eutropha JMP134	thiH protein, putative [Thermotoga maritima MSB8] gb AAD36342.1 thiH protein, putative [Thermotoga maritima MSB8] pir B72274 hypothetical protein TM1267 - Thermotoga maritima (strain MSB8) COG1629: Outer membrane receptor proteins, mostly Fe transport				2.8.1.6
1713, 1714 17131, 17132	29349387 48855487	50 73	1.00E-28 2.00E-37	Bacteroides thetaitaomicron VPI-5482 Cytophaga hutchinsonii	putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79084.1 putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] COG1048: Aconitase A [Cytophaga hutchinsonii]				2.1.1.- 4.2.1.3
17133, 17134	6459446	29	1.00E-21	Deinococcus radiodurans	hypothetical protein [Deinococcus radiodurans] pir G75368 hypothetical protein - Deinococcus radiodurans (strain R1) ref NP_295399.1 hypothetical protein DR1676 [Deinococcus radiodurans R1]				
17135, 17136	9947043	53	1.00E-45	Pseudomonas aeruginosa PAO1	deoxyguanosinetriphosphate triphosphohydrolase [Pseudomonas aeruginosa PAO1] pir H83505 deoxyguanosinetriphosphate triphosphohydrolase PA1124 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_249815.1 deoxyguanosinetriphosphate triphosphohydrolase [Pseudomonas aeruginosa PAO1] sp Q914L1 DGTP_PSEAE Probable deoxyguanosinetriphosphate triphosphohydrolase (dGTPase) (dGTP triphosphohydrolase)				3.1.5.1
17137, 17138	17229920	26	3.00E-13	Nostoc sp. PCC 7120	two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] pir JAE2109 two-component hybrid sensor and regulator alr2428 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB74127.1 two-component hybrid sensor and regulator [Nostoc sp. PCC 7120]				2.7.3.-
17139, 17140	29348537	58	2.00E-59	Bacteroides thetaitaomicron VPI-5482	putative xanthosine triphosphate pyrophosphatase [Bacteroides thetaitaomicron VPI-5482] gb AAO78234.1 putative xanthosine triphosphate pyrophosphatase [Bacteroides thetaiotaomicron VPI-5482]				2.7.7.56
17141, 17142	18309624	40	9.00E-40	Clostridium perfringens str. 13	two-component response regulator [Clostridium perfringens str. 13] dbj BAB80348.1 two-component response regulator [Clostridium perfringens str. 13]				2.7.3.-
17145, 17146	38638619	44	1.00E-36	Burkholderia cenocepacia phage Bcep1	gp12 [Burkholderia cenocepacia phage Bcep1] gb AAQ73358.1 gp12 [Burkholderia cenocepacia phage Bcep1]				
17147, 17148	9654468	44	6.00E-35	Vibrio cholerae O1 biovar eltor str. N16961	sensory box/GGDEF family protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229731.1 sensory box/GGDEF family protein [Vibrio cholerae O1 biovar eltor str. N16961] pir H82367 sensory box/GGDEF family protein VC0072 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				
17149, 17150	51209539	51	6.00E-40	Campylobacter jejuni	cyp27 [Campylobacter jejuni] gb AAR29560.1 cyp27 [Campylobacter jejuni]				

1715, 1716	53731132	40	3.00E-12	Methanococcoides burtonii DSM 6242	COG2097: Ribosomal protein L31E [Methanococcoides burtonii DSM 6242]				
17151, 17152	24214120	37	4.00E-14	Leptospira interrogans serovar Lai str. 56601	hypothetical protein LA1420 [Leptospira interrogans serovar Lai str. 56601] gb AAN48619.1 unknown protein [Leptospira interrogans serovar lai str. 56601]				
17157, 17158	34557543	36	4.00E-39	Wolinella succinogenes DSM 1740	PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10258.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes] emb CAD5552.1 NapL protein [Wolinella succinogenes]				
17163, 17164	34557640	49	8.00E-61	Wolinella succinogenes DSM 1740	POSSIBLE TRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE10355.1 POSSIBLE TRANSFERASE [Wolinella succinogenes]				2.3.2.8
17165, 17166	57241121	39	3.00E-47	Campylobacter lari RM2100	DNA repair protein RecN, putative [Campylobacter lari RM2100] gb EAL54817.1 DNA repair protein RecN, putative [Campylobacter lari RM2100]				
17167, 17168	19338425	41	9.00E-08	Rhizobium leguminosarum bv. viciae	two-component response regulator [Rhizobium leguminosarum bv. viciae]				
17169, 17170	57241290	61	1.00E-40	Campylobacter lari RM2100	Uncharacterized BCR, YceG family COG1559 [Campylobacter lari RM2100] gb EAL54986.1 Uncharacterized BCR, YceG family COG1559 [Campylobacter lari RM2100]	Campylobacter lari subsp. jejuni NCTC 11168 complete genome; segment 2/6	97	3.00E-11	4.---
1717, 1718	48855091	42	3.00E-40	Cytophaga hutchinsonii	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii]				3.1.1.61
17171, 17172	42527788	41	4.00E-50	Treponema denticola ATCC 35405	MazG family protein [Treponema denticola ATCC 35405] gb AAS12805.1 MazG family protein [Treponema denticola ATCC 35405]				
17173, 17174	51246665	37	3.00E-29	Desulfotalea psychrophila LSv54	hypothetical protein DP2813 [Desulfotalea psychrophila LSv54] emb CAG37542.1 conserved hypothetical protein [Desulfotalea psychrophila LSv54]				
17175, 17176	45523887	27	5.00E-09	Crocospira watsonii WH 8501	COG5433: Transposase [Crocospira watsonii WH 8501]				
17179, 17180	50304149	25	6.00E-08	Kluyveromyces lactis	unnamed protein product [Kluyveromyces lactis] emb CAH02417.1 unnamed protein product [Kluyveromyces lactis NRRL Y-1140]				
17185, 17186	21241245	25	6.00E-07	Xanthomonas axonopodis pv. citri str. 306	membrane protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM35363.1 membrane protein [Xanthomonas axonopodis pv. citri str. 306]				

17187, 17188	17228167	30	2.00E-08	Nostoc sp. PCC 7120	WD-repeat protein [Nostoc sp. PCC 7120] dbj BAB72629.1 WD-repeat protein [Nostoc sp. PCC 7120] pir JAF1890 WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120)			
17191, 17192	57158492	31	7.00E-11	Thermococcus kodakaraensis	ribosomal protein-serine acetyltransferase RimL homolog [Thermococcus kodakaraensis] ref YP_182646.1 ribosomal protein-serine acetyltransferase RimL homolog [Thermococcus kodakaraensis]			
17197, 17198	15607008	32	2.00E-17	Aquifex aeolicus VF5	hypothetical protein aq_2027 [Aquifex aeolicus VF5] gb AAC07788.1 hypothetical protein [Aquifex aeolicus VF5] pir J70474 conserved hypothetical protein aq_2027 - Aquifex aeolicus sp O67821 YK27_AQUAE Hypothetical protein Aq_2027			
17199, 17200	34556582	39	4.00E-13	Wolinella succinogenes DSM 1740	PUTATIVE INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09297.1 PUTATIVE INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes]			
17201, 17202	21674385	30	4.00E-14	Chlorobium tepidum TLS	BmrU protein [Chlorobium tepidum TLS] gb AAM72792.1 BmrU protein [Chlorobium tepidum TLS]			
17203, 17204	48853894	44	9.00E-49	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]			
17209, 17210	48860014	40	8.00E-30	Clostridium thermocellum ATCC 27405	COG3321: Polyketide synthase modules and related proteins [Clostridium thermocellum ATCC 27405]			
17213, 17214	34557352	42	8.00E-28	Wolinella succinogenes DSM 1740	hypothetical protein WS0964 [Wolinella succinogenes DSM 1740] emb CAE10067.1 conserved hypothetical protein [Wolinella succinogenes]			2.7.3.-
17215, 17216	34558806	33	3.00E-07	Alvinella pompejana epibiont 6C6	DNA-binding response regulator RprY [Alvinella pompejana epibiont 6C6] DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes]			
17217, 17218	34557665	42	4.00E-36	Wolinella succinogenes DSM 1740	ENSANGP00000019035 [Anopheles gambiae]			2.7.3.-
17219, 17220	31204521	32	5.00E-14	Anopheles gambiae	COG2770: FOG: HAMP domain [Nostoc punctiforme PCC 73102]			4.6.1.1
17221, 17222	23123968	25	1.00E-18	Nostoc punctiforme PCC 73102	Methyl-accepting chemotaxis protein, contain HAMP domain [Clostridium acetobutylicum ATCC 824] gb AAK78885.1 Methyl-accepting chemotaxis protein, contain HAMP domain [Clostridium acetobutylicum ATCC 824] pir B97012 methyl-accepting chemotaxis protein, contain HAMP domain [imported] - Clostridium acetobutylicum			2.7.3.-
17223, 17224	15894196	24	1.00E-06	Clostridium acetobutylicum ATCC 824				2.7.3.-

17225, 17226	34396333	44	6.00E-36	Porphyromonas gingivalis W83	conserved domain protein [Porphyromonas gingivalis W83] ref NP_904501.1 hypothetical protein PG0160 [Porphyromonas gingivalis W83]			
17229, 17230	57242241	43	4.00E-48	NiFe	[NiFe] hydrogenase maturation protein HypF [Campylobacter upsaliensis RM3195] gb EAL53703.1 [NiFe] hydrogenase maturation protein HypF [Campylobacter upsaliensis RM3195]			
1723, 1724	53711817	28	2.00E-20	Bacteroides fragilis YCH46	hypothetical protein BF0526 [Bacteroides fragilis YCH46] dbj BAD47275.1 hypothetical protein [Bacteroides fragilis YCH46]			
17231, 17232	15606085	40	3.00E-35	Aquifex aeolicus VF5	transcriptional regulatory protein HypF [Aquifex aeolicus VF5] gb AAC06863.1 transcriptional regulatory protein HypF [Aquifex aeolicus VF5] pir B70359 transcription regulator HypF - Aquifex aeolicus			
17233, 17234	34558196	33	2.00E-28	Wolinella succinogenes DSM 1740	DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes]			2.7.7.-
17235, 17236	34558196	56	5.00E-80	Wolinella succinogenes DSM 1740	DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes]			2.7.7.-
17239, 17240	32469876	33	4.00E-26	Campylobacter jejuni	VirB4 [Campylobacter jejuni] gb AAN46946.1 VirB4 [Campylobacter jejuni]			
17241, 17242	48846045	36	3.00E-27	Geobacter metallireducens GS- 15	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]			2.7.3.-
17243, 17244	30249663	39	2.00E-49	Nitrosomonas europaea ATCC 19718	possible msrA, pms; peptide methionine sulfoxide reductase [Nitrosomonas europaea ATCC 19718] emb CAD85612.1 possible msrA, pms; peptide methionine sulfoxide reductase [Nitrosomonas europaea ATCC 19718]			1.8.4.6
17245, 17246	ABB4813 5	34	1.00E-17		Desc:Listeria monocytogenes protein #839. Org:Listeria monocytogenes COG1197: Transcription-repair coupling factor (superfamily II helicase)			
17247, 17248	48853984	49	4.00E-62	Cytophaga hutchinsonii	[Cytophaga hutchinsonii]			
17249, 17250	48855632	36	4.00E-13	Cytophaga hutchinsonii	COG0712: F0F1-type ATP synthase, delta subunit (mitochondrial oligomycin sensitivity protein) [Cytophaga hutchinsonii]			3.6.3.14
1725, 1726	53711742	33	5.00E-11	Bacteroides fragilis YCH46	UDP-N-acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate-D-alanyl-D- alanyl ligase [Bacteroides fragilis YCH46] dbj BAD47200.1 UDP-N- acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacteroides fragilis YCH46]			6.3.2.15
17251, 17252	48855632	35	1.00E-25	Cytophaga hutchinsonii	COG0712: F0F1-type ATP synthase, delta subunit (mitochondrial oligomycin sensitivity protein) [Cytophaga hutchinsonii]			3.6.3.15

17257, 17258	34558383	45	4.00E-68	Wollinella succinogenes DSM 1740	RNA POLYMERASE SIGMA-54 FACTOR [Wollinella succinogenes DSM 1740] emb CAE11098.1 RNA POLYMERASE SIGMA-54 FACTOR [Wollinella succinogenes]					
17261, 17262	57168943	59	2.00E-62	Campylobacter coli RM2228	glyceraldehyde-3-phosphate dehydrogenase, type I [Campylobacter coli RM2228] gb EAL56298.1 glyceraldehyde-3-phosphate dehydrogenase, type I [Campylobacter coli RM2228]					1.2.1.12
17263, 17264	53688490	31	2.00E-20	Nostoc punctiforme PCC 73102	COG1100: GTPase SAR1 and related small G proteins [Nostoc punctiforme PCC 73102]					
17265, 17266	34557419	40	4.00E-30	Wollinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes]					2.7.3.-
17269, 17270	46140379	44	5.00E-25	Dechloromonas aromatica RCB	COG0835: Chemotaxis signal transduction protein [Dechloromonas aromatica RCB]					2.7.3.-
1727, 1728	48854018	65	1.00E-120	Cytophaga hutchinsonii	COG0423: Glycyl-tRNA synthetase (class II) [Cytophaga hutchinsonii]	Bacteroides thetaiotaomicron VPI-5482, section 16 of 21 of the complete genome	82	8.00E-16	6.1.1.14	
17271, 17272	48856870	31	6.00E-37	Cytophaga hutchinsonii	COG1555: DNA uptake protein and related DNA-binding proteins [Cytophaga hutchinsonii]					
17273, 17274	34556688	59	9.00E-98	Wollinella succinogenes DSM 1740	ABC TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09403.1 ABC TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wollinella succinogenes]					1.8.-
17275, 17276	56460917	54	9.00E-29	Idiomarina loihensis L2TR	hypothetical protein IL1817 [Idiomarina loihensis L2TR] gb AAV82649.1 Uncharacterized conserved protein [Idiomarina loihensis L2TR]	Vibrio salmonicida partial plasmid pRVS1	82	1.00E-33		
17277, 17278	46401632	42	3.00E-43	Enterobacteria phage P1	Res [Enterobacteria phage P1] gb AAQ14090.1 Res [Enterobacteria phage P1] gb AAQ13982.1 Res [Enterobacteria phage P1] emb CAA29615.1 unnamed protein product [Enterobacteria phage P1] sp P08764 T3RE_BPP1 Type III restriction-modification system EcoPI enzyme res pir S01352 type III site-specific deoxyribonuclease (EC 3.1.21.5) EcoP1 chain res - phage P1					3.1.21.5
17281, 17282	34557246	30	6.00E-33	Wollinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes]					
17283, 17284	48846045	37	1.00E-24	Geobacter metallireducens GS-15	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]					2.7.3.-

17285, 17286	288221	38	1.00E-61	Myxococcus xanthus	ORF2 [Myxococcus xanthus] pilJ[S32169 hypothetical protein 2 - Myxococcus xanthus sp][P54979][CRTJ_MYXXA Phytoene dehydrogenase (Phytoene desaturase)]				
17289, 17290	34556985	38	4.00E-42	Wolinella succinogenes DSM 1740	EXODEOXYRIBONUCLEASE VII LARGE SUBUNIT [Wolinella succinogenes DSM 1740] emb[CAE09700.1] EXODEOXYRIBONUCLEASE VII LARGE SUBUNIT [Wolinella succinogenes]				3.1.1.1.6
17291, 17292	56707780	57	2.00E-73	Francisella tularensis subsp. tularensis Schu 4	DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis Schu 4] emb[CAG45292.1] DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis]				
17295, 17296	39997909	34	2.00E-16	Geobacter sulfurreducens PCA	sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] gbJAAR36210.1] sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA]				
17297, 17298	57237364	33	3.00E-40	Campylobacter jejuni RM1221	membrane protein, putative [Campylobacter jejuni RM1221] gbJAAW34947.1] membrane protein, putative [Campylobacter jejuni RM1221]				
17299, 17300	29348366	41	8.00E-59	Bacteroides thetaiotaomicron VPI-5482	transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] gbJAAO78063.1] transcriptional regulator [Bacteroides thetaiotaomicron VPI- 5482]				
173, 174	21242456	41	1.00E-24	Xanthomonas axonopodis pv. citri str. 306	general stress protein [Xanthomonas axonopodis pv. citri str. 306] gbJAAW36574.1] general stress protein [Xanthomonas axonopodis pv. citri str. 306]				
17301, 17302	48853414	40	1.00E-64	Cytophaga hutchinsonii	COG0686: Alanine dehydrogenase [Cytophaga hutchinsonii]				1.5.1.7
17303, 17304	48855884	40	4.00E-22	Cytophaga hutchinsonii	COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii]				
17305, 17306	48856096	57	4.00E-70	Cytophaga hutchinsonii	COG3129: Predicted SAM-dependent methyltransferase [Cytophaga hutchinsonii]				
17307, 17308	48846045	37	1.00E-29	Geobacter metallireducens GS	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]				2.7.3.-
17309, 17310	46143327	42	2.00E-39	Actinobacillus pleuropneumoniae serovar 1 str. 4074	COG0514: Superfamily II DNA helicase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]				3.6.1.-
1731, 1732	53715782	59	7.00E-91	Bacteroides fragilis YCH46	methionyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj[BAD51240.1] methionyl-tRNA synthetase [Bacteroides fragilis YCH46]	Mus musculus cDNA clone IMAGE:30025832	80	8.00E-25	6.1.1.10
17313, 17314	48895665	48	5.00E-30	Trichodesmium erythraeum IMS101	COG0286: Type I restriction-modification system methyltransferase subunit [Trichodesmium erythraeum IMS101]				2.1.1.72

17315, 17316	34556743	50	4.00E-52	Wolinella succinogenes DSM 1740	hypothetical protein WS0307 [Wolinella succinogenes DSM 1740] emb CAE09458.1 hypothetical protein [Wolinella succinogenes]				
17317, 17318	48892769	34	6.00E-08	Trichodesmium erythraeum IMS101	COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101]				
17319, 17320	29349261	35	1.00E-38	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3853 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78958.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482]				
17321, 17322	46142296	61	1.00E-109	Methanococcoides burtonii DSM 6242	COG4804: Uncharacterized conserved protein [Methanococcoides burtonii DSM 6242]				
17327, 17328	48833879	26	2.00E-17	Magnetococcus sp. MC-1	COG0525: Valyl-tRNA synthetase [Magnetococcus sp. MC-1]				
17329, 17330	ABB4802 6	51	4.00E-46			Clostridium acetobutylicum ATCC 824 section 254 of 356 of the complete genome	87	1.00E-09	2.4.1.8
1733, 1734	AAU3655 0	30	4.00E-19		Desc:Listeria monocytogenes protein #730. Org:Listeria monocytogenes Desc:Staphylococcus aureus cellular proliferation protein #720. Org:Staphylococcus aureus				
17331, 17332	23472835	37	3.00E-16	Pseudomonas syringae pv. syringae B728a	hypothetical protein Psyr03004990 [Pseudomonas syringae pv. syringae B728a]				
17333, 17334	48859668	30	2.00E-24	Clostridium thermocellum ATCC 27405	COG1451: Predicted metal-dependent hydrolase [Clostridium thermocellum ATCC 27405]				3.4.24.-
17335, 17336	57240288	48	2.00E-59	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55402.1 conserved hypothetical protein [Campylobacter lari RM2100]				
17337, 17338	46142567	51	8.00E-30	Methanococcoides burtonii DSM 6242	COG0270: Site-specific DNA methylase [Methanococcoides burtonii DSM 6242]				2.1.1.73
17339, 17340	46142567	38	3.00E-31	Methanococcoides burtonii DSM 6242	COG0270: Site-specific DNA methylase [Methanococcoides burtonii DSM 6242]				2.1.1.73
17343, 17344	34556481	27	1.00E-18	Wolinella succinogenes DSM 1740	hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes]				

17345, 17346	34556481	43	1.00E-41	Wolinella succinogenes DSM 1740	hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes]			2.7.3.-
17349, 17350	51245709	40	6.00E-10	Desulfotalea psychrophila LSV54	hypothetical protein DP1857 [Desulfotalea psychrophila LSV54] emb CAG36586.1 hypothetical protein [Desulfotalea psychrophila LSV54]			2.3.1.51
1735, 1736	48847199	50	5.00E-55	Geobacter metallireducens GS-15	COG0861: Membrane protein TerC, possibly involved in tellurium resistance [Geobacter metallireducens GS-15]			
17351, 17352	48859385	24	9.00E-18	Clostridium thermocellum ATCC 27405	COG0858: Predicted membrane metal-binding protein [Clostridium thermocellum ATCC 27405]			
17353, 17354	29347784	44	2.00E-21	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT2374 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77481.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
17355, 17356	4234793	27	1.00E-09	Leptospira borgpetersenii	unknown [Leptospira borgpetersenii]			
17357, 17358	45657982	49	5.00E-20	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	sugar transferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711831.1 hemolysin hemolytic protein hlpA [Leptospira interrogans serovar Lai str. 56601] gb AA448849.1 hemolysin hemolytic protein hlpA [Leptospira interrogans serovar lai str. 56601] gb AAK19900.1 unknown [Leptospira interrogans] gb AAD52178.1 unknown [Leptospira interrogans] gb AAS70705.1 sugar transferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			
17359, 17360	48855350	32	3.00E-19	Cytophaga hutchinsonii	COG2849: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
17361, 17362	15605941	48	3.00E-52	Aquifex aeolicus VF5	hypothetical protein aq_321 [Aquifex aeolicus VF5] gb AAC06618.1 putative protein [Aquifex aeolicus VF5] pir [F70328 hypothetical protein aq_321 - Aquifex aeolicus]			
17363, 17364	20806660	49	1.00E-50	Thermoanaerobact er tengcongensis MB4	Hydrogenase maturation factor [Thermoanaerobacter tengcongensis MB4] gb AAM23435.1 Hydrogenase maturation factor [Thermoanaerobacter tengcongensis MB4]			3.6.1.7
17365, 17366	46580951	39	3.00E-26	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	transcriptional regulator, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS97019.1 transcriptional regulator, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			
17367, 17368	31615651	33	1.00E-06		Chain B, Design Of Stable Alpha-Helical Arrays From An Idealized Tpr Motif pdb 1NA0 A Chain A, Design Of Stable Alpha-Helical Arrays From An Idealized Tpr Motif			

17369, 17370	48855217	37	2.00E-39	Cytophaga hutchinsonii	COG5635: Predicted NTPase (NACHT family) [Cytophaga hutchinsonii]			
1737, 1738	48847199	46	2.00E-48	Geobacter metallireducens GS-15	COG0861: Membrane protein TerC, possibly involved in tellurium resistance [Geobacter metallireducens GS-15]			
17371, 17372	23506369	31	6.00E-10	Francisella tularensis subsp. novicida	galactose epimerase [Francisella tularensis subsp. novicida]			5.1.3.2
17373, 17374	17940062	42	2.00E-32	Leptospira interrogans	unknown [Leptospira interrogans]			2.4.1.-
17375, 17376	39996515	41	2.00E-57	Geobacter sulfurreducens PCA	sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] gblAAR34789.1] sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA]			2.7.3.-
17377, 17378	52548677	37	5.00E-07	uncultured archaeon GZfos18C8	hypothetical protein GZ18C8_3 [uncultured archaeon GZfos18C8]			
17379, 17380	48858932	43	2.00E-41	Clostridium thermocellum ATCC 27405	COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405]			2.7.3.-
17381, 17382	34556868	28	5.00E-23	Wolinella succinogenes DSM 1740	hypothetical protein WS0441 [Wolinella succinogenes DSM 1740] embjCAE09583.1] conserved hypothetical protein [Wolinella succinogenes] PUTATIVE HOLLIDAY JUNCTION DNA HELICASE [Wolinella succinogenes DSM 1740] embjCAE09582.1] PUTATIVE HOLLIDAY JUNCTION DNA HELICASE [Wolinella succinogenes] spjQ7MA70 RUVA_WOLSU Holliday junction DNA helicase ruva			
17383, 17384	34556867	50	2.00E-38	Wolinella succinogenes DSM 1740	rfbL protein [Vibrio cholerae O1 biovar eltor str. N16961] refjNP_229906.1] rfbL protein [Vibrio cholerae O1 biovar eltor str. N16961] embjCAA42142.1] rfbL [Vibrio cholerae] pirjS28476 rfbL protein VC0249 [similarity] - Vibrio cholerae (strain N16961 serogroup O1) prfj2203284B rfbL gene			6.2.1.3
17385, 17386	9654658	25	4.00E-13	Vibrio cholerae O1 biovar eltor str. N16961	hypothetical protein WS0802 [Wolinella succinogenes DSM 1740] embjCAE09915.1] conserved hypothetical protein [Wolinella succinogenes] probable acylaminoacyl-peptidase [Rhodopirellula baltica SH 1] embjCAD71387.1] probable acylaminoacyl-peptidase [Pirellula sp.] 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE [Wolinella succinogenes DSM 1740] embjCAE10998.1] 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE [Wolinella succinogenes] spjQ7M720jDXS_WOLSU 1-deoxy-D-xylulose-5-phosphate synthase (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS)			
17389, 17390	34557200	31	2.00E-30	Wolinella succinogenes DSM 1740				
1739, 1740	32470723	27	7.00E-22	Rhodopirellula baltica SH 1				
17391, 17392	34558283	67	1.00E-105	Wolinella succinogenes DSM 1740				4.1.3.37

17393, 17394	AAU3592 8	58	6.00E-66			Desc: Helicobacter pylori cellular proliferation protein #241. Org: Helicobacter pylori			4.6.1.4
17395, 17396	57240635	41	2.00E-36	Campylobacter lari RM2100		peptidase, M23/M37 family [Campylobacter lari RM2100] gb EAL55749.1 peptidase, M23/M37 family [Campylobacter lari RM2100]			
17397, 17398	20808841	47	2.00E-59	Thermoanaerobact er tengcongensis MB4		NADH dehydrogenase, FAD-containing subunit [Thermoanaerobacter tengcongensis MB4] NADH dehydrogenase, FAD-containing subunit [Thermoanaerobacter tengcongensis MB4]			1.6.99.3
17399, 17400	53715372	67	1.00E-45	Bacteroides fragilis YCH46		putative GTP-binding protein [Bacteroides fragilis YCH46] dbj BAD50830.1 putative GTP-binding protein [Bacteroides fragilis YCH46]			
17401, 17402	48845271	43	4.00E-43	Geobacter metallireducens GS 15		COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]			2.7.3.-
17403, 17404	55822185	49	1.00E-37	Streptococcus thermophilus CNRZ1066		undecaprenyl pyrophosphate synthetase [Streptococcus thermophilus CNRZ1066] ref YP_138737.1 undecaprenyl pyrophosphate synthetase [Streptococcus thermophilus LMG 18311] gb AAV61811.1 undecaprenyl pyrophosphate synthetase [Streptococcus thermophilus CNRZ1066] gb AAV59922.1 undecaprenyl pyrophosphate synthetase [Streptococcus thermophilus LMG 18311]			2.5.1.31
17411, 17412	37519590	36	6.00E-44	Geobacter violaceus PCC 7421		HlyB/MsbA family ABC transporter [Geobacter violaceus PCC 7421] dbj BAC87962.1 HlyB/MsbA family ABC transporter [Geobacter violaceus PCC 7421]			3.4.21.-
17413, 17414	34557946	43	2.00E-29	Wolinella succinogenes DSM 1740		RESPONSE REGULATOR PROTEIN-CheY-like nd an HD-GYP domain [Wolinella succinogenes DSM 1740] emb CAE10661.1 RESPONSE REGULATOR PROTEIN-CheY-like nd an HD-GYP domain [Wolinella succinogenes]			2.7.3.-
17415, 17416	34557665	50	4.00E-39	Wolinella succinogenes DSM 1740		DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10380.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes]			2.7.3.-
17417, 17418	34558399	44	9.00E-26	Wolinella succinogenes DSM 1740		3-DEOXY-D-MANNO-OCTULOSONIC-ACID TRANSFERASE KDTA [Wolinella succinogenes DSM 1740] emb CAE11114.1 3-DEOXY-D-MANNO-OCTULOSONIC-ACID TRANSFERASE KDTA [Wolinella succinogenes]			2.4.99.-
17419, 17420	16330004	37	4.00E-34	Synechocystis sp. PCC 6803		hypothetical protein slr2077 [Synechocystis sp. PCC 6803] dbj BAA17412.1 slr2077 [Synechocystis sp. PCC 6803] pir S77565 hypothetical protein slr2077 - Synechocystis sp. (strain PCC 6803)			

17421, 17422	15895797	40	2.00E-20	Clostridium acetobutylicum ATCC 824	HD_GYP hydrolase domain fused to HD hydrolase domain [Clostridium acetobutylicum ATCC 824] gb AAK80486.1 HD_GYP hydrolase domain fused to HD hydrolase domain [Clostridium acetobutylicum ATCC 824] pir C97212 HD_GYP hydrolase domain fused to HD hydrolase domain [imported] - Clostridium acetobutylicum			
17423, 17424	54301944	38	2.00E-44	Photobacterium profundum SS9	putative response regulator protein [Photobacterium profundum SS9] emb CAG22137.1 putative response regulator protein [Photobacterium profundum]			2.7.3.-
17427, 17428	46202456	36	2.00E-58	Magnetospirillum magnetotacticum MS-1	COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1]			2.7.3.-
17429, 17430	48853400	53	7.00E-44	Cytophaga hutchinsonii	COG0732: Restriction endonuclease S subunits [Cytophaga hutchinsonii]			3.1.21.-
1743, 1744	22797876	45	2.00E-62	uncultured crenarchaeote	putative alpha/beta hydrolase [uncultured crenarchaeote]			3.7.1.-
17431, 17432	48853400	56	5.00E-33	Cytophaga hutchinsonii	COG0732: Restriction endonuclease S subunits [Cytophaga hutchinsonii]			3.1.21.3
17433, 17434	17938569	37	3.00E-12	Agrobacterium tumefaciens str. C58	transcriptional regulator, AraC family [Agrobacterium tumefaciens str. C58] gb AAL45674.1 transcriptional regulator, AraC family [Agrobacterium tumefaciens str. C58] pir AD3157 transcription regulator, AraC family Atu4880 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)			
17437, 17438	34557782	39	4.00E-41	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]			2.7.3.-
17439, 17440	53713728	40	2.00E-21	Bacteroides fragilis YCH46	putative protease [Bacteroides fragilis YCH46] dbj BAD49186.1 putative protease [Bacteroides fragilis YCH46]			3.4.21.-
17443, 17444	48833126	35	3.00E-25	Magnetococcus sp. MC-1	COG1355: Predicted dioxygenase [Magnetococcus sp. MC-1]			
17447, 17448	27382617	34	3.00E-30	Bradyrhizobium japonicum USDA 110	hypothetical protein bli7506 [Bradyrhizobium japonicum USDA 110] dbj BAC5277.1 bli7506 [Bradyrhizobium japonicum USDA 110]			3.1.-
17449, 17450	15894828	64	3.00E-50	Clostridium acetobutylicum ATCC 824	Methionine sulfoxide reductase C-terminal domain related protein, YPPQ ortholog [Clostridium acetobutylicum ATCC 824] gb AAK79517.1 Methionine sulfoxide reductase C-terminal domain related protein, YPPQ ortholog [Clostridium acetobutylicum ATCC 824] pir B97091 methionine sulfoxide reductase C-terminal domain related protein, YPPQ ortholog [imported] - Clostridium acetobutylicum sp Q971U0 MSRB_CLOAB Peptide methionine sulfoxide reductase msrB			1.8.4.6

1745,	48847433	42	2.00E-49	15	Geobacter metallireducens GS	COG0058: Glucan phosphorylase [Geobacter metallireducens GS-15]				2.4.1.1
1746						probable phosphate acetyltransferase [Desulfotalea psychrophila LSV54]				
17451,					Desulfotalea	emb CAG35287.1 probable phosphate acetyltransferase [Desulfotalea				
17452	51244410	32	1.00E-35		psychrophila LSV54	psychrophila LSV54]				2.3.1.8
17453,						probable phosphate acetyltransferase [Desulfotalea psychrophila LSV54]				
17454	51244410	29	3.00E-26		Desulfotalea	emb CAG35287.1 probable phosphate acetyltransferase [Desulfotalea				2.3.1.8
					psychrophila LSV54]	psychrophila LSV54]				
17457,					Chlorobium	rubredoxin:oxygen oxidoreductase, putative [Chlorobium tepidum TLS]				
17458	21675091	54	1.00E-85		tepidum TLS	gb AAM73498.1 rubredoxin:oxygen oxidoreductase, putative [Chlorobium				
					Campylobacter coli	tepidum TLS]				
17459,					RM2228	probable flagellar protein Cj1312 [Campylobacter coli RM2228]				
17460	57168227	41	2.00E-31		Campylobacter coli	gb EAL57270.1 probable flagellar protein Cj1312 [Campylobacter coli				
17461,					Cytophaga	RM2228]				
17462	48855342	64	1.00E-105		hutchinsonii	COG0612: Predicted Zn-dependent peptidases [Cytophaga hutchinsonii]				3.4.---
17463,					Cytophaga					
17464	48854183	66	2.00E-94		hutchinsonii	COG0438: Glycosyltransferase [Cytophaga hutchinsonii]				
					Bacteroides	threonine synthase [Bacteroides thetaiotaomicron VPI-5482]				
17469,					thetataomicron	gb AAO77508.1 threonine synthase [Bacteroides thetaiotaomicron VPI-				4.2.99.2
17470	29347811	58	7.00E-81		VPI-5482	5482]				
					Bacteroides	threonine synthase [Bacteroides thetaiotaomicron VPI-5482]				
17471,					thetataomicron	gb AAO77508.1 threonine synthase [Bacteroides thetaiotaomicron VPI-				4.2.99.2
17472	29347811	44	7.00E-41		VPI-5482	5482]				
					Desulfovibrio	glycerophosphoryl diester phosphodiesterase family protein [Desulfovibrio				
17473,					vulgaris subsp.	vulgaris subsp. vulgaris str. Hildenborough] gb AAS94660.1				
17474	46578593	34	2.00E-32		vulgaris str.	glycerophosphoryl diester phosphodiesterase family protein [Desulfovibrio				3.1.4.46
					Hildenborough	vulgaris subsp. vulgaris str. Hildenborough]				
					Clostridium					
17475,					thermocellum	COG1905: NADH:ubiquinone oxidoreductase 24 kD subunit [Clostridium				1.6.5.3
17476	48858102	46	4.00E-37		ATCC 27405	thermocellum ATCC 27405]				
					Desulfotalea					
17477,					hafnense DCB-2	COG0095: Lipote-protein ligase A [Desulfotalea hafnense DCB-2]				6.---
17478	53685137	59	1.00E-66		Thermoanaerobact	transposase [Thermoanaerobacter tengcongensis MB4] gb AAM24980.1				
					er tengcongensis	transposase [Thermoanaerobacter tengcongensis MB4]				
17479,					MB4					
17480	20808205	29	2.00E-21		Cytophaga					
17481,					hutchinsonii					
17482	48855753	47	1.00E-33			COG0058: Glucan phosphorylase [Cytophaga hutchinsonii]				2.4.1.1

17483, 17484	34557416	62	3.00E-31	1740	Wollinella succinogenes DSM 1740	PHOSPHOGLYCERATE KINASE [Wollinella succinogenes DSM 1740] emb CAE10131.1 PHOSPHOGLYCERATE KINASE [Wollinella succinogenes] sp Q7M9C1 PGK_WOLSU Phosphoglycerate kinase	Dictyostellium discoideum phosphoglycerate kinase (pgkA) mRNA, complete cds	91	1.00E-09	2.7.2.3
17485, 17486	52841303	39	2.00E-49	1740	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	AbiD phage protein-like [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27155.1 AbiD phage protein-like [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]				
17487, 17488	53729000	27	1.00E-10	4074	Actinobacillus pleuropneumoniae serovar 1 str. 4074	hypothetical protein Aple02000727 [Actinobacillus pleuropneumoniae serovar 1 str. 4074]				
17491, 17492	46580427	27	2.00E-25	1740	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	hypothetical protein DVU2020 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96495.1 conserved hypothetical protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]				
17493, 17494	20807204	44	3.00E-62	MB4	Thermoanaerobact er tengcongensis MB4	NtrC family Transcriptional regulator, ATPase domain [Thermoanaerobacter tengcongensis MB4] gb AAM23979.1 NtrC family Transcriptional regulator, ATPase domain [Thermoanaerobacter tengcongensis MB4]				
17497, 17498	48855019	43	1.00E-35	hutchinsonii	Cytophaga hutchinsonii	COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii]				2.4.1.18 2
17499, 17500	48853636	48	4.00E-35	hutchinsonii	Cytophaga hutchinsonii	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii]				2.7.3.-
175, 176	48853385	45	2.00E-18	hutchinsonii	Cytophaga hutchinsonii	hypothetical protein Chut02003884 [Cytophaga hutchinsonii]				
17503, 17504	37680074	35	2.00E-09	YJ016	Vibrio vulnificus YJ016	hypothetical protein VV1890 [Vibrio vulnificus YJ016] db BAC94654.1 hypothetical protein [Vibrio vulnificus YJ016]				
17505, 17506	57240635	48	3.00E-68	RM2100	Campylobacter lari RM2100	peptidase, M23/M37 family [Campylobacter lari RM2100] gb EAL55749.1 peptidase, M23/M37 family [Campylobacter lari RM2100]				3.5.1.-
17507, 17508	57240635	42	1.00E-49	RM2100	Campylobacter lari RM2100	peptidase, M23/M37 family [Campylobacter lari RM2100] gb EAL55749.1 peptidase, M23/M37 family [Campylobacter lari RM2100]				
17509, 17510	34556616	44	2.00E-35	1740	Wollinella succinogenes DSM 1740	CATION EFFLUX (ACRB/ACRDI/ACRF FAMILY) [Wollinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRDI/ACRF FAMILY) [Wollinella succinogenes]				

1751,	AAU3668	50	3.00E-69			Desc: Staphylococcus aureus cellular proliferation protein #857. Org: Staphylococcus aureus			4.1.1.49
1752	7								
17513,									
17514	34557339	43	5.00E-18	Wolinetia succinogenes DSM 1740		SENSORY TRANSDUCTION REGULATOR [Wolinetia succinogenes DSM 1740] emb CAE10054.1 SENSORY TRANSDUCTION REGULATOR [Wolinetia succinogenes]			
17515,									
17516	48844440	24	4.00E-18	Geobacter metallireducens GS-15		COG0859: ADP-heptose:LPS heptosyltransferase [Geobacter metallireducens GS-15]			
17517,									
17518	42527456	58	8.00E-76	Treponema denticola ATCC 35405		metallo-beta-lactamase family protein [Treponema denticola ATCC 35405] gb AAS12465.1 metallo-beta-lactamase family protein [Treponema denticola ATCC 35405] sp Q73LB4 RNZ_TREDE Ribonuclease Z (RNase Z) (RNase Z) (RNA 3 endonuclease)			
17519,									
17520	53713699	30	3.00E-37	Bacteroides fragilis YCH46		putative patatin-like phospholipase [Bacteroides fragilis YCH46] dbj BAD49157.1 putative patatin-like phospholipase [Bacteroides fragilis YCH46]			
17521,									
17522	53731000	92	2.00E-67	Methanococcoides burtonii DSM 6242		COG0661: Predicted unusual protein kinase [Methanococcoides burtonii DSM 6242]			
17523,									
17524	45358779	34	1.00E-31	Methanococcus maripaludis S2		Histidinol-phosphate aminotransferase [Methanococcus maripaludis S2] emb CAF30772.1 Histidinol-phosphate aminotransferase [Methanococcus maripaludis S2] sp P61003 HIS8_METMP Histidinol-phosphate aminotransferase (mldazole acetol-phosphate transaminase)		2.6.1.9	
17525,									
17526	27525016	31	2.00E-13	Bacillus circulans		BtrN protein [Bacillus circulans] dbj BAC41205.1 BtrN [Bacillus circulans]			
17527,									
17528	34557232	37	8.00E-16	Wolinetia succinogenes DSM 1740		NIFS PROTEIN (FRAGMENT) [Wolinetia succinogenes DSM 1740] emb CAE09947.1 NIFS PROTEIN (FRAGMENT) [Wolinetia succinogenes]		4.4.1.-	
1753,									
1754	53712185	41	2.00E-49	Bacteroides fragilis YCH46		alanine racemase [Bacteroides fragilis YCH46] dbj BAD47643.1 alanine racemase [Bacteroides fragilis YCH46]		6.3.2.15	
17531,									
17532	48890454	36	4.00E-22	Trichodesmium erythraeum IMS101		COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101]			
17533,									
17534	22960166	55	2.00E-99	Rhodobacter sphaeroides 2.4.1		COG3825: Uncharacterized protein conserved in bacteria [Rhodobacter sphaeroides 2.4.1]			
17535,									
17536	39996008	41	6.00E-15	Geobacter sulfurreducens PCA		hypothetical protein GSJ0905 [Geobacter sulfurreducens PCA] gb AAR34232.1 hypothetical protein GSJ0905 [Geobacter sulfurreducens PCA]			
17539,									
17540	20809022	26	5.00E-12	Thermoanaerobacter tengcongensis MB4		hypothetical protein TTE2678 [Thermoanaerobacter tengcongensis MB4] gb AAM25797.1 hypothetical protein TTE2678 [Thermoanaerobacter tengcongensis MB4]		4.1.99.-	

17541, 17542	28899897	46	4.00E-37	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VPA0042 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61385.1 hypothetical protein [Vibrio parahaemolyticus]				
17543, 17544	28212141	62	1.00E-69	Clostridium tetani E88	methylaspartate ammonia-lyase [Clostridium tetani E88] gb AAO37022.1 methylaspartate ammonia-lyase [Clostridium tetani E88]				
17545, 17546	21242902	40	1.00E-11	Xanthomonas axonopodis pv. citri str. 306	two-component system sensor protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM37020.1 two-component system sensor protein [Xanthomonas axonopodis pv. citri str. 306]				
17549, 17550	29346178	39	4.00E-24	Bacteroides thetaiotaomicron VPI-5482	putative para-aminobenzoate synthase component I [Bacteroides thetaiotaomicron VPI-5482] gb AAO75875.1 putative para-aminobenzoate synthase component I [Bacteroides thetaiotaomicron VPI-5482]				4.---
1755, 1756	42523059	57	1.00E-55	Bdellovibrio bacteriovorus HD100	probable zinc proteinase [Bdellovibrio bacteriovorus HD100] emb CAE79432.1 probable zinc proteinase [Bdellovibrio bacteriovorus HD100]				3.4.99.-
17555, 17556	19705092	26	1.00E-08	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Tetratricopeptide repeat family protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93886.1 Tetratricopeptide repeat family protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]	Homo sapiens BAC clone RP11-457D4 from 2, complete sequence	97	4.00E-07	
17557, 17558	34557437	45	7.00E-57	Wolinella succinogenes DSM 1740	FLAGELLAR BIOSYNTHESIS/REGULATION PROTEIN FLBA [Wolinella succinogenes DSM 1740] emb CAE107152.1 FLAGELLAR BIOSYNTHESIS/REGULATION PROTEIN FLBA [Wolinella succinogenes]				
17559, 17560	57240611	63	5.00E-40	Campylobacter lari RM2100	phosphoenolpyruvate carboxykinase (ATP) [Campylobacter lari RM2100] gb EAL55725.1 phosphoenolpyruvate carboxykinase (ATP) [Campylobacter lari RM2100]				4.1.1.49
17565, 17566	34557324	21	6.00E-20	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10039.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]				
17567, 17568	34556675	46	9.00E-26	Wolinella succinogenes DSM 1740	hypothetical protein WS0233 [Wolinella succinogenes DSM 1740] emb CAE09390.1 conserved hypothetical protein [Wolinella succinogenes]				
17569, 17570	34556675	35	2.00E-12	Wolinella succinogenes DSM 1740	hypothetical protein WS0233 [Wolinella succinogenes DSM 1740] emb CAE09390.1 conserved hypothetical protein [Wolinella succinogenes]				
17571, 17572	48854303	32	2.00E-12	Cytophaga hutchinsonii	COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii]				

17573, 17574	42525591	29	5.00E-11	Treponema denticola ATCC 35405	methyl-accepting chemotaxis protein [Treponema denticola ATCC 35405] gb AAS10570.1 methyl-accepting chemotaxis protein [Treponema denticola ATCC 35405]				
17577, 17578	34556775	67	4.00E-89	Wolinella succinogenes DSM 1740	UTP-GLUCOSE-1-PHOSPHATE URIDYL TRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09490.1 UTP-GLUCOSE-1- PHOSPHATE URIDYL TRANSFERASE [Wolinella succinogenes]				2.7.7.9
17579, 17580	15920920	42	6.00E-56	Sulfolobus tokodaii str. 7	hypothetical protein ST0692 [Sulfolobus tokodaii str. 7] dbj BAB65698.1 470aa long conserved hypothetical protein [Sulfolobus tokodaii str. 7]				2.3.1.48
17581, 17582	57505845	59	2.00E-52	Campylobacter upsaliensis RM3195	GTP cyclohydrolase II [Campylobacter upsaliensis RM3195] gb EAL52664.1 GTP cyclohydrolase II [Campylobacter upsaliensis RM3195]				3.5.4.25
17583, 17584	34556603	39	3.00E-21	Wolinella succinogenes DSM 1740	DKSA-LIKE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09318.1 DKSA-LIKE PROTEIN [Wolinella succinogenes]				
17587, 17588	32261568	32	1.00E-16	Helicobacter hepaticus ATCC 51449	two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] ref NP_859552.1 two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449]				2.7.3.-
17589, 17590	34558196	34	6.00E-33	Wolinella succinogenes DSM 1740	DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes]				2.7.7.-
1759, 1760	34895012	45	8.00E-65	Oryza sativa (japonica cultivar- group)	putative polyprotein [Oryza sativa (japonica cultivar-group)]				3.4.23.-
17591, 17592	34558196	52	2.00E-60	Wolinella succinogenes DSM 1740	DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes]				2.7.7.-
17593, 17594	48833487	50	3.00E-32	Magnetococcus sp. MC-1	COG2326: Uncharacterized conserved protein [Magnetococcus sp. MC-1]				2.-.-.-
17595, 17596	34556523	60	5.00E-99	Wolinella succinogenes DSM 1740	hypothetical protein WS0069 [Wolinella succinogenes DSM 1740] emb CAE09238.1 conserved hypothetical protein [Wolinella succinogenes]				
17597, 17598	34397452	57	5.00E-74	Porphyromonas gingivalis W83	type I restriction-modification system, M subunit, putative [Porphyromonas gingivalis W83] ref NP_905615.1 type I restriction-modification system, M subunit, putative [Porphyromonas gingivalis W83]	Porphyromonas gingivalis W83 section 6 of 8 of the complete genome	86	1.00E-07	2.1.1.72

17599, 17600	12964608	56	4.00E-78	Clostridium difficile	formylglycinamide ribonucleotide synthetase (FGAM synthetase) [Clostridium difficile] probable ATP-dependent DNA helicase [Azoarcus sp. EbN1] emb CA109453.1 probable ATP-dependent DNA helicase [Azoarcus sp. EbN1]	Clostridium difficile purL gene for formylglycinamide ribonucleotide synthetase (FGAM synthetase), complete cds	88	3.00E-21	6.3.5.3
17603, 17604	56478765	54	2.00E-39	Azoarcus sp. EbN1	aldose 1-epimerase [Rhodopirellula baltica SH 1] emb CAD74867.1 aldose 1-epimerase [Pirellula sp.]				3.6.1.-
17605, 17606	32474327	42	7.00E-47	Rhodopirellula baltica SH 1	ribulose-phosphate 3-epimerase [Campylobacter jejuni RM1221] gb AAW35088.1 ribulose-phosphate 3-epimerase [Campylobacter jejuni RM1221]				5.1.3.3
17607, 17608	57237505	29	1.00E-13	Campylobacter jejuni RM1221	Sigma factor sigB regulation protein rsbU [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] protein rsbU [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] adenylosuccinate synthetase [Porphyromonas gingivalis W83] ref NP_904762.1 adenylosuccinate synthetase [Porphyromonas gingivalis W83] sp Q7MWW8 PURA_PORGI Adenylosuccinate synthetase (IMP-aspartate ligase) (AdSS) (AMPSase)				5.1.3.1
17609, 17610	19704426	29	1.00E-23	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	DNA polymerase I [Rhodopirellula baltica SH 1] emb CAD77785.1 DNA polymerase I [Pirellula sp.]				3.1.3.16
1761, 1762	34396595	63	3.00E-39	Porphyromonas gingivalis W83	polysaccharide deacetylase family protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]				6.3.4.4
17617, 17618	32477714	52	7.00E-70	Rhodopirellula baltica SH 1	putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD47859.1 , putative glycosyltransferase [Bacteroides fragilis YCH46] hypothetical protein HH0918 [Helicobacter hepaticus ATCC 51449] ref NP_860449.1 hypothetical protein HH0918 [Helicobacter hepaticus ATCC 51449]				2.7.7.7
17619, 17620	46562204	32	1.00E-11	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough					3.5.1.-
17623, 17624	53712401	42	1.00E-18	Bacteroides fragilis YCH46					
17625, 17626	32262467	41	3.00E-17	Helicobacter hepaticus ATCC 51449					

17627, 17628	47778153	42	3.00E-22	Bacillus anthracis str. 'Ames Ancestor'	abc transporter, atp-binding protein [Bacillus anthracis str. 'Ames Ancestor'] ref YP_029415.1 ABC transporter, ATP-binding protein [Bacillus anthracis str. Sterne] ref NP_845690.1 ABC transporter, ATP-binding protein [Bacillus anthracis str. Ames] gb AAP27176.1 ABC transporter, ATP-binding protein [Bacillus anthracis str. Ames] gb AAT35373.1 ABC transporter, ATP-binding protein [Bacillus anthracis str. 'Ames Ancestor'] gb AAT55468.1 ABC transporter, ATP-binding protein [Bacillus anthracis str. Sterne] EXTRACELLULAR SOLUTE-BINDING PROTEIN, PUTATIVE [Wollinella succinogenes DSM 1740] emb CAE09521.1 EXTRACELLULAR SOLUTE-BINDING PROTEIN, PUTATIVE [Wollinella succinogenes]	1.8.-.-			
17629, 17630	34556806	53	2.00E-89	Wollinella succinogenes DSM 1740	hypothetical protein WS0023 [Wollinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wollinella succinogenes]				
17631, 17632	34556481	33	9.00E-48	Wollinella succinogenes DSM 1740	hypothetical protein WS0023 [Wollinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wollinella succinogenes]				
17633, 17634	34556481	51	1.00E-34	Wollinella succinogenes DSM 1740	hypothetical protein WS0023 [Wollinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wollinella succinogenes]	2.7.3.-			
17635, 17636	57242456	39	4.00E-10	Campylobacter upsaliensis RM3195	probable periplasmic protein Cj0530 [Campylobacter upsaliensis RM3195] gb EAL53524.1 probable periplasmic protein Cj0530 [Campylobacter upsaliensis RM3195]				
17637, 17638	32473273	58	7.00E-65	Rhodopirellula baltica SH 1	hypothetical protein RB4721 [Rhodopirellula baltica SH 1] emb CAD73953.1 conserved hypothetical protein [Pirellula sp.] glycosyl transferase [Symbiobacterium thermophilum IAM 14863] dbj BAD40347.1 glycosyl transferase [Symbiobacterium thermophilum IAM 14863]				
17639, 17640	51892500	33	1.00E-09	Symbiobacterium thermophilum IAM 14863	COG1106: Predicted ATPases [Crocospaera watsonii WH 8501] Membrane permease, predicted cation efflux pumps [Clostridium acetobutylicum ATCC 824] gb AAK78299.1 Membrane permease, predicted cation efflux pumps [Clostridium acetobutylicum ATCC 824] p H96938 membrane permease, probable cation efflux pumps [imported] - Clostridium acetobutylicum				
17645, 17646	46119894	41	2.00E-41	Crocospaera watsonii WH 8501	hypothetical protein BF3327 [Bacteroides fragilis YCH46] dbj BAD50071.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
17647, 17648	15693610	25	9.00E-14	Clostridium acetobutylicum ATCC 824	unnamed protein product [Escherichia coli] sp P17222 T1SP_ECOLI Type I restriction enzyme Ecoprt1 specificity protein (S protein) (S.Ecoprt1) p H96926 prB protein - Escherichia coli				
17649, 17650	53714613	35	3.00E-17	Bacteroides fragilis YCH46	hypothetical protein CPE0283 [Clostridium perfringens str. 13] dbj BAB79989.1 conserved hypothetical protein [Clostridium perfringens str. 13]	3.1.21.-			
17651, 17652	42512	74	3.00E-37	Escherichia coli					
17653, 17654	18309265	42	5.00E-42	Clostridium perfringens str. 13					

17655, 17656	52006159	38	6.00E-50	Thiobacillus denitrificans ATCC 25259	COG3587: Restriction endonuclease [Thiobacillus denitrificans ATCC 25259]				
17657, 17658	48844551	35	7.00E-13	Geobacter metallireducens GS-15	COG1061: DNA or RNA helicases of superfamily II [Geobacter metallireducens GS-15]				
17661, 17662	34556604	52	4.00E-29	Wolinella succinogenes DSM 1740	hypothetical protein WS0156 [Wolinella succinogenes DSM 1740] emb CAE09319.1 conserved hypothetical protein [Wolinella succinogenes]				
17663, 17664	54401435	49	6.00E-73	Salmonella enterica subsp. salamae serovar Greenside	UDP-GlcNAc 4-epimerase [Salmonella enterica subsp. salamae serovar (Greenside)]				5.1.3.2
17665, 17666	34558271	67	1.00E-111	Wolinella succinogenes DSM 1740	DNA POLYMERASE III ALPHA SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10986.1 DNA POLYMERASE III ALPHA SUBUNIT [Wolinella succinogenes]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6	95	2.00E-07	2.7.7.7
17667, 17668	51248483	50	1.00E-31	Desulfotalea psychrophila LSV54	probable peptide synthase [Desulfotalea psychrophila LSV54] emb CAG37360.1 probable peptide synthase [Desulfotalea psychrophila LSV54]				
17669, 17670	56459317	31	8.00E-24	Idiomarina lohiensis L2TR	Intracellular signaling protein (GAF, GGDEF, EAL domains) [Idiomarina lohiensis L2TR] gb AAV81049.1 Intracellular signaling protein (GAF, GGDEF, EAL domains) [Idiomarina lohiensis L2TR]				2.7.3.-
1767, 1768	14591553	34	7.00E-39	Pyrococcus horikoshii OT3	chromosome assembly protein [Pyrococcus horikoshii OT3] dbj BAA30917.1 1179aa long hypothetical chromosome assembly protein [Pyrococcus horikoshii OT3] pir F71190 probable chromosome assembly protein - Pyrococcus horikoshii				3.1.3.3
17671, 17672	29349780	48	5.00E-21	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT4372 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79477.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
17673, 17674	48854899	60	3.00E-56	Cytophaga hutchinsonii	COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii]				2.1.1.-
17675, 17676	34557975	71	1.00E-122	Wolinella succinogenes DSM 1740	AAA FAMILY ATPASE [Wolinella succinogenes DSM 1740] emb CAE10690.1 AAA FAMILY ATPASE [Wolinella succinogenes]	Helicobacter hepaticus ATCC 51449 section 2 of 6 of the complete genome	93	2.00E-13	3.4.24.-
17677, 17678	32262066	45	3.00E-46	Helicobacter hepaticus ATCC 51449	riboflavin kinase/FAD synthase RibF [Helicobacter hepaticus ATCC 51449] ref NP_860049.1 riboflavin kinase/FAD synthase RibF [Helicobacter hepaticus ATCC 51449]				2.7.1.26

17679, 17680	34557551	30	5.00E-19	Wollinella succinogenes DSM 1740	hypothetical protein WS1181 [Wollinella succinogenes DSM 1740] emb CAE10266.1 hypothetical protein [Wollinella succinogenes]			
17681, 17682	32261560	51	1.00E-25	Helicobacter hepaticus ATCC 51449	glucose inhibited division protein A [Helicobacter hepaticus ATCC 51449] ref NP_859544.1 glucose inhibited division protein A [Helicobacter hepaticus ATCC 51449]			
17683, 17684	57238060	52	2.00E-66	Campylobacter jejuni RM1221	glucose inhibited division protein A [Campylobacter jejuni RM1221] gb AAW35643.1 glucose inhibited division protein A [Campylobacter jejuni RM1221]	Mycoplasma mobile 163K complete genome	88	9.00E-09
17685, 17686	34558795	43	2.00E-58	Alvinella pompejana epibiont 6C6	TonB-dependent receptor [Alvinella pompejana epibiont 6C6] S-ADENOSYLMETHIONINE-DEPENDENT METHYLTRANSFERASE			
17687, 17688	34557883	32	8.00E-20	Wollinella succinogenes DSM 1740	[Wollinella succinogenes DSM 1740] emb CAE10598.1 S- ADENOSYLMETHIONINE-DEPENDENT METHYLTRANSFERASE [Wollinella succinogenes]			2.1.1.-
17689, 17690	17230890	33	7.00E-17	Nostoc sp. PCC 7120	hypothetical protein all3398 [Nostoc sp. PCC 7120] pir AG2230 hypothetical protein all3398 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75097.1 all3398 [Nostoc sp. PCC 7120]			
1769, 1770	29347079	37	6.00E-16	Bacteroides thetaiotaomicron VPI-5482	phenylalanyl-tRNA synthetase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76776.1 phenylalanyl-tRNA synthetase alpha chain [Bacteroides thetaiotaomicron VPI-5482] sp Q8A756 SYFA_BACTN Phenylalanyl-tRNA synthetase alpha chain (Phenylalanine-tRNA ligase alpha chain) (PheRS)			6.1.1.20
17691, 17692	14518364	60	6.00E-74	Microscilla sp. PRE1	putative transposase [Microscilla sp. PRE1] gb AAK62881.1 MS159, putative transposase [Microscilla sp. PRE1]			
17693, 17694	48833941	36	2.00E-26	Magnetococcus sp. MC-1	COG5421: Transposase [Magnetococcus sp. MC-1]			
17695, 17696	50084270	74	5.00E-64	Acinetobacter sp. ADP1	cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAG67958.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAA86930.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] sp Q43989 COBQ_ACIAD Cobyrinic acid synthase			3.-.-.-
17697, 17698	50084270	40	5.00E-22	Acinetobacter sp. ADP1	cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAG67958.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAA86930.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] sp Q43989 COBQ_ACIAD Cobyrinic acid synthase			
17699, 17700	34557966	52	1.00E-49	Wollinella succinogenes DSM 1740	ATP-DEPENDENT HELICASE [Wollinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wollinella succinogenes]			3.6.1.-

17701,	34557966	55	1.00E-55	Wollinella succinogenes DSM 1740	ATP-DEPENDENT HELICASE [Wollinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wollinella succinogenes]				3.6.1.-
17702	AAU3601	40	2.00E-33		Desc:Helicobacter pylori cellular proliferation protein #326. Org:Helicobacter pylori				
17703,	48837900	42	5.00E-19	Methanosarcina barkeri str. fusaro	COG1817: Uncharacterized protein conserved in archaea [Methanosarcina barkeri str. fusaro]				
17709,	48837900	44	5.00E-54	Methanosarcina barkeri str. fusaro	COG1817: Uncharacterized protein conserved in archaea [Methanosarcina barkeri str. fusaro]				
17710,	57241815	29	8.00E-22	Campylobacter lari RM2100	signal-transducing protein, histidine kinase [Campylobacter lari RM2100] gb EAL54233.1 signal-transducing protein, histidine kinase [Campylobacter lari RM2100]				2.7.3.-
17711,	53691904	32	2.00E-16	Desulfovibrio desulfuricans G20	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Desulfovibrio desulfuricans G20]				
17712,	57167845	55	4.00E-94	Campylobacter coli RM2228	glutamyl-tRNA synthetase [Campylobacter coli RM2228] gb EAL57631.1 glutamyl-tRNA synthetase [Campylobacter coli RM2228]				6.1.1.17
17727,	34557946	41	2.00E-23	Wollinella succinogenes DSM 1740	RESPONSE REGULATOR PROTEIN-CheY-like nd an HD-GYP domain [Wollinella succinogenes DSM 1740] emb CAE10661.1 RESPONSE REGULATOR PROTEIN-CheY-like nd an HD-GYP domain [Wollinella succinogenes]				2.7.3.-
17733,	57242733	41	1.00E-49	Campylobacter upsaliensis RM3195	sensor histidine kinase, putative [Campylobacter upsaliensis RM3195] gb EAL53446.1 sensor histidine kinase, putative [Campylobacter upsaliensis RM3195]				2.7.3.-
17734,	7592813	52	7.00E-68	Actinobacillus actinomycetemcom itans	GDP-mannose pyrophosphorylase homolog [Actinobacillus actinomycetemcomitans]				2.7.7.22
17737,	48855454	31	1.00E-34	Cytophaga hutchinsonii	hypothetical protein Chut02001791 [Cytophaga hutchinsonii]				
17739,	31194301	42	4.00E-31	Anopheles gambiae	ENSANGP00000000011 [Anopheles gambiae]				
17740,	21228716	30	1.00E-10	Methanosarcina mazei Go1	hypothetical protein MM2614 [Methanosarcina mazei Go1] gb AAM32310.1 hypothetical protein [Methanosarcina mazei Go1]				
17741,	50591466	37	5.00E-13	Streptococcus suis 89/1591	COG1011: Predicted hydrolase (HAD superfamily) [Streptococcus suis 89/1591]				3.8.1.2
17743,	34556770	37	5.00E-29	Wollinella succinogenes DSM 1740	Putative Dethiobiotin synthetase [Wollinella succinogenes DSM 1740] emb CAE09485.1 Putative Dethiobiotin synthetase [Wollinella succinogenes]				6.3.3.3
17744,	34557808	58	6.00E-70	Wollinella succinogenes DSM 1740	hypothetical protein WS1465 [Wollinella succinogenes DSM 1740] emb CAE10523.1 conserved hypothetical protein [Wollinella succinogenes]				

1775,	48856903	39	1.00E-52	Cytophaga hutchinsonii	COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii]				
1776					COG3279: Response regulator of the LytR/AlgR family [Cytophaga hutchinsonii]				2.7.3.-
17757,	48854415	40	1.00E-39	Cytophaga hutchinsonii	hypothetical protein VVA1493 [Vibrio vulnificus YJ016] dbj BAC97519.1				
17758					hypothetical protein [Vibrio vulnificus YJ016]				
17759,	37677153	33	2.00E-25	Vibrio vulnificus	phosphoglycerate dehydrogenase [Campylobacter coli RM2228]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6	84	1.00E-07	1.1.1.95
17760					phosphoglycerate dehydrogenase [Campylobacter coli RM2228]				
17761,	57168512	60	3.00E-78	Campylobacter coli RM2228	UDP-N-acetylmuramoyl-D-glutamate ligase [Campylobacter lari RM2100]				6.3.2.13
17762					UDP-N-acetylmuramoyl-D-glutamate ligase [Campylobacter lari RM2100]				
17763,	57240646	60	2.00E-42	Campylobacter lari RM2100	APOLIPOPROTEIN N-ACYLTRANSFERASE [Wolnella succinogenes DSM 1740] emb CAE09249.1 APOLIPOPROTEIN N-ACYLTRANSFERASE [Wolnella succinogenes] sp Q7MAR3 LNT_WOLSU.Apolipoprotein N-acyltransferase (ALP N-acyltransferase)				2.3.1.-
17764					citrate lyase alpha chain [Clostridium tetani E88] gb AAO37018.1 citrate lyase alpha chain [Clostridium tetani E88]				2.8.3.10
17765,	34556534	45	7.00E-28	Wolnella succinogenes DSM 1740	glycosyltransferase, putative [Deinococcus radiodurans R1] gb AAF12451.1 glycosyltransferase, putative [Deinococcus radiodurans] pir F75587 probable glycosyltransferase - Deinococcus radiodurans (strain R1)				
17766					COG0500: SAM-dependent methyltransferases [Mesorhizobium sp. BNC1]				2.1.1.64
17767,	15807989	39	3.00E-18	Deinococcus radiodurans R1	spore coat polysaccharide biosynthesis protein; SpsA [Synecocystis sp. PCC 6803] dbj BAA18053.1 spore coat polysaccharide biosynthesis protein; SpsA [Synecocystis sp. PCC 6803] pir S75492 spore coat polysaccharide biosynthesis protein spsA - Synecocystis sp. (strain PCC 6803)				
17768,	45916450	25	4.00E-10	Mesorhizobium sp. BNC1	COG2202: FOG: PAS/PAC domain [Pseudomonas aeruginosa UCBPP-PA14]				
17769,					Phospho-2-dehydro-3-deoxyheptonate aldolase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93688.1 Phospho-2-dehydro-3-deoxyheptonate aldolase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]				4.1.2.15
17770	28212137	50	1.00E-63	Clostridium tetani E88					
17771,									
17772									
17773,									
17774	16330645	44	8.00E-28	Synechocystis sp. PCC 6803					
17775,									
17776	53727219	44	4.00E-20	Pseudomonas aeruginosa UCBPP-PA14					
17777,									
17778	19704894	54	2.00E-63	Fusobacterium nucleatum subsp. nucleatum ATCC 25586					

17781, 17782	34557551	39	1.00E-33	1740	Wolinella succinogenes DSM	hypothetical protein WS1181 [Wolinella succinogenes DSM 1740] emb CAE10266.1 hypothetical protein [Wolinella succinogenes]				
17787, 17788	48862510	47	4.00E-18	degradans 2-40	Microbulbifer	COG0778: Nitroreductase [Microbulbifer degradans 2-40] Desc: Helicobacter pylori cellular proliferation protein #241. Org: Helicobacter pylori				1.-.-.-
17789, 17790	AAU3592 6	62	6.00E-46							4.6.1.4
17791, 17792	57168806	70	9.00E-47	RM2228	Campylobacter coli	chorismate synthase [Campylobacter coli RM2228] gb EAL56536.1 chorismate synthase [Campylobacter coli RM2228]				
17795, 17796	34557593	48	3.00E-81	1740	Wolinella succinogenes DSM	hypothetical protein WS1227 [Wolinella succinogenes DSM 1740] emb CAE10308.1 hypothetical protein [Wolinella succinogenes] sp P59893 TRUD_WOLSU tRNA pseudouridine synthase D (Pseudouridylate synthase) [Uracil hydrolyase]				
17797, 17798	29348698	45	2.00E-66	VPI-5482	Bacteroides thetaiotaomicron	hypothetical protein BT3289 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78395.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
17799, 17800	57167799	24	3.00E-14	RM2228	Campylobacter coli	conserved hypothetical protein [Campylobacter coli RM2228] gb EAL57585.1 conserved hypothetical protein [Campylobacter coli RM2228]				
17801, 17802	34556868	30	7.00E-33	1740	Wolinella succinogenes DSM	hypothetical protein WS0441 [Wolinella succinogenes DSM 1740] emb CAE09583.1 conserved hypothetical protein [Wolinella succinogenes]				
17803, 17804	53715372	63	4.00E-88	YCH46	Bacteroides fragilis	putative GTP-binding protein [Bacteroides fragilis YCH46] db BAD50830.1 putative GTP-binding protein [Bacteroides fragilis YCH46]				
17805, 17806	48854613	32	8.00E-20	hutchinsonii	Cytophaga	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] hypothetical protein TM0744 [Thermotoga maritima MSB8] gb AAD35825.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir C72340 probable hexosyltransferase (EC 2.4.1.-) TM0744 - Thermotoga maritima (strain MSB8)				2.7.3.-
17807, 17808	15643507	38	2.00E-31	maritima MSB8	Thermotoga					2.4.1.-
17815, 17816	34557673	29	4.00E-11	1740	Wolinella succinogenes DSM	hypothetical protein WS1312 [Wolinella succinogenes DSM 1740] emb CAE10388.1 hypothetical protein [Wolinella succinogenes]				
17817, 17818	57505998	29	4.00E-19	RM3195	Campylobacter upsaliensis	partitioning protein, putative [Campylobacter upsaliensis RM3195] gb EAL52588.1 partitioning protein, putative [Campylobacter upsaliensis RM3195]				

17819, 17820	42518123	37	6.00E-11	Lactobacillus johnsonii NCC 533	hypothetical protein LJ0037 [Lactobacillus johnsonii NCC 533] gb AA08019.1 hypothetical protein LJ0037 [Lactobacillus johnsonii NCC 533]			
17823, 17824	53715360	76	1.00E-112	Bacteroides fragilis YCH46	ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] dbj BAD50818.1 ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46]	Coxiella burnetii strain RSA 493, section 2 of 7 of the complete genome	95	1.00E-07 3.6.1.-
17825, 17826	48854506	42	2.00E-24	Cytophaga hutchinsonii	hypothetical protein Chut02002705 [Cytophaga hutchinsonii] hypothetical protein air4323 [Nostoc sp. PCC 7120] pir AD2346 hypothetical protein air4323 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB76022.1 air4323 [Nostoc sp. PCC 7120]			3.6.1.-
17827, 17828	17231815	34	8.00E-11	Nostoc sp. PCC 7120	Amylovoran biosynthesis AmsK [Bacillus cereus ATCC 14579] gb AAP12133.1 Amylovoran biosynthesis AmsK [Bacillus cereus ATCC 14579]			
17829, 17830	30023301	29	5.00E-10	Bacillus cereus ATCC 14579	COG3569: Topoisomerase IB [Cytophaga hutchinsonii]			
1783, 1784	48855551	55	6.00E-57	Cytophaga hutchinsonii	COG0835: Chemotaxis signal transduction protein [Geobacter metallireducens GS-15]			2.7.3.-
17831, 17832	48845934	49	6.00E-32	Geobacter metallireducens GS-15	Histidinol-phosphatase; UDP-N-acetylmuramoylalanine-D-glutamyl-meso- diaminopimelate-D-alanine ligase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95654.1 Histidinol-phosphatase; UDP-N-acetylmuramoylalanine-D-glutamyl-meso-diaminopimelate-D-alanine- D-alanine ligase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] putative alginase O-acetylation protein [Nitrosomonas europaea ATCC 19718] emb CAD84965.1 putative alginase O-acetylation protein [Nitrosomonas europaea ATCC 19718]			3.1.3.15
17835, 17836	19704793	35	2.00E-20	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	hypothetical protein WS1181 [Wolonia succinogenes DSM 1740] emb CAE10266.1 hypothetical protein [Wolonia succinogenes]			
17837, 17838	30249053	57	9.00E-66	Nitrosomonas europaea ATCC 19718	nitrous oxide reductase [Wolonia succinogenes] DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis Schu 4] emb CAG45292.1 DNA recombination protein RmuC family protein [Francisella tularensis subsp. tularensis]			1.7.99.6
17839, 17840	34557551	38	1.00E-35	Wolonia succinogenes DSM 1740				
17841, 17842	46934822	70	1.00E-133	Wolonia succinogenes				
17847, 17848	56707780	57	1.00E-73	Francisella tularensis subsp. tularensis Schu 4				

17849, 17850, 17851, 17852	12512884 45528155	42 59	7.00E-30 9.00E-23	Escherichia coli O157:H7 Crocospaera watsonii WH 8501	deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] ref NP_285856.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7 EDL933] ref NP_308191.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] sp Q8X8Y9 DGT_P_ECO57 Deoxyguanosinetriphosphate triphosphohydrolase (dGTPase) (dGTP triphosphohydrolase) pir D85500 deoxyguanosine triphosphate triphosphohydrolase [imported] - Escherichia coli (strain O157:H7, substrain EDL933) dbj BAB33587.1 deoxyguanosine triphosphate triphosphohydrolase [Escherichia coli O157:H7] pir D90649 deoxyguanosine triphosphate triphosphohydrolase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)	3.1.5.1			
17853, 17854	28901031	57	4.00E-34	Vibrio parahaemolyticus RIMD 2210633	COG0662: Mannose-6-phosphate isomerase [Crocospaera watsonii WH 8501] hypothetical protein VPA1176 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62519.1 hypothetical protein [Vibrio parahaemolyticus]				
17855, 17856	15669145	31	2.00E-11	Methanocaldococ- cus jannaschii DSM 2661	histidinol-phosphate aminotransferase (hisC) [Methanocaldococcus jannaschii DSM 2661] gb AAB98960.1 histidinol-phosphate aminotransferase (hisC) [Methanocaldococcus jannaschii DSM 2661] pir C64419 histidinol-phosphate transaminase (EC 2.6.1.9) - Methanococcus jannaschii sp Q58365 HIS8_METJA Histidinol-phosphate aminotransferase (imidazole acetol-phosphate transaminase)	2.6.1.9			
17857, 17858	29349895	51	9.00E-68	Bacteroides thetaiotaomicron VPI-5482	putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79592.1 putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicron VPI-5482]	3.2.1.-			
17861, 17862	46135621	37	3.00E-36	Anabaena variabilis ATCC 29413	COG1201: Lhr-like helicases [Anabaena variabilis ATCC 29413]	3.6.1.-			
17865, 17866	42781306	54	1.00E-90	Bacillus cereus ATCC 10987	isoleucyl-tRNA synthetase [Bacillus cereus ATCC 10987] gb AAS41161.1 isoleucyl-tRNA synthetase [Bacillus cereus ATCC 10987]	6.1.1.5			
17867, 17868	28210025	34	2.00E-25	Clostridium tetani E88	isoleucyl-tRNA synthetase [Clostridium tetani E88] gb AAO34906.1 isoleucyl- tRNA synthetase [Clostridium tetani E88]	6.1.1.5			
1787, 1788	29349217	53	4.00E-78	Bacteroides thetaiotaomicron VPI-5482	ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78914.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482]				

17871,	11498895	37	2.00E-41	Archaeoglobus fulgidus DSM 4304	cell division control protein 48, AAA family (cdc48-1) [Archaeoglobus fulgidus DSM 4304] gb AAB89948.1 cell division control protein 48, AAA family (cdc48-1) [Archaeoglobus fulgidus DSM 4304] pir H69411 cell division control protein 48, AAA family (cdc48-1) homolog - Archaeoglobus fulgidus sp O28972 YC97_ARCFU Cell division cycle protein 48 homolog AF1297				2.7.1.-
17873,	53715849	63	1.00E-106	Bacteroides fragilis YCH46	ribonuclease R [Bacteroides fragilis YCH46] dbj BAD51307.1 ribonuclease R [Bacteroides fragilis YCH46]				3.1.-
17875,				Wolnella succinogenes DSM 1740	TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolnella succinogenes DSM 1740] emb CAE09862.1 TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolnella succinogenes]				2.7.3.-
17876,	34557247	66	6.00E-41	Kluyveromyces fragilis	unnamed protein product [Kluyveromyces fragilis] emb CAH02614.1				2.7.3.-
17877,	50302185	34	2.00E-14	Bacteroides fragilis YCH46	hypothetical protein BF1778 [Bacteroides fragilis YCH46] dbj BAD48525.1				
17879,	53713067	25	1.00E-10	Bacteroides fragilis YCH46	hypothetical protein [Bacteroides fragilis YCH46]				
17880,				Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3127 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78233.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
17883,	29348536	43	4.00E-35	Aquifex aeolicus VF5	hypothetical protein aq_321 [Aquifex aeolicus VF5] gb AAC06618.1 putative protein [Aquifex aeolicus VF5] pir F70328 hypothetical protein aq_321 - Aquifex aeolicus				
17885,	15605841	53	4.00E-47	Desulfovibrio desulfuricans G20	COG0840: Methyl-accepting chemotaxis protein [Desulfovibrio desulfuricans G20]				
17886,	23474422	29	5.00E-17	Cytophaga hutchinsonii	COG3124: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
17889,	48853925	47	2.00E-45	Cytophaga hutchinsonii	COG1793: ATP-dependent DNA ligase [Cytophaga hutchinsonii]				6.5.1.1
1789,	48854052	57	4.00E-95	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	glycerophosphoryl diester phosphodiesterase family protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94660.1				
17891,	46578593	35	6.00E-33	Desulfovibrio vulgaris str. Hildenborough	glycerophosphoryl diester phosphodiesterase family protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]				3.1.4.46
17892,				Bacillus licheniformis ATCC 14580	ribosomal protein L22 (BL17) [Bacillus licheniformis ATCC 14580] gb AAU21767.1 ribosomal protein L22 (BL17) [Bacillus licheniformis ATCC 14580] ref YP_089805.1 RplV [Bacillus licheniformis ATCC 14580] gb AAU39112.1 RplV [Bacillus licheniformis DSM 13]				
17893,	52078614	47	2.00E-21	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	mannose-1-phosphate guanylyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70773.1 mannose-1-phosphate guanylyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				2.7.7.13

17901, 17902	21228306	75	1.00E-104	Methanosarcina mazel Go1	hypothetical protein MIM2204 [Methanosarcina mazel Go1] gb AAM31900.1 hypothetical protein [Methanosarcina mazel Go1]	Desc: Methanococcus jannaschii large circular extrachromosomal element. Org: Methanococcus jannaschii	95	1.00E-07	3.1.21.3
17903, 17904	34557740	48	2.00E-54	Wolinella succinogenes DSM 1740	NIFEN2 [Wolinella succinogenes DSM 1740] emb CAE10455.1 NIFEN2 [Wolinella succinogenes]				1.18.6.1
17905, 17906	53730557	39	7.00E-44	Dechloromonas aromatica RCB	COG3696: Putative silver efflux pump [Dechloromonas aromatica RCB]				
17907, 17908	51246943	38	8.00E-21	Desulfotalea psychrophila LSV54	hypothetical protein DP3091 [Desulfotalea psychrophila LSV54] emb CAG37820.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]				
17909, 17910	39997909	26	9.00E-07	Geobacter sulfurreducens PCA	sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] gb AAR36210.1 sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA]				
1791, 1792	15643716	55	8.00E-48	Thermotoga maritima MSB8	ribose ABC transporter, ATP-binding protein [Thermotoga maritima MSB8] gb AAD36035.1 ribose ABC transporter, ATP-binding protein [Thermotoga maritima MSB8] pir E72314 ribose ABC transporter, ATP-binding protein - Thermotoga maritima (strain MSB8)				
17911, 17912	14602171	35	2.00E-09	Aeropyrum permix K1	polysulfide reductase [Aeropyrum permix K1] dbj BAA81623.1 250aa long hypothetical polysulfide reductase [Aeropyrum permix K1] pir G72495 probable polysulfide reductase APE2605 - Aeropyrum permix (strain K1)	Bacillus cereus ZK, complete genome	97	1.00E-07	1.8.-.-
17917, 17918	32262428	63	1.00E-44	Helicobacter hepaticus ATCC 51449	ATP-dependent zinc metalloproteinase [Helicobacter hepaticus ATCC 51449] ref NP_860410.1 ATP-dependent zinc metalloproteinase. [Helicobacter hepaticus ATCC 51449]				1.2.7.-
17921, 17922	57241365	40	2.00E-51	Campylobacter lari RM2100	NADH-ubiquinone oxidoreductase, NQO3 subunit (NQO3) [Campylobacter lari RM2100] gb EAL54477.1 NADH-ubiquinone oxidoreductase, NQO3 subunit (NQO3) [Campylobacter lari RM2100]				3.4.24.-
17923, 17924	29348867	37	1.00E-48	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3458 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78564.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				1.6.5.3
17925, 17926	34556460	45	3.00E-33	Wolinella succinogenes DSM 1740	DNA POLYMERASE III, BETA CHAIN [Wolinella succinogenes DSM 1740] emb CAE09175.1 DNA POLYMERASE III, BETA CHAIN [Wolinella succinogenes]				
17927, 17928	34556459	43	4.00E-27	Wolinella succinogenes DSM 1740	dnaA, probable chromosomal replication initiator protein [Wolinella succinogenes DSM 1740] emb CAE09174.1 dnaA, probable chromosomal replication initiator protein [Wolinella succinogenes]				2.7.7.7

1793, 1794	15897063	29	6.00E-18	Sulfolobus solfataricus P2	Esterase, tropinesterase related protein [Sulfolobus solfataricus P2] gblAAK40458.1 Esterase, tropinesterase related protein [Sulfolobus solfataricus P2] emb CAA69549.1 orf c04020 [Sulfolobus solfataricus pfl S75387 hypothetical protein c04020 - Sulfolobus solfataricus SEPTUM SITE-DETERMINING PROTEIN MIND CELL DIVISION INHIBITOR MIND [Wolinella succinogenes DSM 1740] emb CAE10889.1 SEPTUM SITE-DETERMINING PROTEIN MIND CELL DIVISION INHIBITOR MIND [Wolinella succinogenes]	3.1.-
17931, 17932	34558174	55	1.00E-70	Wolinella succinogenes DSM 1740	membrane fusion efflux protein [Bacteroides fragilis YCH46] dbj BAD47307.1 membrane fusion efflux protein [Bacteroides fragilis YCH46]	
17933, 17934	53711849	28	2.00E-08	Bacteroides fragilis YCH46		
17935, 17936	34557146	47	9.00E-88	Wolinella succinogenes DSM 1740	A/G-SPECIFIC ADENINE GLYCOSYLASE EC 3.2.2. [Wolinella succinogenes DSM 1740] emb CAE09861.1 A/G-SPECIFIC ADENINE GLYCOSYLASE EC 3.2.2. [Wolinella succinogenes]	3.2.2.-
17939, 17940	46580602	35	2.00E-15	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	site-specific recombinase, phage integrase family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gblAAS96670.1 site-specific recombinase, phage integrase family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]	
17941, 17942	34558334	48	2.00E-74	Wolinella succinogenes DSM 1740	PENICILLIN-BINDING PROTEIN 1A PBP-1A [Wolinella succinogenes DSM 1740] emb CAE11049.1 PENICILLIN-BINDING PROTEIN 1A PBP-1A [Wolinella succinogenes]	2.4.2.-
17943, 17944	21227351	53	9.00E-79	Methanosarcina mazei Gø1	Ribulose biphosphate carboxylase large chain [Methanosarcina mazei Gø1] gblAAM30945.1 Ribulose biphosphate carboxylase large chain [Methanosarcina mazei Gø1] sp Q8PXC9 RBL_METMA Ribulose biphosphate carboxylase (RuBisCO)	4.1.1.39
17947, 17948	34558179	47	2.00E-24	Wolinella succinogenes DSM 1740	conserved hypothetical protein-Predicted endonuclease [Wolinella succinogenes DSM 1740] emb CAE10894.1 conserved hypothetical protein-Predicted endonuclease [Wolinella succinogenes]	
17951, 17952	48853472	47	1.00E-16	Cytophaga hutchinsonii	hypothetical protein Chut02003804 [Cytophaga hutchinsonii]	
17953, 17954	34557966	59	4.00E-40	Wolinella succinogenes DSM 1740	ATP-DEPENDENT HELICASE [Wolinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wolinella succinogenes]	3.6.1.-
17955, 17956	48856952	51	3.00E-83	Cytophaga hutchinsonii	COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii]	4.1.3.27
17957, 17958	40062476	41	4.00E-54	uncultured bacterium 105	hypothetical protein EBAC750-01A01.2 [uncultured bacterium 105]	
17959, 17960	29348819	36	8.00E-08	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3410 [Bacteroides thetaiotaomicron VPI-5482] gblAAO78516.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A295 Y10_BACTN Hypothetical UPF0145 protein BT3410	

17961, 17962	9657465	32	5.00E-08	Vibrio cholerae O1 biovar eltor str. N16961	GGDEF family protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_232481.1 GGDEF family protein [Vibrio cholerae O1 biovar eltor str. N16961] pir JF82502 GGDEF family protein VCA0080 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				
17963, 17964	45358725	53	9.00E-71	Methanococcus maripaludis S2	Flavodoxin:Beta-lactamase-like [Methanococcus maripaludis S2] (emb CAF30718.1 Flavodoxin:Beta-lactamase-like [Methanococcus maripaludis S2])				
17967, 17968	48854285	32	3.00E-13	Cytophaga hutchinsonii	COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
17969, 17970	54310375	26	3.00E-14	Photobacterium profundum SS9	putative MSHA biogenesis protein MshH [Photobacterium profundum SS9] emb CAG21593.1 putative MSHA biogenesis protein MshH [Photobacterium profundum]				
17971, 17972	20091095	35	5.00E-23	Methanosarcina acetivorans C2A	sensory transduction histidine kinase [Methanosarcina acetivorans C2A] gb AAAM05650.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A]				2.7.3.-
17973, 17974	AAR2046 0	36	1.00E-41		Desc:Glutamine 2-oxo-glutarate amino transferase. Org:Zea mays				1.4.7.1
17975, 17976	16125068	32	2.00E-18	Caulobacter crescentus CB15	TonB-dependent receptor, putative [Caulobacter crescentus CB15] gb AAK22800.1 TonB-dependent receptor, putative [Caulobacter crescentus CB15] pir D87350 TonB-dependent receptor, probable [imported] - Caulobacter crescentus				
17977, 17978	48855401	35	3.00E-12	Cytophaga hutchinsonii	COG2332: Cytochrome c-type biogenesis protein CcmE [Cytophaga hutchinsonii]				
17983, 17984	53756233	36	2.00E-40	Methylococcus capsulatus str. Bath	paraquat-inducible protein B [Methylococcus capsulatus str. Bath] ref YP_112894.1 paraquat-inducible protein B [Methylococcus capsulatus str. Bath]				
17985, 17986	48854120	53	1.00E-74	Cytophaga hutchinsonii	COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii]				6.2.1.3
17987, 17988	48854120	41	2.00E-55	Cytophaga hutchinsonii	COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii]				6.2.1.3
17991, 17992	52856660	21	1.00E-08	Xylella fastidiosa Ann-1	COG0671: Membrane-associated phospholipid phosphatase [Xylella fastidiosa Ann-1]				
17993, 17994	9657891	34	7.00E-24	Vibrio cholerae O1 biovar eltor str. N16961	conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_232879.1 hypothetical protein VCA0487 [Vibrio cholerae O1 biovar eltor str. N16961] pir D82453 conserved hypothetical protein VCA0487 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				
17997, 17998	51246705	44	3.00E-53	Desulfotalea psychrophila LSV54	hypothetical protein DP2853 [Desulfotalea psychrophila LSV54] emb CAG37582.1 hypothetical protein [Desulfotalea psychrophila LSV54]				

17999, 18000	5531408	51	1.00E-49	Pseudomonas putida	aldehyde dehydrogenase [Pseudomonas putida]				1.2.1.3
18003, 18004	39996595	55	4.00E-39	Geobacter sulfurreducens PCA	sigma-54 dependent DNA-binding response regulator [Geobacter sulfurreducens PCA] gb AAR34889.1 sigma-54 dependent DNA-binding response regulator [Geobacter sulfurreducens PCA]				2.7.3.-
18005, 18006	29348659	42	2.00E-43	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3250 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78356.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
18007, 18008	48854999	49	6.00E-24	Cytophaga hutchinsonii	COG1832: Predicted CoA-binding protein [Cytophaga hutchinsonii]				
18009, 18010	29349404	47	1.00E-56	Bacteroides thetaiotaomicron VPI-5482	putative peptidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79101.1 putative peptidase [Bacteroides thetaiotaomicron VPI-5482]				3.5.1.-
18011, 18012	48853377	62	5.00E-48	Cytophaga hutchinsonii	COG3832: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
18015, 18016	34556560	34	4.00E-18	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]				2.7.3.-
18017, 18018	48853783	51	8.00E-43	Cytophaga hutchinsonii	COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii]				2.7.7.7
18023, 18024	48853984	37	5.00E-31	Cytophaga hutchinsonii	COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii]				
18025, 18026	29346467	25	1.00E-15	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT1057 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76164.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
18029, 18030	51595992	54	5.00E-78	Yersinia pseudotuberculosis IP 32953	oligopeptidase B [Yersinia pseudotuberculosis IP 32953] ref NP_992969.1 oligopeptidase B [Yersinia pestis biovar Medievalis str. 91001] ref NP_405347.1 oligopeptidase B [Yersinia pestis CO92] gb AAS61846.1 oligopeptidase B [Yersinia pestis biovar Medievalis str. 91001] emb CAC90598.1 oligopeptidase B [Yersinia pestis CO92] emb CAH20895.1 oligopeptidase B [Yersinia pseudotuberculosis IP 32953] pir AB0217 oligopeptidase B (EC 3.4.21.83) [imported] - Yersinia pestis (strain CO92)				3.4.21.8 3
1803, 1804	46135321	51	1.00E-81	Anabaena variabilis ATCC 29413	hypothetical protein Avar03000604 [Anabaena variabilis ATCC 29413]				
18037, 18038	48854617	53	2.00E-40	Cytophaga hutchinsonii	COG1576: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
18039, 18040	53714521	35	7.00E-19	Bacteroides fragilis YCH46	hypothetical protein BF3234 [Bacteroides fragilis YCH46] db BAD49979.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				

18043,	9857170	24	1.00E-11	Streptomyces coelicolor A3(2)	hypothetical protein [Streptomyces coelicolor A3(2)] ref NP_628388.1				
18044				coelicolor A3(2)	hypothetical protein SCO4213 [Streptomyces coelicolor A3(2)]				
18047,				Cytophaga	COG2812: DNA polymerase III, gamma/tau subunits [Cytophaga hutchinsonii]				2.7.7.7
18048	48855172	31	2.00E-14	hutchinsonii					
18049,				Thiobacillus					
18050	52006378	54	1.00E-35	denitrificans ATCC 25259	COG0225: Peptide methionine sulfoxide reductase [Thiobacillus denitrificans ATCC 25259]				1.8.4.6
18053,				Methanosarcina					
18054	21227543	48	2.00E-17	mazei Go1	Inorganic pyrophosphatase [Methanosarcina mazei Go1] gb AAM31137.1				
18057,				Campylobacter coli	Inorganic pyrophosphatase [Methanosarcina mazei Go1]				3.6.1.1
18058	57169084	37	3.00E-13	RM2228	conserved hypothetical protein [Campylobacter coli RM2228]				
18059,				Psychrobacter sp.	gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228]				
18060	46141189	43	9.00E-39	273-4	hypothetical protein Psyc03002392 [Psychrobacter sp. 273-4]				
18063,				Haemophilus					
18064	33148938	33	3.00E-23	ducreyi 35000HP	type III restriction enzyme [Haemophilus ducreyi 35000HP] ref NP_874067.1				
18069,				Haemophilus	type III restriction enzyme [Haemophilus ducreyi 35000HP]				3.1.21.5
18070	46129161	54	1.00E-60	influenzae R2846	COG0259: Pyridoxamine-phosphate oxidase [Haemophilus influenzae R2846]				
18073,				Haemophilus					1.4.3.5
18074	48868784	40	1.00E-18	influenzae 86-028NP	COG1393: Arsenate reductase and related proteins, glutaredoxin family [Haemophilus influenzae 86-028NP]				
18085,				Pseudomonas	hypothetical protein PA0043 [Pseudomonas aeruginosa PAO1] pir F83639				
18086	9945865	39	2.00E-25	aeruginosa PAO1	hypothetical protein PA0043 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_248733.1 hypothetical protein PA0043 [Pseudomonas aeruginosa PAO1]				
18089,				Clostridium					
18090	48859484	42	1.00E-17	thermocellum ATCC 27405	COG1015: Phosphopentomutase [Clostridium thermocellum ATCC 27405]				5.4.2.1
18093,				Streptococcus	coproporphyrinogen III oxidase [Streptococcus thermophilus CNRZ1066]				
18094	55823155	31	4.00E-31	thermophilus CNRZ1066	gb AAV62781.1 coproporphyrinogen III oxidase [Streptococcus thermophilus CNRZ1066]				1.---
18095,				Legionella					
18096	45656817	91	1.00E-103	interrogans serovar Copenhageni str. Fioeruz L1-130	type I restriction enzyme [Legionella interrogans serovar Copenhageni str. Fioeruz L1-130] gb AAS69540.1 type I restriction enzyme [Legionella interrogans serovar Copenhageni str. Fioeruz L1-130]				
18097,				Cytophaga					
18098	48856925	33	8.00E-23	hutchinsonii	COG1309: Transcriptional regulator [Cytophaga hutchinsonii]				

18099, 18100	29347468	47	7.00E-58	Bacteroides thetaiotaomicron VPI-5482	putative isoprenyl synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77165.1 putative isoprenyl synthetase [Bacteroides thetaiotaomicron VPI-5482]			2.5.1.1
18101, 18102	20093291	28	5.00E-19	Methanosarcina acetivorans C2A	Na-K-Cl cotransporter [Methanosarcina acetivorans C2A] gb AAM07846.1 Na-K-Cl cotransporter [Methanosarcina acetivorans str. C2A]			
18103, 18104	53756837	34	1.00E-20	Methylococcus capsulatus str. Bath	nitrogen regulation protein NtrY, putative [Methylococcus capsulatus str. Bath] ref YP_115241.1 nitrogen regulation protein NtrY, putative [Methylococcus capsulatus str. Bath]			2.7.3.-
18105, 18106 1811, 1812	48854978	45	6.00E-60	Cytophaga hutchinsonii	COG1410: Methionine synthase I, cobalamin-binding domain [Cytophaga hutchinsonii]	Vibrio fischeri gene for cobalamin- dependent methionine synthase, Na+/H+ antiporter and aspartokinase III, partial and complete cds	93 9.00E-09	2.1.1.13
18111, 18112	48854664	37	1.00E-42	Cytophaga hutchinsonii	COG2217: Cation transport ATPase [Cytophaga hutchinsonii]			3.6.1.-
18113, 18114	51246929	50	1.00E-65	Desulfotalea psychrophila LSV54	probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSV54] emb CAG37806.1 probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSV54]			3.4.21.-
18117, 18118	32475768	43	6.00E-47	Rhodopirellula baltica SH 1	conserved hypothetical protein-putative secreted protein [Rhodopirellula baltica SH 1] emb CAD76137.1 conserved hypothetical protein-putative secreted protein [Pirellula sp.]			
18119, 18120	56962313	38	1.00E-26	Bacillus clausii KSM-K16	hypothetical protein ABC0537 [Bacillus clausii KSM-K16] dbj BAD63077.1 conserved hypothetical protein [Bacillus clausii KSM-K16]			
18121, 18122	54309817	71	1.00E-63	Photobacterium profundum SS9	putative UDP-glucose dehydrogenase [Photobacterium profundum SS9] emb CAG21035.1 putative UDP-glucose dehydrogenase [Photobacterium profundum]			1.1.1.22
18123, 18124	48854132	41	3.00E-19	Cytophaga hutchinsonii	COG0367: Asparagine synthase (glutamine-hydrolyzing) [Cytophaga hutchinsonii]			6.3.5.4
	49236610	35	2.00E-31	Moorella thermoacetica	COG0247: Fe-S oxidoreductase [Moorella thermoacetica ATCC 39073]			1.1.99.5

18129, 18130	21229550	55	5.00E-18	Xanthomonas campestris pv: campestris str. ATCC 33913	hypothetical protein XCC0072 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM39391.1 conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913]				
1813, 1814	28901110	27	3.00E-13	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VPA1255 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62598.1 hypothetical protein [Vibrio parahaemolyticus]				
18133, 18134	29346307	50	2.00E-56	Bacteroides thetaiotaomicron VPI-5482	chaperone protein htpG (heat shock protein htpG) [Bacteroides thetaiotaomicron VPI-5482] gb AAO76004.1 chaperone protein htpG (heat shock protein htpG) [Bacteroides thetaiotaomicron VPI-5482]				
18135, 18136	34397856	45	4.00E-18	Porphyromonas gingivalis W83	ribosomal protein L23 [Porphyromonas gingivalis W83] ref NP_906018.1 ribosomal protein L23 [Porphyromonas gingivalis W83]				
18137, 18138	24373378	43	8.00E-14	Shewanella oneidensis MR-1	DNA-binding protein, putative [Shewanella oneidensis MR-1] gb AAN54865.1 DNA-binding protein, putative [Shewanella oneidensis MR- 1]				
18139, 18140	56675038	33	7.00E-17	uncultured bacterium	cellulase [uncultured bacterium]				
18141, 18142	20809032	36	4.00E-39	Thermoanaerobact er tengcongensis MB4	Sensory transduction histidine kinases [Thermoanaerobacter tengcongensis MB4] gb AAM25807.1 Sensory transduction histidine kinases [Thermoanaerobacter tengcongensis MB4]				2.7.3.-
18145, 18146	53713022	44	1.00E-42	Bacteroides fragilis YCH46	beta-mannosidase [Bacteroides fragilis YCH46] dbj BAC56899.2 beta- mannosidase [Bacteroides fragilis YCH46] dbj BAD48480.1 beta- mannosidase [Bacteroides fragilis YCH46]				3.2.1.25
18149, 18150	48855136	60	3.00E-43	Cytophaga hutchinsonii	COG0118: Glutamine amidotransferase [Cytophaga hutchinsonii]				2.4.2.-
1815, 1816	17547338	38	3.00E-12	Ralstonia solanacearum GMI1000	hypothetical protein RS00923 [Ralstonia solanacearum GMI1000] emb CAD16326.1 CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum]				
18151, 18152	48853807	33	6.00E-23	Cytophaga hutchinsonii	COG0793: Periplasmic protease [Cytophaga hutchinsonii]				
18153, 18154	48854129	42	5.00E-24	Cytophaga hutchinsonii	COG0172: Seryl-tRNA synthetase [Cytophaga hutchinsonii]				6.1.1.11
18155, 18156	34557419	39	2.00E-21	Wolnella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolnella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolnella succinogenes]				2.7.3.-
18157, 18158	45250013	69	4.00E-58	Aneurinibacillus thermoaerophilus	dTDP-glucose 4,6-dehydratase [Aneurinibacillus thermoaerophilus]				4.2.1.46

18159, 18160	9632024	42	6.00E-12	Paramedium bursaria Chlorella virus 1	contains ATP/GTP-binding site motif A [Paramedium bursaria Chlorella virus 1] pif1 17959 hypothetical protein A456L - Chlorella virus PBCV-1				
18161, 18162	24214410	50	9.00E-61	Leptospira interrogans serovar Lai str. 56601	Sensory transduction histidine kinase [Leptospira interrogans serovar Lai str. 56601]				2.7.3.-
18163, 18164	53712683	45	9.00E-45	Bacteroides fragilis YCH46	tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]				
18165, 18166	48854288	39	2.00E-34	Cytophaga hutchinsonii	COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii]				
18167, 18168	7445809	47	6.00E-39	Thermoanaerobact erium thermosulfurigenes	hypothetical ABC exporter component A - Thermoanaerobacterium thermosulfurigenes gb AAB0804.1 AbcA [Thermoanaerobacterium thermosulfurigenes]				3.4.21.-
18169, 18170	53712391	65	1.00E-45	Bacteroides fragilis YCH46	UDP-ManNAc dehydrogenase [Bacteroides fragilis YCH46] dbj BAD47849.1				1.1.1.-
1817, 1818	34104413	49	1.00E-43	Chromobacterium violaceum ATCC 12472	probable Bifunctional: UDP-N-acetylglucosamineglucose-1-phosphate thymidyltransferase; Glucosamine-1-phosphate [Chromobacterium violaceum ATCC 12472] ref NP_902773.1 probable Bifunctional: UDP-N-acetylglucosamineglucose-1-phosphate thymidyltransferase; Glucosamine-1-phosphate [Chromobacterium violaceum ATCC 12472]				2.7.7.24
18173, 18174	48854571	54	8.00E-49	Cytophaga hutchinsonii	COG0707: UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase [Cytophaga hutchinsonii]				2.4.1.-
18175, 18176	22960110	39	4.00E-10	Rhodobacter sphaeroides 2.4.1	COG2808: Transcriptional regulator [Rhodobacter sphaeroides 2.4.1]				
18179, 18180	20807925	38	1.00E-11	Thermoanaerobact er tengcongensis MB4	Acetate kinase [Thermoanaerobacter tengcongensis MB4] sp Q8R9V4 ACKA_THETN Acetate kinase (Acetokinase)				2.7.2.1
18183, 18184	24372586	25	7.00E-07	Shewanella oneidensis MR-1	rhomboid family protein [Shewanella oneidensis MR-1]				
18185, 18186	18309557	30	5.00E-10	Clostridium perfringens str. 13	two-component response regulator [Clostridium perfringens str. 13] dbj BAB80281.1 two-component response regulator [Clostridium perfringens str. 13]				
18191, 18192	32470867	34	5.00E-18	Rhodopirellula baltica SH 1	hypothetical protein RB360 [Rhodopirellula baltica SH 1] emb CAD71533.1 hypothetical protein [Pirellula sp.]				

18193, 18194	47527329	44	4.00E-35	Bacillus anthracis str. 'Ames Ancestor'	methyalted-dna--protein-cysteine s-methyltransferase [Bacillus anthracis str. 'Ames Ancestor'] ref YP_028156.1 methyalted-DNA--protein-cysteine S- methyltransferase [Bacillus anthracis str. Sterne] ref NP_844441.1 methyalted-DNA--protein-cysteine S-methyltransferase [Bacillus anthracis str. Ames] gb AAP25927.1 methyalted-DNA--protein-cysteine S- methyltransferase [Bacillus anthracis str. Ames] gb AAT31153.1 methyalted- DNA--protein-cysteine S-methyltransferase [Bacillus anthracis str. 'Ames Ancestor'] gb AAT54207.1 methyalted-DNA--protein-cysteine S- methyltransferase [Bacillus anthracis str. Sterne]				2.1.1.63
18195, 18196	24372116	53	2.00E-32	Shewanella oneidensis MR-1	large conductance mechanosensitive channel protein [Shewanella oneidensis MR-1] gb AAN53603.1 large conductance mechanosensitive channel protein [Shewanella oneidensis MR-1]				
18197, 18198	21242288	35	1.00E-30	Xanthomonas axonopodis pv. citri str. 306	hypothetical protein XAC1537 [Xanthomonas axonopodis pv. citri str. 306] gb AAM36406.1 conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306]				
18203, 18204	27367689	57	4.00E-73	Vibrio vulnificus CMCP6	Pseudouridylylase, 23S RNA-specific [Vibrio vulnificus CMCP6] gb AAO08206.1 Pseudouridylylase synthase, 23S RNA-specific [Vibrio vulnificus CMCP6]				4.2.1.70
18205, 18206	29349619	69	1.00E-70	Bacteroides thetaiotaomicron VPI-5482	putative phosphoribosylglycinamide cyclo-ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79316.1 putative phosphoribosylglycinamide cyclo-ligase [Bacteroides thetaiotaomicron VPI-5482]				6.3.3.1
18207, 18208	AAW7163 9	25	8.00E-18		Desc:Omega-cyclohexane fatty acid biosynthesis enzyme #2 ORF1. Org:Alcyclobacillus acidocaldarius				
18209, 18210	53713904	69	1.00E-93	Bacteroides fragilis YCH46	exonuclease ABC subunit A [Bacteroides fragilis YCH46] db BAD49362.1 exonuclease ABC subunit A [Bacteroides fragilis YCH46]				1.8.-.-
1821, 1822	14520906	39	2.00E-48	Pyrococcus abyssal GE5	hypothetical protein PAB1903 [Pyrococcus abyssi GE5] emb CAB49612.1 Hypothetical protein [Pyrococcus abyssi] pir C75112 hypothetical protein PAB1903 - Pyrococcus abyssi (strain Orsay)				
18213, 18214	29350165	29	2.00E-08	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT4757 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79862.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482]				
18215, 18216	49653726	28	1.00E-08	Debaryomyces hansenii CBS767	unnamed protein product [Debaryomyces hansenii CBS767] ref XP_458060.1 unnamed protein product [Debaryomyces hansenii]				
18219, 18220	32471625	48	9.00E-51	Rhodopirellula baltica SH 1	hypothetical protein RB1854 [Rhodopirellula baltica SH 1] emb CAD72299.1 conserved hypothetical protein [Pirellula sp.]				

18221,	48856921	58	4.00E-49	Cytophaga hutchinsonii	COG0388: Predicted amidohydrolase [Cytophaga hutchinsonii]	Wollnella succinogenes, complete genome, segment 5/7	93	2.00E-08	6.3.2.1
18222	48854699	70	5.00E-30	Cytophaga hutchinsonii	COG3324: Predicted enzyme related to lactoylglutathione lyase [Cytophaga hutchinsonii]				
18231,	48854699	70	5.00E-30	Cytophaga hutchinsonii	Deoxycytidylate deaminase [Vibrio vulnificus CMCP6] gb AAO07156.1]				
18232	48854699	70	5.00E-30	Cytophaga hutchinsonii	Deoxycytidylate deaminase [Vibrio vulnificus CMCP6]				
18235,	27366639	42	4.00E-27	Vibrio vulnificus CMCP6	Smf protein DNA processing chain A [Bacteroides fragilis YCH46]				3.5.4.12
18236	27366639	42	4.00E-27	Vibrio vulnificus CMCP6	Smf protein DNA processing chain A [Bacteroides fragilis YCH46]				
18239,	53715841	51	6.00E-46	Bacteroides fragilis YCH46	mannose-6-phosphate isomerase [Bacteroides fragilis YCH46]				
18240	53715841	51	6.00E-46	Bacteroides fragilis YCH46	mannose-6-phosphate isomerase [Bacteroides fragilis YCH46]				
18241,	53712946	59	7.00E-42	Bacteroides fragilis YCH46	mannose-6-phosphate isomerase [Bacteroides fragilis YCH46]				5.3.1.8
18242	53712946	59	7.00E-42	Bacteroides fragilis YCH46	mannose-6-phosphate isomerase [Bacteroides fragilis YCH46]				
18243,	56461099	57	6.00E-99	Idiomarina loihiensis L2TR	Carboxynorspermidine dehydrogenase [Idiomarina loihiensis L2TR]	Geobacter sulfurreducens PCA, complete genome	83	5.00E-17	1.1.1.-
18244	56461099	57	6.00E-99	Idiomarina loihiensis L2TR	Carboxynorspermidine dehydrogenase [Idiomarina loihiensis L2TR]				
18249,	48854777	45	6.00E-42	Cytophaga hutchinsonii	COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii]				
18250	48854777	45	6.00E-42	Cytophaga hutchinsonii	COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii]				
1825,	23127068	64	3.00E-91	Nostoc punctiforme PCC 73102	COG1002: Type II restriction enzyme, methylase subunits [Nostoc punctiforme PCC 73102]				
1826	23127068	64	3.00E-91	Nostoc punctiforme PCC 73102	COG1002: Type II restriction enzyme, methylase subunits [Nostoc punctiforme PCC 73102]				
18253,	52080825	31	5.00E-13	Bacillus licheniformis ATCC 14580	two-component sensor histidine kinase ResE [Bacillus licheniformis ATCC 14580] gb AAU23978.1] two-component sensor histidine kinase ResE [Bacillus licheniformis ATCC 14580] ref YP_092025.1] ResE1 [Bacillus licheniformis ATCC 14580] gb AAU41332.1] ResE1 [Bacillus licheniformis DSM 13]				
18254	52080825	31	5.00E-13	Bacillus licheniformis ATCC 14580	two-component sensor histidine kinase ResE [Bacillus licheniformis ATCC 14580] gb AAU23978.1] two-component sensor histidine kinase ResE [Bacillus licheniformis ATCC 14580] ref YP_092025.1] ResE1 [Bacillus licheniformis DSM 13]				2.7.3.-
18255,	56677219	24	3.00E-11	Silicibacter pomeroyi DSS-3	conserved hypothetical protein [Silicibacter pomeroyi DSS-3] ref YP_165830.1] hypothetical protein SPO0570 [Silicibacter pomeroyi DSS-3]				
18256	56677219	24	3.00E-11	Silicibacter pomeroyi DSS-3	conserved hypothetical protein [Silicibacter pomeroyi DSS-3] ref YP_165830.1] hypothetical protein SPO0570 [Silicibacter pomeroyi DSS-3]				
18257,	21242288	40	9.00E-29	Xanthomonas axonopodis pv. citri str. 306	hypothetical protein XAC1537 [Xanthomonas axonopodis pv. citri str. 306] gb AAM36406.1] conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306]				
18258	21242288	40	9.00E-29	Xanthomonas axonopodis pv. citri str. 306	hypothetical protein XAC1537 [Xanthomonas axonopodis pv. citri str. 306] gb AAM36406.1] conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306]				
18259,	45547643	33	7.00E-10	Rubrobacter xylanophilus DSM 9941	COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Rubrobacter xylanophilus DSM 9941]				
18260	45547643	33	7.00E-10	Rubrobacter xylanophilus DSM 9941	COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Rubrobacter xylanophilus DSM 9941]				
18261,	48855790	32	9.00E-15	Cytophaga hutchinsonii	COG5343: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
18262	48855790	32	9.00E-15	Cytophaga hutchinsonii	COG5343: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				

18263, 18264, 18265, 18266	39997854 48853741	44 41	9.00E-53 2.00E-10	Geobacter sulfurreducens PCA Cytophaga hutchinsonii	FAD-dependent glycerol-3-phosphate dehydrogenase subunit [Geobacter sulfurreducens PCA] gb AA36155.1 FAD-dependent glycerol-3-phosphate dehydrogenase subunit [Geobacter sulfurreducens PCA]	1.1.99.5 2.7.3.-
18267, 18268	48853741 34556853	41 53	2.00E-10 2.00E-65	Wolinella succinogenes DSM 1740	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] TRIOSEPHOSPHATE ISOMERASE TIM [Wolinella succinogenes DSM 1740] emb CAE09568.1 TRIOSEPHOSPHATE ISOMERASE TIM [Wolinella succinogenes] sp Q7MA77 TPIS_WOLSU Triosephosphate isomerase (TIM) (Triose-phosphate isomerase)	5.3.1.1
18271, 18272	53735964	32	6.00E-07	Crocospaera watsonii WH 8501	hypothetical protein Cwat03001091 [Crocospaera watsonii WH 8501]	
18275, 18276	52011137	85	1.00E-105	Silicibacter sp. TM1040	COG0086: DNA-directed RNA polymerase, beta' subunit/160 kD subunit [Silicibacter sp. TM1040]	Brucella suis 1330 chromosome I, complete sequence 85 1.00E-22 2.7.7.6
18279, 18280	29350007	35	2.00E-31	Bacteroides thetataoimicron VPI-5482	putative transcriptional regulator [Bacteroides thetataoimicron VPI-5482] gb AAO79704.1 putative transcriptional regulator [Bacteroides thetataoimicron VPI-5482]	
18283, 18284	48855914	30	4.00E-28	Cytophaga hutchinsonii	COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii]	
18285, 18286	46580986	36	2.00E-09	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	transcriptional regulator, TetR family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS97054.1 transcriptional regulator, TetR family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]	
1829, 1830	48853635	48	4.00E-42	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]	2.7.3.-
18291, 18292	34398079	38	1.00E-13	Porphyromonas gingivalis W83	ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65301.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_906240.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904402.1 ISPg4, transposase [Porphyromonas gingivalis W83]	
18295, 18296	34102201	33	3.00E-11	Chromobacterium violaceum ATCC 12472	probable 5-carboxymethyl-2-hydroxymuconate D-isomerase [Chromobacterium violaceum ATCC 12472] ref NP_900563.1 probable 5-carboxymethyl-2-hydroxymuconate D-isomerase [Chromobacterium violaceum ATCC 12472]	5.3.3.10
18297, 18298	56708912	35	9.00E-18	Silicibacter pomeroiyi DSS-3	hypothetical protein SPOA0125 [Silicibacter pomeroiyi DSS-3] gb AAV97262.1 hypothetical protein SPOA0125 [Silicibacter pomeroiyi DSS-3]	
18299, 18300	23128981	39	3.00E-27	Nostoc punctiforme PCC 73102	COG2319: FOG: WD40 repeat [Nostoc punctiforme PCC 73102]	2.7.1.37

183, 184	20808046	41	1.00E-52	Thermoanaerobacter tengcongensis MB4	predicted GTPases [Thermoanaerobacter tengcongensis MB4] gb AAM24821.1 predicted GTPases [Thermoanaerobacter tengcongensis MB4] sp Q8R9J1 ENGA_THETN GTP-binding protein engA				
18301, 18302	34557235	45	3.00E-29	Wolinella succinogenes DSM 1740	PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR [Wolinella succinogenes DSM 1740] emb CAE0950.1 PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR [Wolinella succinogenes]				
18305, 18306	53711360	46	5.00E-50	Bacteroides fragilis YCH46	putative Tricorn-like protease [Bacteroides fragilis YCH46] dbj BAD46818.1 putative Tricorn-like protease [Bacteroides fragilis YCH46]				3.4.21.-
18307, 18308	34396235	42	1.00E-33	Porphyromonas gingivalis W83	sensor histidine kinase [Porphyromonas gingivalis W83] ref NP_904403.1 sensor histidine kinase [Porphyromonas gingivalis W83]				2.7.3.-
1831, 1832	ABU5672	25	4.00E-13		Desc:Lung cancer-associated polypeptide #317. Org:Unidentified				2.7.1.-
18311, 18312	48855398	29	6.00E-29	Cytophaga hutchinsonii	COG0612: Predicted Zn-dependent peptidases [Cytophaga hutchinsonii] type I restriction-modification system methyltransferase subunit [Vibrio vulnificus YJ016] dbj BAC93580.1 type I restriction-modification system methyltransferase subunit [Vibrio vulnificus YJ016]				3.4.-
18313, 18314	37679000	70	1.00E-102	Vibrio vulnificus YJ016					2.1.1.72
18315, 18316	31196343	55	1.00E-20	Anopheles gambiae	ENSANGP0000001688 [Anopheles gambiae]				3.1.21.3
18321, 18322	48853833	56	2.00E-38	Cytophaga hutchinsonii	COG0576: Molecular chaperone GrpE (heat shock protein) [Cytophaga hutchinsonii]				
18333, 18334	48853635	46	5.00E-36	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]				
18337, 18338	48831369	40	1.00E-45	Magnetococcus sp. MC-1	COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Magnetococcus sp. MC-1]			87	2.00E-09/2.7.3.-
18343, 18344	15837098	29	3.00E-13	Xylella fastidiosa 9a5c	hypothetical protein XF0496 [Xylella fastidiosa 9a5c] gb AAF83306.1 conserved hypothetical protein [Xylella fastidiosa 9a5c] pir A82801 conserved hypothetical protein XF0496 [imported] - Xylella fastidiosa (strain 9a5c)				1.2.7.-
18345, 18346	48859741	49	8.00E-51	Clostridium thermocellum ATCC 27405	COG2360: Leu/Phe-tRNA-protein transferase [Clostridium thermocellum ATCC 27405]				2.3.2.6

18347, 18348	29608580	31	3.00E-18	Streptomyces avermittilis MA-4680	hypothetical protein [Streptomyces avermittilis MA-4680] ref NP_826099.1 hypothetical protein SAV4922 [Streptomyces avermittilis MA-4680]				
1835, 1836	46202632	51	1.00E-25	Magnetospirillum magnetotacticum MS-1	COG2202: FOG: PAS/PAC domain [Magnetospirillum magnetotacticum MS-1]				
18353, 18354	49485641	32	4.00E-27	Staphylococcus aureus subsp. aureus MSSA476	hypothetical protein SAS0734 [Staphylococcus aureus subsp. aureus MSSA476] ref NP_645548.1 hypothetical protein MW0731 [Staphylococcus aureus subsp. aureus MW2] emb CAG42510.1 conserved hypothetical protein [Staphylococcus aureus subsp. aureus MSSA476] db JBA894596.1 MW0731 [Staphylococcus aureus subsp. aureus MW2]				
18357, 18358	48853890	67	2.00E-49	Cytophaga hutchinsonii	COG0210: Superfamily I DNA and RNA helicases [Cytophaga hutchinsonii]				3.6.1.-
18359, 18360	48856934	47	4.00E-48	Cytophaga hutchinsonii	COG1058: Predicted nucleotide-utilizing enzyme related to molybdopterin-biosynthesis enzyme MoeA [Cytophaga hutchinsonii]				
18361, 18362	48854804	60	8.00E-24	Cytophaga hutchinsonii	COG0661: Predicted unusual protein kinase [Cytophaga hutchinsonii]				
18365, 18366	AB8477	49	6.00E-31		Desc:DNA polymerase III holoenzyme delta subunit related protein SEQ ID:144. Org: Cytophaga hutchinsonii				
18367, 18368	48836151	41	4.00E-33	Thermobifida fusca	COG0210: Superfamily I DNA and RNA helicases [Thermobifida fusca]				3.6.1.-
18369, 18370	23128175	46	2.00E-13	Nostoc punctiforme PCC 73102	COG0463: Glycosyltransferases Involved in cell wall biogenesis [Nostoc punctiforme PCC 73102]				2.4.1.-
18371, 18372	48895505	46	1.00E-18	Trichodesmium erythraeum IMS101	COG3222: Uncharacterized protein conserved in bacteria [Trichodesmium erythraeum IMS101]				
18373, 18374	48825855	29	6.00E-09	Enterococcus faecium	hypothetical protein Efae03000852 [Enterococcus faecium]				
18375, 18376	48854895	54	1.00E-55	Cytophaga hutchinsonii	COG0491: Zn-dependent hydrolases, including glyoxylases [Cytophaga hutchinsonii]				
18377, 18378	48854970	30	1.00E-11	Cytophaga hutchinsonii	COG0308: Aminopeptidase N [Cytophaga hutchinsonii]				
18383, 18384	53712046	63	5.00E-32	Bacteroides fragilis YCH46	putative alpha-1,2-mannosidase [Bacteroides fragilis YCH46] db BAD47504.1 putative alpha-1,2-mannosidase [Bacteroides fragilis YCH46]				
18389, 18390	15606814	41	6.00E-29	Aquifex aeolicus VF5	beta 1,4 glucosyltransferase [Aquifex aeolicus VF5] gb AAC07593.1 beta 1,4 glucosyltransferase [Aquifex aeolicus VF5] pir B70450 beta 1,4 glucosyltransferase - Aquifex aeolicus				2.4.-

18391, 18392	15895588	32	7.00E-27	Clostridium acetobutylicum ATCC 824	Predicted glycosyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK80277.1 Predicted glycosyltransferase [Clostridium acetobutylicum ATCC 824] pir B97186 probable glycosyltransferase CAC2321 [imported] - Clostridium acetobutylicum				2.4.1.-
18393, 18394	48856925	30	2.00E-10	Cytophaga hutchinsonii	COG1309: Transcriptional regulator [Cytophaga hutchinsonii]				
18395, 18396	48856042	45	6.00E-20	Cytophaga hutchinsonii	COG0465: ATP-dependent Zn proteases [Cytophaga hutchinsonii] Probable sigma(54) modulation protein; SSU ribosomal protein S30P, putative [Campylobacter lari RM2100] gb EAL55561.1 Probable sigma(54) modulation protein; SSU ribosomal protein S30P, putative [Campylobacter lari RM2100]				3.4.24.-
18399, 18400	57240447	47	4.00E-38	Campylobacter lari RM2100	COG0793: Periplasmic protease [Cytophaga hutchinsonii] hypothetical protein BT3977 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79082.1 conserved hypothetical protein [Bacteroides thetaitotaomicron VPI-5482]				3.4.21.-
18401, 18402	48853807	38	7.00E-45	Cytophaga hutchinsonii	Branched-chain amino acid aminotransferase [Methanopyrus kandleri AV19] gb AAM02840.1 Branched-chain amino acid aminotransferase [Methanopyrus kandleri AV19]				2.6.1.42
18403, 18404	29349385	32	8.00E-10	Bacteroides thetaitotaomicron VPI-5482	ORF5 [Moritella marina]				3.4.21.-
18405, 18406	20095063	30	8.00E-13	Methanopyrus kandleri AV19	putative phenylacetic acid degradation NADH oxidoreductase [Corynebacterium efficiens YS-314] db BAC17481.1 putative phenylacetic acid degradation NADH oxidoreductase [Corynebacterium efficiens YS-314] ribonuclease HII [Porphyromonas gingivalis W83] ref NP_905006.1 ribonuclease HII [Porphyromonas gingivalis W83] sp Q51832 RNH2_PORGI Ribonuclease HII (RNase HII) COG1381: Recombinational DNA repair protein (RecF pathway) [Cytophaga hutchinsonii]				1.6.99.7
18407, 18408	6691651	35	7.00E-24	Moritella marina	GldB [Flavobacterium johnsoniae]				3.1.26.4
18409, 18410	25027227	39	3.00E-27	Corynebacterium efficiens YS-314	GldB [Flavobacterium johnsoniae]				
1841, 1842	34396840	57	8.00E-39	Porphyromonas gingivalis W83	GldB [Flavobacterium johnsoniae]				
18413, 18414	48856963	43	3.00E-19	Cytophaga hutchinsonii	GldB [Flavobacterium johnsoniae]				
18415, 18416	5360168	38	6.00E-19	Flavobacterium johnsoniae	GldB [Flavobacterium johnsoniae]				
18417, 18418	5360168	38	2.00E-18	Flavobacterium johnsoniae	GldB [Flavobacterium johnsoniae]				
18421, 18422	29346727	61	4.00E-52	Bacteroides thetaitotaomicron VPI-5482	riboflavin synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76424.1 riboflavin synthase alpha chain [Bacteroides thetaitotaomicron VPI-5482]				2.5.1.9
18423, 18424	46446120	54	2.00E-25	Parachlamydia sp. UWE25	hypothetical protein pc0486 [Parachlamydia sp. UWE25] emb CAF23210.1 hypothetical protein [Parachlamydia sp. UWE25]				

18425, 18426	32404060	26	1.00E-07	Neurospora crassa	predicted protein [Neurospora crassa] emb CAD70330.1 putative protein [Neurospora crassa] gb EAA27596.1 predicted protein [Neurospora crassa]				
18427, 18428	AAU7962 2	24	3.00E-07		Desc:Corynebacterium glutamicum Org:Corynebacterium glutamicum				
1843, 1844	55376565	37	6.00E-18	Haloarcula marismortui ATCC 43049	DNA polymerase B2 exonuclease domain [Haloarcula marismortui ATCC 43049] gb AAV44711.1 DNA polymerase B2 exonuclease domain [Haloarcula marismortui ATCC 43049]			2.7.7.7	
18431, 18432	24373054	31	4.00E-18	Shewanella oneidensis MR-1	GGDEF family protein [Shewanella oneidensis MR-1] gb AAN54541.1				
18433, 18434	48854489	52	9.00E-26	Cytophaga hutchinsonii	GGDEF family protein [Shewanella oneidensis MR-1] hypothetical protein Chut02002688 [Cytophaga hutchinsonii]				
18443, 18444	34397294	55	1.00E-28	Porphyrromonas gingivalis W83	UDP-glucose-6 dehydrogenase, putative [Porphyrromonas gingivalis W83]				
18445, 18446	48854228	39	1.00E-48	Cytophaga hutchinsonii	ref NP_905458.1 UDP-glucose-6 dehydrogenase, putative [Porphyrromonas gingivalis W83] COG1819: Glycosyl transferases, related to UDP-glucuronosyltransferase [Cytophaga hutchinsonii]			1.1.1.-	
18447, 18448	26991195	45	6.00E-34	Pseudomonas putida KT2440	hypothetical protein PP4510 [Pseudomonas putida KT2440] gb AAN70084.1 conserved hypothetical protein [Pseudomonas putida KT2440]				
18449, 18450	53714730	63	2.00E-83	Bacteroides fragilis YCH46	2-isopropylmalate synthase LeuA [Bacteroides fragilis YCH46] dbj BAD50188.1 2-isopropylmalate synthase LeuA [Bacteroides fragilis YCH46]			4.1.3.12	
18451, 18452	48856112	40	2.00E-53	Cytophaga hutchinsonii	COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
18453, 18454	23098370	53	1.00E-41	Oceanobacillus iheynensis HTE831	hypothetical protein OB0915 [Oceanobacillus iheynensis HTE831] dbj BAC12871.1 hypothetical conserved protein [Oceanobacillus iheynensis HTE831]				
18457, 18458	53711798	58	6.00E-67	Bacteroides fragilis YCH46	riboflavin biosynthesis protein RibD [Bacteroides fragilis YCH46] dbj BAD47256.1 riboflavin biosynthesis protein RibD [Bacteroides fragilis YCH46]			1.1.1.19 3	
18459, 18460	29653730	55	7.00E-59	Coxiella burnetii RSA 493	DNA-3-methyladenine glycosidase I [Coxiella burnetii RSA 493] gb AAO89936.1 DNA-3-methyladenine glycosidase I [Coxiella burnetii RSA 493]			3.2.2.20	
18463, 18464	20559950	44	3.00E-17	Pseudomonas aeruginosa	ORF_10; similar to Zinc-binding dehydrogenases [Pseudomonas aeruginosa] gb AAM27562.1 ORF_10; similar to Zinc-binding dehydrogenases [Pseudomonas aeruginosa]			1.1.1.-	
18465, 18466	48860575	31	1.00E-12	Microbulbifer degradans 2-40	hypothetical protein Mdeg02004210 [Microbulbifer degradans 2-40]				

18467, 18468, 18469, 18470	29655030 58003149	50 58	2.00E-22 3.00E-33	Coxiella burnetii RSA 493 Gluconobacter oxydans 621H	conserved hypothetical protein TIGR00252 [Coxiella burnetii RSA 493] gb AAO91236.1 conserved hypothetical protein TIGR00252 [Coxiella burnetii RSA 493] sp Q83AY5 YH42_COXBU Hypothetical UPF0102 protein CBU1742			3.1.-.-
1847, 1848	53712890	48	1.00E-57	Bacteroides fragilis YCH46	Serine hydroxymethyl transferase [Gluconobacter oxydans 621H] putative NADH dehydrogenase [Bacteroides fragilis YCH46] db BAD48348.1 putative NADH dehydrogenase [Bacteroides fragilis YCH46]			2.1.2.1
18471, 18472	55769919	52	2.00E-68	Oryza sativa (japonica cultivar-group)	putative leucyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)] db BAD52586.1 putative leucyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)]	Desc:Staphylococcus aureus DNA for cellular proliferation protein #863. Org:Staphylococcus aureus	91 1.00E-07 6.1.1.4	1.6.99.3
18475, 18476	47459121	27	4.00E-08	Mycoplasma mobile 163K	type I restriction enzyme m protein [Mycoplasma mobile 163K] gb AA27772.1 type I restriction enzyme m protein [Mycoplasma mobile 163K]			
18477, 18478	48854976	45	4.00E-42	Cytophaga hutchinsonii	COG0119: Isopropylmalate/homocitrate/citramalate synthases [Cytophaga hutchinsonii]			4.1.3.4
18479, 18480	48854542	40	2.00E-39	Cytophaga hutchinsonii	COG1748: Saccharopine dehydrogenase and related proteins [Cytophaga hutchinsonii]			1.5.1.7
18481, 18482	29346142	38	1.00E-39	Bacteroides thetaiotaomicron VPI-5482	two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO75839.1 two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482]			2.7.3.-
18483, 18484	28897283	24	3.00E-11	Vibrio parahaemolyticus RIMD 2210633	integrase/recombinase XerD [Vibrio parahaemolyticus RIMD 2210633] db BAC58772.1 integrase/recombinase XerD [Vibrio parahaemolyticus]			
18485, 18486	48855767	43	4.00E-21	Cytophaga hutchinsonii	COG0123: Deacetylases, including yeast histone deacetylase and acetoin utilization protein [Cytophaga hutchinsonii]			
18487, 18488	47529986	54	9.00E-21	Bacillus anthracis str. 'Ames Ancestor'	septom formation protein maf [Bacillus anthracis str. 'Ames Ancestor'] ref YP_030599.1 septum formation protein Maf [Bacillus anthracis str. Ames] ref NP_846900.1 septum formation protein Maf [Bacillus anthracis str. Ames] ref NP_658486.1 Maf, Maf-like protein [Bacillus anthracis str. A2012] gb AAP28386.1 septum formation protein Maf [Bacillus anthracis str. Ames] gb AAAT33810.1 septum formation protein Maf [Bacillus anthracis str. Ames] gb AAAT56650.1 septum formation protein Maf [Bacillus anthracis str. Ames] sp Q81LD6 MAF_BACAN Septum formation protein Maf			

18489, 18490	21241606	45	1.00E-07	Xanthomonas axonopodis pv. citri str. 306	hypothetical protein XAC0836 [Xanthomonas axonopodis pv. citri str. 306] gb AAAM35724.1 conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306]				
1849, 1850	45510657	55	2.00E-63	Anabaena variabilis ATCC 29413	COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Anabaena variabilis ATCC 29413]				3.1.21.3
18491, 18492	37520843	51	5.00E-24	Gloeobacter violaceus PCC 7421	hypothetical protein glr1374 [Gloeobacter violaceus PCC 7421] dbj BAC89315.1 glr1374 [Gloeobacter violaceus PCC 7421]				
18493, 18494	29349247	54	7.00E-56	Bacteroides thetaiotaomicron VPI-5482	ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO78944.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482]				1.8.-.-
18495, 18496	8886019	50	2.00E-41	Chryseobacterium meningosepticum	PI-irrepressible alkaline phosphatase PafA [Chryseobacterium meningosepticum]				
18497, 18498	53715368	36	1.00E-07	Bacteroides fragilis YCH46	hypothetical protein BF4084 [Bacteroides fragilis YCH46] dbj BAD50826.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				-
18501, 18502	48839680	27	5.00E-08	Methanoscarchina barkeri str. fusaro	COG1668: ABC-type Na ⁺ efflux pump, permease component [Methanoscarchina barkeri str. fusaro]				
18503, 18504	48856549	58	6.00E-32	Cytophaga hutchinsonii	COG3204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Cytophaga hutchinsonii]				2.7.-.-
18505, 18506	9655931	56	3.00E-48	Vibrio cholerae O1 biovar eltor str. N16961	conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_231075.1 hypothetical protein VC1432 [Vibrio cholerae O1 biovar eltor str. N16961] plr D82199 conserved hypothetical protein VC1432 [Imported] - Vibrio cholerae (strain N16961 serogroup O1)				
18507, 18508	48856923	32	1.00E-28	Cytophaga hutchinsonii	COG0845: Membrane-fusion protein [Cytophaga hutchinsonii]				
18509, 18510	53758661	52	2.00E-43	Methylococcus capsulatus str. Bath	pyruvate ferredoxin/flavodoxin oxidoreductase family protein [Methylococcus capsulatus str. Bath] ref YP_113272.1 pyruvate ferredoxin/flavodoxin oxidoreductase family protein [Methylococcus capsulatus str. Bath]				1.2.7.1
1851, 1852	48856045	24	9.00E-11	Cytophaga hutchinsonii	hypothetical protein Chut02001277 [Cytophaga hutchinsonii]				
18511, 18512	28199976	28	2.00E-13	Xylella fastidiosa Temecula1	hypothetical protein PD2120 [Xylella fastidiosa Temecula1] gb AAO29939.1 conserved hypothetical protein [Xylella fastidiosa Temecula1]				
18513, 18514	52425551	37	1.00E-25	Mannheimia succiniciproducens MBEL55E	RfaG protein [Mannheimia succiniciproducens MBEL55E] gb AAU38103.1 RfaG protein [Mannheimia succiniciproducens MBEL55E]				2.4.1.-

18517, 18518	29347648	39	3.00E-22	Bacteroides thetaiotaomicron VPI-5482	putative biotin-(acetyl-CoA carboxylase) synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77345.1 putative biotin-(acetyl-CoA carboxylase) synthetase [Bacteroides thetaiotaomicron VPI-5482]				6.3.4.15
18533, 18534	56708241	50	1.00E-41	Francisella tularensis subsp. tularensis Schu 4	DNA-methyltransferase, type I restriction-modification enzyme subunit M [Francisella tularensis subsp. tularensis Schu 4] emb CAG45804.1 DNA- methyltransferase, type I restriction-modification enzyme subunit M [Francisella tularensis subsp. tularensis]				
18535, 18536	58000733	33	1.00E-08	Gluconobacter oxydans 621H	Type I restriction-modification enzyme S subunit [Gluconobacter oxydans 621H]				3.1.21.3
18537, 18538	ABB4904	41	3.00E-37		Desc:Listeria monocytogenes protein #1747. Org:Listeria monocytogenes				6.2.1.26
18539, 18540	46202152	36	4.00E-33	Magnetospirillum magnetotacticum MS-1	COG0582: Integrase [Magnetospirillum magnetotacticum MS-1]				
18541, 18542	23004335	33	2.00E-10	Magnetospirillum magnetotacticum MS-1	COG1974: SOS-response transcriptional repressors (RecA-mediated autopeptidases) [Magnetospirillum magnetotacticum MS-1]				3.4.21.8 8
18545, 18546	21243533	30	3.00E-24	Xanthomonas axonopodis pv. citri str. 306	beta-lactamase [Xanthomonas axonopodis pv. citri str. 306] gb AAM37651.1 beta-lactamase [Xanthomonas axonopodis pv. citri str. 306]				
18547, 18548	34397294	38	2.00E-12	Porphyrromonas gingivalis W83	UDP-glucose-6 dehydrogenase, putative [Porphyrromonas gingivalis W83] ref NP_905458.1 UDP-glucose-6 dehydrogenase, putative [Porphyrromonas gingivalis W83]				1.1.1.-
18549, 18550	48854895	57	5.00E-53	Cytophaga hutchinsonii	COG0491: Zn-dependent hydrolases, including glyoxylases [Cytophaga hutchinsonii]				
18551, 18552	56678640	78	7.00E-46	Silicibacter pomeroiy DSS-3	RecA [Silicibacter pomeroiy DSS-3] ref YP_167265.1 RecA [Silicibacter pomeroiy DSS-3]				
18555, 18556	39996620	44	6.00E-09	Geobacter sulfurreducens PCA	phenylalanyl-tRNA synthetase, beta subunit [Geobacter sulfurreducens PCA] gb AAR34894.1 phenylalanyl-tRNA synthetase, beta subunit [Geobacter sulfurreducens PCA]		89	5.00E-12	3.1.-.-
18557, 18558	53714985	30	3.00E-14	Bacteroides fragilis YCH46	putative membrane peptidase [Bacteroides fragilis YCH46] db BAD50443.1 putative membrane peptidase [Bacteroides fragilis YCH46]				6.1.1.20
18559, 18560	48856025	29	8.00E-18	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]				

18561,	29027481	58	5.00E-57	Aster yellows phytoplasma	threonine dehydratase [Aster yellows phytoplasma]	Streptococcus mutans UA159 section 21 of 185 of the complete genome	93	2.00E-08	4.2.1.16
18562					ABC transporter ATP-binding protein [Clostridium tetani E88]				
18563,	28210316	69	5.00E-24	Clostridium tetani E88	gb AAO35197.1 ABC transporter ATP-binding protein [Clostridium tetani E88]				
18564									
18565,	56962820	37	1.00E-33	Bacillus clausii KSM-K16	multidrug ABC transporter ATP-binding protein [Bacillus clausii KSM-K16]				1.8.-.-
18566					dbj BAD63585.1 multidrug ABC transporter ATP-binding protein [Bacillus clausii KSM-K16]				
18571,	48854785	37	1.00E-18	Cytophaga hutchinsonii	COG0513: Superfamily II DNA and RNA helicases [Cytophaga hutchinsonii]				2.7.7.-
18575,									
18576	48856042	52	3.00E-26	Cytophaga hutchinsonii	COG0465: ATP-dependent Zn proteases [Cytophaga hutchinsonii]				3.4.24.-
18577,									
18578	48854859	39	2.00E-22	Cytophaga hutchinsonii	COG0108: 3,4-dihydroxy-2-butanone 4-phosphate synthase [Cytophaga hutchinsonii]				3.5.4.25
18579,									
18580	48853829	57	2.00E-58	Cytophaga hutchinsonii	COG0498: Threonine synthase [Cytophaga hutchinsonii]				4.2.99.2
18581,									
18582	34557291	40	3.00E-33	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740]				
18585,					emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]				
18586	48855019	50	2.00E-62	Cytophaga hutchinsonii	COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii]				2.4.1.18 2
18587,									
18588	48853588	26	7.00E-12	Cytophaga hutchinsonii	COG1388: FOG: LysM repeat [Cytophaga hutchinsonii]				
18589,									
18590	48856321	57	6.00E-43	Cytophaga hutchinsonii	COG4430: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
18591,									
18592	18310383	39	4.00E-45	Clostridium perfringens str. 13	probable DNA polymerase III epsilon chain [Clostridium perfringens str. 13] dbj BAB81107.1 probable DNA polymerase III epsilon chain [Clostridium perfringens str. 13]				2.7.7.7
18595,									
18596	48846657	40	1.00E-37	Geobacter metallireducens GS-15	COG4191: Signal transduction histidine kinase regulating C4-dicarboxylate transport system [Geobacter metallireducens GS-15]				2.7.3.-
18597,									
18598	37520287	46	2.00E-47	Geobacter violaceus PCC 7421	two-component hybrid sensor and regulator [Geobacter violaceus PCC 7421] dbj BAC38659.1 two-component hybrid sensor and regulator [Geobacter violaceus PCC 7421]				2.7.3.-
18599,									
18600	14590306	31	6.00E-10	Pyrococcus horikoshii OT3	hypothetical protein PH0398 [Pyrococcus horikoshii OT3] dbj BAA29473.1 334aa long hypothetical protein [Pyrococcus horikoshii OT3] pir D71148 hypothetical protein PH0398 - Pyrococcus horikoshii				

18601, 18602	54295894	42	3.00E-56	Legionella pneumophila str. Paris	hypothetical protein plpp0051 [Legionella pneumophila str. Paris] emb CAH17228.1 hypothetical protein [Legionella pneumophila str. Paris]			
18603, 18604	54295894	61	2.00E-81	Legionella pneumophila str. Paris	hypothetical protein plpp0051 [Legionella pneumophila str. Paris] emb CAH17228.1 hypothetical protein [Legionella pneumophila str. Paris]			
18605, 18606	42523942	49	3.00E-25	Bdellovibrio bacteriovorus HD100	SEC-independent protein translocase protein TATC [Bdellovibrio bacteriovorus HD100] emb CAE80315.1 SEC-independent protein translocase protein TATC [Bdellovibrio bacteriovorus HD100]			
18609, 18610	AAB1851 5	44	1.00E-33		Desc:Amino acid sequence of prolyl-tripeptidyl peptidase DPP. Org:Porphyromonas gingivalis			3.4.14.-
18611, 18612	48855584	31	1.00E-40	Cytophaga hutchinsonii	COG0010: Arginase/agmatinase/formimionoglutamyl hydrolase, arginase family [Cytophaga hutchinsonii]			3.5.3.1
18615, 18616	48856329	60	1.00E-82	Cytophaga hutchinsonii	COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii]			1.8.-
18619, 18620	21675046	45	4.00E-15	Chlorobium tepidum TLS	hypothetical protein CT2237 [Chlorobium tepidum TLS] gb AAM73453.1 hypothetical protein [Chlorobium tepidum TLS]			
18623, 18624	29347938	42	2.00E-17	Bacteroides thetaiotaomicron VPI-5482	putative Na+-dependent phosphate transporter [Bacteroides thetaiotaomicron VPI-5482] gb AAO77635.1 putative Na+-dependent phosphate transporter [Bacteroides thetaiotaomicron VPI-5482]			
18625, 18626	57158781	44	2.00E-17	Thermococcus kodakaraensis	carbohydrate esterase, family 1 [Thermococcus kodakaraensis] ref YP_182935.1 carbohydrate esterase, family 1 [Thermococcus kodakaraensis]			3.2.1.41
1863, 1864	48855446	32	3.00E-32	Cytophaga hutchinsonii	COG1173: ABC-type dipeptide/oligopeptide/nickel transport systems, permease components [Cytophaga hutchinsonii]			
18631, 18632	34398049	55	8.00E-40	Porphyromonas gingivalis W83	conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_906210.1 hypothetical protein PG2158 [Porphyromonas gingivalis W83]			
18633, 18634	55246965	69	1.00E-36	Anopheles gambiae str. PEST	ENSANGP000000000220 [Anopheles gambiae str. PEST] ref XP_561052.1 ENSANGP000000000220 [Anopheles gambiae str. PEST]			2.3.1.30
18635, 18636	48850961	69	1.00E-40	Novosphingobium aromaticivorans DSM 12444	COG0250: Transcription antiterminator [Novosphingobium aromaticivorans DSM 12444]			
18637, 18638	27366639	50	1.00E-22	Vibrio vulnificus CMCP6	Deoxycytidylate deaminase [Vibrio vulnificus CMCP6] gb AAO07156.1 Deoxycytidylate deaminase [Vibrio vulnificus CMCP6]			
18639, 18640	21702210	34	9.00E-18	Flavobacterium sp. 92	cyclomaltodextrinase [Flavobacterium sp. 92]			
18643, 18644	28974569	28	1.00E-11	Pseudomonas sp. Y2	putative ring-oxydation complex protein 5 [Pseudomonas sp. Y2]			1.18.1.2

18647, 18648	29348988	50	2.00E-71	Bacteroides thetaiotaomicron VPI-5482	topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] gb AAO78685.1 topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482]				5.99.1.-
18651, 18652	48855884	46	5.00E-21	Cytophaga hutchinsonii	COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii]				
18653, 18654	15643161	33	5.00E-25	Thermotoga maritima MSB8	NADH oxidase, putative [Thermotoga maritima MSB8] gb AAD35480.1 NADH oxidase, putative [Thermotoga maritima MSB8] pir J72382 hypothetical protein TM0395 - Thermotoga maritima (strain MSB8)				1.6.-
18655, 18656	48853860	65	1.00E-40	Cytophaga hutchinsonii	hypothetical protein Chut02003506 [Cytophaga hutchinsonii]	Desulfotalea psychrophila LSv54 chromosome	81	5.00E-12	
18657, 18658	21674610	55	1.00E-10	Chlorobium tepidum TLS	hypothetical protein CT1796 [Chlorobium tepidum TLS] gb AAM73017.1 hypothetical protein [Chlorobium tepidum TLS]				
18659, 18660	53691661	55	3.00E-43	Desulfovibrio desulfuricans G20	COG3039: Transposase and inactivated derivatives, IS5 family [Desulfovibrio desulfuricans G20]				
18661, 18662	29349972	62	1.00E-79	Bacteroides thetaiotaomicron VPI-5482	putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79669.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.4.1.83
18663, 18664	29349649	44	9.00E-74	Bacteroides thetaiotaomicron VPI-5482	beta-galactosidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79346.1 beta-galactosidase [Bacteroides thetaiotaomicron VPI- 5482]				3.2.1.23
18669, 18670	45658173	27	8.00E-10	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	hypothetical protein LIC12325 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_711602.1 hypothetical protein LA1421 [Leptospira interrogans serovar Lai str. 56601] gb AAN48620.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS70896.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				
18671, 18672	48837936	44	2.00E-43	Methanosarcina barkeri str. fusaro	COG1162: Predicted GTPases [Methanosarcina barkeri str. fusaro]				3.6.1.-
18677, 18678	39997048	43	2.00E-30	Geobacter sulfurreducens PCA	capK related-protein [Geobacter sulfurreducens PCA] gb AAR35326.1 capK related-protein [Geobacter sulfurreducens PCA]				
18679, 18680	48854755	54	8.00E-71	Cytophaga hutchinsonii	COG0774: UDP-3-O-acetyl-N-acetylglucosamine deacetylase [Cytophaga hutchinsonii]				4.2.1.-
18681, 18682	34397292	52	2.00E-24	Porphyromonas gingivalis W83	translation elongation factor P [Porphyromonas gingivalis W83] ref NP_905456.1 translation elongation factor P [Porphyromonas gingivalis W83] sp Q7MV32 EFP2_PORGI Elongation factor P 2 (EF-P 2)	Orion yellows phytoplasma OY-M DNA, complete genome	92	2.00E-11	

18683, 18684	29345629	43	5.00E-17	Bacteroides thetaiotaomicron VPI-5482	thioredoxin C-2 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75326.1] thioredoxin C-2 [Bacteroides thetaiotaomicron VPI-5482]				1.6.4.5
18685, 18686	15614651	68	3.00E-45	Bacillus halodurans C-125	hypothetical protein BH2088 [Bacillus halodurans C-125] dbj BAB05807.1] BH2088 [Bacillus halodurans C-125] pir H83910 hypothetical protein BH2088 [imported] - Bacillus halodurans (strain C-125) dbj BAA75367.1] Ydel [Bacillus halodurans]				
18687, 18688	53712279	24	3.00E-16	Bacteroides fragilis YCH46	outer membrane assembly protein [Bacteroides fragilis YCH46] dbj BAD47737.1] outer membrane assembly protein [Bacteroides fragilis YCH46]				
18689, 18690	48854415	42	1.00E-44	Cytophaga hutchinsonii	COG3279: Response regulator of the LysR/AigR family [Cytophaga hutchinsonii]				
18691, 18692	48860518	52	6.00E-21	Clostridium thermocellum ATCC 27405	COG0261: Ribosomal protein L21 [Clostridium thermocellum ATCC 27405]				
18693, 18694	48856677	37	6.00E-44	Cytophaga hutchinsonii	COG0232: dGTP triphosphohydrolase [Cytophaga hutchinsonii]				3.1.5.1
18695, 18696	48856576	46	7.00E-45	Cytophaga hutchinsonii	COG1071: Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, alpha subunit [Cytophaga hutchinsonii]				1.2.4.1
18697, 18698	46202152	37	3.00E-40	Magnetospirillum magnetotacticum MS-1	COG0582: Integrase [Magnetospirillum magnetotacticum MS-1]				
18701, 18702	31195865	75	3.00E-46	Anopheles gambiae	ENSANGP00000000381 [Anopheles gambiae]	Anopheles gambiae ENSANGP00000000 0381 (ENSANGG00000000 00361) mRNA, partial cds	87	3.00E-10	4.4.1.11
18703, 18704	29345661	69	5.00E-88	Bacteroides thetaiotaomicron VPI-5482	dolichol-phosphate mannosyltransferase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO75358.1] dolichol-phosphate mannosyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.4.1.83
18709, 18710	48856872	57	7.00E-70	Cytophaga hutchinsonii	COG1533: DNA repair photolyase [Cytophaga hutchinsonii]				
18711, 18712	21229991	39	1.00E-16	Xanthomonas campestris pv. campestris str. ATCC 33913	hypothetical protein XCC0516 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM39832.1] conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913]				

18713, 18714	56460818	32	5.00E-19	Idiomarina loihensis L2TR	Secreted enzyme, contains two amidohydrolase related domains [Idiomarina loihensis L2TR] gb AAV82550.1 Secreted enzyme, contains two amidohydrolase related domains [Idiomarina loihensis L2TR]				
18715, 18716	48859742	30	1.00E-31	Clostridium thermocellum ATCC 27405	hypothetical protein Chte02000885 [Clostridium thermocellum ATCC 27405]				
18717, 18718	37522197	25	5.00E-13	Gloeobacter violaceus PCC 7421	hypothetical protein gli2628 [Gloeobacter violaceus PCC 7421] dbj BAC90569.1 gli2628 [Gloeobacter violaceus PCC 7421]				
18719, 18720	32474463	47	3.00E-15	Rhodopirellula baltica SH 1	choline sulfatase [Rhodopirellula baltica SH 1] emb CAD75003.1 choline sulfatase [Pirellula sp.]				
18723, 18724	29347646	45	3.00E-20	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT2236 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77343.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A5K3 YM36_BACTN Hypothetical UPF0102 protein BT2236				3.1--
18725, 18726	48853984	42	1.00E-30	Cytophaga hutchinsonii	COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii]				
1873, 1874	48858374	35	1.00E-19	Clostridium thermocellum ATCC 27405	COG2908: Uncharacterized protein conserved in bacteria [Clostridium thermocellum ATCC 27405]				
18731, 18732	45659049	26	1.00E-14	Leptospira interrogans serovar Copenhageni str. Floeruz L1-130	hypothetical protein LIC13227 [Leptospira interrogans serovar Copenhageni str. Floeruz L1-130] ref NP_714224.1 hypothetical protein LA4044 [Leptospira interrogans serovar Lai str. 56601] gb AAN51242.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS71772.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Floeruz L1-130]				
18733, 18734	53734828	31	3.00E-08	Crocospaera watsonii WH 8501	COG0463: Glycosyltransferases involved in cell wall biogenesis [Crocospaera watsonii WH 8501]				
18735, 18736	53729796	64	5.00E-69	Dechloromonas aromatica RCB	COG0178: Excinuclease ATPase subunit [Dechloromonas aromatica RCB]				
18739, 18740	48853553	37	2.00E-19	Cytophaga hutchinsonii	COG0715: ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components [Cytophaga hutchinsonii]				
18741, 18742	48855418	66	2.00E-79	Cytophaga hutchinsonii	COG0535: Predicted Fe-S oxidoreductases [Cytophaga hutchinsonii]				
18743, 18744	28212164	56	3.00E-52	Clostridium tetani E88	LSU ribosomal protein L6P [Clostridium tetani E88] gb AAO37045.1 LSU ribosomal protein L6P [Clostridium tetani E88]				
18745, 18746	29606128	37	2.00E-14	Streptomyces avermittis MA-4680	hypothetical protein [Streptomyces avermittis MA-4680] ref NP_823656.1 hypothetical protein SAV2480 [Streptomyces avermittis MA-4680]				

18747, 18748	46119348	43	5.00E-08	Crocospaera watsonii WH 8501	COG0607: Rhodanese-related sulfotransferase [Crocospaera watsonii WH 8501]				
18749, 18750	29348486	60	1.00E-65	Bacteroides thetataoamicon VPI-5482	ribonuclease R [Bacteroides thetataoamicon VPI-5482] gb AAO78183.1 ribonuclease R [Bacteroides thetataoamicon VPI-5482]	Apis mellifera similar to SD10981p (LOC413944), mRNA	91	5.00E-10	3.1.-
18751, 18752 18753, 18754	56459804	29	4.00E-20	Idiomarina lohiensis L2TR	Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina lohiensis L2TR] gb AAV81536.1 Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina lohiensis L2TR]				
18755, 18756	19068097	57	3.00E-26	Bacteroides fragilis	unknown [Bacteroides fragilis]	Treponema denticola ATCC 35405, section 3 of 10 of the complete genome	95	1.00E-07	
18757, 18758	48853695	46	2.00E-52	Cytophaga hutchinsonii	hypothetical protein Chut02003551 [Cytophaga hutchinsonii]				
18761, 18762	29349192	60	5.00E-83	Bacteroides thetataoamicon VPI-5482	putative alpha-1,2-mannosidase [Bacteroides thetataoamicon VPI-5482] gb AAO78889.1 putative alpha-1,2-mannosidase [Bacteroides thetataoamicon VPI-5482]				
18763, 18764	48856934	36	7.00E-49	Cytophaga hutchinsonii	COG1058: Predicted nucleotide-utilizing enzyme related to molybdopterh- biosynthesis enzyme MoeA [Cytophaga hutchinsonii]				
	49482329	59	7.00E-43	Staphylococcus aureus subsp. aureus MRSA252	putative restriction enzyme [Staphylococcus aureus subsp. aureus MRSA252] emb CAG39114.1 putative restriction enzyme [Staphylococcus aureus subsp. aureus MRSA252]				3.1.21.-

18765, 18766	57285120	36	4.00E-14	Staphylococcus aureus subsp. aureus COL	transcriptional regulatory protein DegU, putative [Staphylococcus aureus subsp. aureus COL] ref YP_044394.1 putative response regulator [Staphylococcus aureus subsp. aureus MSSA476] ref NP_647130.1 hypothetical protein MW2313 [Staphylococcus aureus subsp. aureus MW2] ref NP_375502.1 hypothetical protein SA2179 [Staphylococcus aureus subsp. aureus N315] emb CAG44095.1 putative response regulator [Staphylococcus aureus subsp. aureus MSSA476] db BAB58553.1 response regulators of two-component regulatory [Staphylococcus aureus subsp. aureus Mu50] db BAB96178.1 MW2313 [Staphylococcus aureus subsp. aureus MW2] db BAB43481.1 SA2179 [Staphylococcus aureus subsp. aureus N315] pir H90039 hypothetical protein SA2179 [imported] - Staphylococcus aureus (strain N315) ref NP_372915.1 response regulators of two-component regulatory [Staphylococcus aureus subsp. aureus Mu50] ref YP_187192.1 transcriptional regulatory protein DegU, putative [Staphylococcus aureus subsp. aureus COL]				
18767, 18768	39995500	43	1.00E-08	Geobacter sulfurreducens PCA	efflux transporter, RND family, MFP subunit [Geobacter sulfurreducens PCA] gb AAR33724.1 efflux transporter, RND family, MFP subunit [Geobacter sulfurreducens PCA]				
18769, 18770	48847126	48	2.00E-64	Geobacter metallireducens GS-15	COG0841: Cation/multidrug efflux pump [Geobacter metallireducens GS-15]				
18773, 18774	24214680	36	5.00E-28	Leptospira interrogans serovar Lai str. 56601	hypothetical protein LA1980 [Leptospira interrogans serovar Lai str. 56601] gb AAN49179.1 hypothetical protein [Leptospira interrogans serovar lai str. 56601]				
18779, 18780	17232048	61	6.00E-20	Nostoc sp. PCC 7120	hypothetical protein al4556 [Nostoc sp. PCC 7120] db BAB76255.1 al4556 [Nostoc sp. PCC 7120] pir AD2375 hypothetical protein al4556 [imported] - Nostoc sp. (strain PCC 7120)				
18781, 18782	48853836	59	2.00E-85	Cytophaga hutchinsonii	COG1363: Cellulase M and related proteins [Cytophaga hutchinsonii]				3.2.1.4
18783, 18784	48861416	75	2.00E-50	Microbulifer degradans 2-40	COG0177: Predicted Endolli-related endonuclease [Microbulifer degradans 2-40]				4.2.99.1
18787, 18788	29346789	62	2.00E-55	Bacteroides thetaiotaomicron VPI-5482	phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide (ProFAR) isomerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76486.1 phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide (ProFAR) isomerase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A7Z5 HIS4_BACTN 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase (Phosphoribosylformimino-5-aminimidazole carboxamide ribotide isomerase)				5.3.1.16

1879, 1880	29608208	42	1.00E-23	Streptomyces avermitilis MA-4680	putative aminotransferase [Streptomyces avermitilis MA-4680] ref NP_825728.1 putative aminotransferase [Streptomyces avermitilis MA-4680]				2.6.1.-
18791, 18792	12518097	52	2.00E-79	Escherichia coli O157:H7	gamma-glutamyltranspeptidase [Escherichia coli O157:H7] ref NP_289992.1 gamma-glutamyltranspeptidase [Escherichia coli O157:H7 EDL933] ref NP_312320.1 gamma-glutamyltranspeptidase [Escherichia coli O157:H7] dbj BAB37716.1 gamma-glutamyltranspeptidase [Escherichia coli O157:H7] pir E86011 gamma-glutamyltranspeptidase [imported] - Escherichia coli (strain O157:H7, substrain EDL933) pir E91165 gamma- glutamyltranspeptidase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)				2.3.2.2
18797, 18798	21674986	60	3.00E-52	Chlorobium tepidum TLS	ribosomal protein L5 [Chlorobium tepidum TLS] gb AAM73393.1 ribosomal protein L5 [Chlorobium tepidum TLS] sp Q8KA4 RL5_CHL TE 50S ribosomal protein L5				
18799, 18800	47568001	38	3.00E-22	Bacillus cereus G9241	phospholipid N-methyltransferase, putative [Bacillus cereus G9241] gb EAL13649.1 phospholipid N-methyltransferase, putative [Bacillus cereus G9241]				2.1.1.17
18801, 18802	56750401	31	1.00E-18	Synechococcus elongatus PCC 6301	hypothetical protein syc0392_d [Synechococcus elongatus PCC 6301] dbj BAD78582.1 hypothetical protein [Synechococcus elongatus PCC 6301]				2.7.3.-
18803, 18804	23098185	28	4.00E-09	Oceanobacillus ihayensis HTE831	hypothetical protein OB0730 [Oceanobacillus ihayensis HTE831] dbj BAC12686.1 hypothetical conserved protein [Oceanobacillus ihayensis HTE831]				
18809, 18810	16329452	51	3.00E-42	Synechocystis sp. PCC 6803	hypothetical protein sil1188 [Synechocystis sp. PCC 6803] dbj BAA16860.1 sil1188 [Synechocystis sp. PCC 6803] pir S74709 hypothetical protein sil1188 - Synechocystis sp. (strain PCC 6803)				
18811, 18812	34396325	55	2.00E-30	Porphyromonas gingivalis W83	signal recognition particle-docking protein FtsY [Porphyromonas gingivalis W83] ref NP_904493.1 signal recognition particle-docking protein FtsY [Porphyromonas gingivalis W83]				
18813, 18814	48854229	54	8.00E-74	Cytophaga hutchinsonii	COG2723: Beta-glucosidase/6-phospho-beta-glucosidase/beta- galactosidase [Cytophaga hutchinsonii]				3.2.1.21
18815, 18816	52420939	44	2.00E-57	Escherichia coli	putative restriction modification enzyme S subunit [Escherichia coli]				3.1.21.3
18817, 18818	22297790	33	2.00E-37	Thermosynechococ cus elongatus BP-1	putative glycosyltransferase [Thermosynechococcus elongatus BP-1] dbj BAC07799.1 tr0246 [Thermosynechococcus elongatus BP-1]				
18821, 18822	54294788	30	2.00E-21	Legionella pneumophila str. Lens	hypothetical protein lp1865 [Legionella pneumophila str. Lens] emb CAH16104.1 hypothetical protein [Legionella pneumophila str. Lens]				2.4.1.-

18827, 18828	17229587	41	3.00E-35	Nostoc sp. PCC 7120	two-component sensor histidine kinase [Nostoc sp. PCC 7120] pir A 2067 two-component sensor histidine kinase all2095 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73794.1 two-component sensor histidine kinase [Nostoc sp. PCC 7120]				2.7.3.-
1883, 1884	23128083	44	9.00E-60	Nostoc punctiforme PCC 73102	COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102]				2.7.3.-
18831, 18832	46117862	33	2.00E-20	Crocospaera watsonii WH 8501	COG0500: SAM-dependent methyltransferases [Crocospaera watsonii WH 8501]				2.1.1.64
18839, 18840	48868784	40	1.00E-18	Haemophilus influenzae 86- 028NP	COG1393: Arsenate reductase and related proteins, glutaredoxin family [Haemophilus influenzae 86-028NP]				1.-.-.-
18843, 18844	48853747	64	2.00E-73	Cytophaga hutchinsonii	COG0441: Threonyl-tRNA synthetase [Cytophaga hutchinsonii]				6.1.1.3
18845, 18846	53715747	76	7.00E-76	Bacteroides fragilis YCH46	adenosylhomocysteinase [Bacteroides fragilis YCH46] dbj BAD51205.1 adenosylhomocysteinase [Bacteroides fragilis YCH46]	Bdellovibrio bacteriovorus complete genome, strain HD 100; segment 4/11	89	4.00E-13	3.3.1.1
1885, 1886	28211485	34	1.00E-19	Clostridium tetani E88	two-component sensor kinase yesM [Clostridium tetani E88]				2.7.3.-
18853, 18854	46202304	25	7.00E-16	Magnetospirillum magnetotacticum MS-1	COG2931: RTX toxins and related Ca ²⁺ -binding proteins [Magnetospirillum magnetotacticum MS-1]				
18863, 18864	23452763	35	7.00E-10	Campylobacter jejuni	RloA [Campylobacter jejuni]				
18867, 18868	48863689	45	2.00E-19	Microbulbifer degradans 2-40	COG0346: Lactoylglutathione lyase and related lyases [Microbulbifer degradans 2-40]				
1887, 1888	34397532	69	2.00E-63	Porphyromonas gingivalis W83	dTDP-glucose 4,6-dehydratase [Porphyromonas gingivalis W83] ref NP_905695.1 dTDP-glucose 4,6-dehydratase [Porphyromonas gingivalis W83] dbj BAD18851.1 dTDP-glucose 4,6-dehydratase [Porphyromonas gingivalis]				4.2.1.46
18873, 18874	23002261	30	2.00E-17	Lactobacillus gasseri	COG1074: ATP-dependent exoDNase (exonuclease V) beta subunit (contains helicase and exonuclease domains) [Lactobacillus gasseri]				3.6.1.-

18875,						oligoendopeptidase f [Bacillus anthracis str. 'Ames Ancestor'] ref NP_027386.1 oligoendopeptidase F [Bacillus anthracis str. Sterne]					
18876	47526469	40	2.00E-18		Bacillus anthracis str. 'Ames Ancestor'						3.4.24.-
18879,											
18880	22726420	45	6.00E-53		Ruegeria sp. PR1b	RC142 [Ruegeria sp. PR1b] ref NP_788129.1 putative pirin-like protein					
18881,											
18882	48855993	54	5.00E-83		Cytophaga hutchinsonii	COG1233: Phytoene dehydrogenase and related proteins [Cytophaga hutchinsonii]					
1889,											
1890	34397532	69	2.00E-63		Porphyromonas gingivalis W83	dTDP-glucose 4,6-dehydratase [Porphyromonas gingivalis W83] ref NP_905695.1 dTDP-glucose 4,6-dehydratase [Porphyromonas gingivalis W83] db BAD18851.1 dTDP-glucose 4,6-dehydratase [Porphyromonas gingivalis]				4.2.1.46	
18891,											
18892	31195605	73	5.00E-93		Anopheles gambiae	ENSANGP0000013686 [Anopheles gambiae]					
18893,											
18894	48855393	30	5.00E-33		Cytophaga hutchinsonii	COG0665: Glycine/D-amino acid oxidases (deaminating) [Cytophaga hutchinsonii]				88 2.00E-25	
18895,											
18896	42525629	32	1.00E-25		Treponema denticola ATCC 35405	M23/M37 peptidase domain protein [Treponema denticola ATCC 35405] gb AAS10608.1 M23/M37 peptidase domain protein [Treponema denticola ATCC 35405]					3.5.1.-
189,											
190	56675038	38	4.00E-14		uncultured bacterium	cellulase [uncultured bacterium]					
18901,											
18902	48854129	48	2.00E-41		Cytophaga hutchinsonii	COG0172: Seryl-tRNA synthetase [Cytophaga hutchinsonii]					6.1.1.11
18903,											
18904	45658998	58	6.00E-80		Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	Tas [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714153.1 Aldo/keto reductase family protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51171.1 Aldo/keto reductase family protein [Leptospira interrogans serovar Lai str. 56601] gb AAS71721.1 Tas [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]					1.1.1.-
18905,											
18906	53759004	54	9.00E-45		Methylococcus capsulatus str. Bath	peptidyl-prolyl cis-trans isomerase B [Methylococcus capsulatus str. Bath] ref YP_113035.1 peptidyl-prolyl cis-trans isomerase B [Methylococcus capsulatus str. Bath]					5.2.1.8

18909,	27366639	38	9.00E-07	Vibrio vulnificus	Deoxycytidylate deaminase [Vibrio vulnificus CMCP6] gb AAO07156.1]			
18910				CMCP6	Deoxycytidylate deaminase [Vibrio vulnificus CMCP6]			
1891,				Chloroflexus	COG2172: Anti-sigma regulatory factor (Ser/Thr protein kinase)			
1892	53795040	38	3.00E-21	aurantiacus	[Chloroflexus aurantiacus]			
18911,				Cytophaga				
18912	48856125	44	5.00E-16	hutchinsonii	COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii]			
18913,				Bacillus cereus	conserved hypothetical protein [Bacillus cereus G9241]			
18914	47566234	29	2.00E-10	G9241	gb EAL15118.1] conserved hypothetical protein [Bacillus cereus G9241]			
18915,				Wolinella				
18916	34557509	54	1.00E-73	succinogenes DSM 1740	hypothetical protein WS1135 [Wolinella succinogenes DSM 1740]			
18917,				Chlorobium	emb CAE10224.1] hypothetical protein [Wolinella succinogenes]			
18918	21672873	24	1.00E-09	tepidum TLS	FtsQ protein, putative [Chlorobium tepidum TLS] gb AAM71280.1] FtsQ protein, putative [Chlorobium tepidum TLS]			
18923,				Leptospira	Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN4862.1] Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601]			
18924	24214122	31	6.00E-31	Lai str. 56601				
18931,				Includes: Adenine-specific				
18932	586070	40	1.00E-35	methyltransferase activity	Restriction enzyme Bgl alpha subunit [Includes: Adenine-specific methyltransferase activity] pir J53125 restriction enzyme Bgl alpha chain -			2.1.1.72
18933,				Cytophaga	Bacillus coagulans gb AAA16626.1] restriction endonuclease alpha subunit			
18934	48855702	34	7.00E-35	hutchinsonii	COG3279: Response regulator of the LysR/AlaR family [Cytophaga hutchinsonii]			2.7.3.-
18935,				Cytophaga				
18936	48855017	42	2.00E-53	hutchinsonii	COG0501: Zn-dependent protease with chaperone function [Cytophaga hutchinsonii]			3.4.24.-
18937,				Cytophaga				
18938	48854863	58	2.00E-97	hutchinsonii	COG0358: DNA primase (bacterial type) [Cytophaga hutchinsonii]			2.7.7.-
18939,				Methanosarcina	(S)-2-hydroxy-acid dehydrogenase [Methanosarcina mazel Go1]			
18940	21227393	42	4.00E-32	mazel Go1	gb AAM30987.1] (S)-2-hydroxy-acid dehydrogenase [Methanosarcina mazel Go1]			1.1.3.15
18945,				Oenococcus oeni	COG2017: Galactose mutarotase and related enzymes [Oenococcus oeni PSU-1]			
18946	48865028	42	6.00E-26	PSU-1				
18947,				Cytophaga				
18948	48855111	71	3.00E-65	hutchinsonii	COG0262: Dihydrofolate reductase [Cytophaga hutchinsonii]			3.4.24.-
18949,				Erwinia carotovora	long-chain-fatty-acid--CoA ligase [Erwinia carotovora subsp. atroseptica SCR11043] emb CAG75275.1] long-chain-fatty-acid--CoA ligase [Erwinia carotovora subsp. atroseptica SCR11043]			
18950	50121300	58	2.00E-70	SCR11043				6.2.1.3

1895, 1896									Desc:Drosophila melanogaster expressed polynucleotide SEQ ID NO 38933. Org:Drosophila melanogaster	97	2.00E-07	
18951, 18952	29349255	24	2.00E-10	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3847 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78952.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]							
18953, 18954	28900645	34	4.00E-20	Vibrio parahaemolyticus RIMD 2210633	putative YnfP protein [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62133.1 putative YnfP protein [Vibrio parahaemolyticus]							
18955, 18956	56677851	30	3.00E-21	Silicibacter pomeroyi DSS-3	site-specific recombinase, resolvase family [Silicibacter pomeroyi DSS-3] ref YP_166469.1 site-specific recombinase, resolvase family [Silicibacter pomeroyi DSS-3]							
18957, 18958	48854777	43	2.00E-44	Cytophaga hutchinsonii	COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii]							
18959, 18960	48853532	32	6.00E-29	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]							
18961, 18962	48853531	51	1.00E-54	Cytophaga hutchinsonii	COG0020: Undecaprenyl pyrophosphate synthase [Cytophaga hutchinsonii]							
18963, 18964	34396493	35	2.00E-36	Porphyromonas gingivalis W83	ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83] ref NP_904660.1 ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83]					##	5.00E-07	2.5.1.31
18967, 18968	21243825	32	5.00E-24	Xanthomonas axonopodis pv. citri str. 306	PilL protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM37943.1 PilL protein [Xanthomonas axonopodis pv. citri str. 306]							3.6.1.-
1897, 1898	16273484	45	9.00E-49	Haemophilus influenzae Rd KW20	hypothetical protein HI1590 [Haemophilus influenzae Rd KW20] gb AAC23238.1 conserved hypothetical protein [Haemophilus influenzae Rd KW20] pir F64172 hypothetical protein HI1590 - Haemophilus influenzae (strain Rd KW20) sp P45262 YCAJ_HAEIN Hypothetical protein HI1590							2.7.7.7
18971, 18972	52550067	34	1.00E-21	uncultured archaeon GZfos34H9	conserved hypothetical protein [uncultured archaeon GZfos34H9]							

18977, 18978	AAV3437 2	28	2.00E-08		Desc:Porphorymonas gingivalis protein PG39. Org:Porphorymonas gingivalis				
18981, 18982	13123737	70	3.00E-54	Campylobacter jejuni	putative acetyltransferase [Campylobacter jejuni]				
18983, 18984	57241824	46	1.00E-58	Campylobacter lari RM2100	phosphoribosylamine-glycine ligase [Campylobacter lari RM2100]				
18985, 18986	20091554	36	8.00E-08	Methanosarcina acetivorans C2A	hypothetical protein MA2730 [Methanosarcina acetivorans C2A]				
18987, 18988	48854785	36	1.00E-29	Cytophaga hutchinsonii	gb AAM06109.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A]				2.1.1.-
18989, 18990	48786618	42	6.00E-19	Burkholderia fungorum LB400	COG0513: Superfamily II DNA and RNA helicases [Cytophaga hutchinsonii]				2.7.7.-
1899, 1900	53712491	29	5.00E-32	Bacteroides fragilis YCH46	COG3324: Predicted enzyme related to lactoylglycine lyase [Burkholderia fungorum LB400]				
18991, 18992	34558170	29	1.00E-10	Wolinella succinogenes DSM 1740	putative nitrogen utilization substance protein [Bacteroides fragilis YCH46]				
18993, 18994	53713723	31	4.00E-30	Bacteroides fragilis YCH46	RIBONUCLEASE [Wolinella succinogenes DSM 1740] emb CAE10885.1				
18997, 18998	53713728	36	1.00E-37	Bacteroides fragilis YCH46	RIBONUCLEASE [Wolinella succinogenes]				
18999, 19000	30249662	45	2.00E-42	Nitrosomonas europaea ATCC 19718	hypothetical protein BF2432 [Bacteroides fragilis YCH46] db BAD49181.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
19001, 19002	26988709	32	1.00E-22	Pseudomonas putida KT2440	putative protease [Bacteroides fragilis YCH46] db BAD49186.1 putative protease [Bacteroides fragilis YCH46]				3.4.21.-
					Diguanylate cyclase/phosphodiesterase domain 2 [EAL] [Nitrosomonas europaea ATCC 19718] emb CAD85611.1 Diguanylate cyclase/phosphodiesterase domain 2 [EAL] [Nitrosomonas europaea ATCC 19718]				
					sensory box protein [Pseudomonas putida KT2440] gb AAN67598.1				
					sensory box protein [Pseudomonas putida KT2440]				2.7.3.-

19005, 19006	38233405	42	3.00E-38	Corynebacterium diphtheriae NCTC 13129	hypothetical protein DIP0806 [Corynebacterium diphtheriae NCTC 13129] emb CAE49324.1 Putative phage protein [Corynebacterium diphtheriae]				
19007, 19008	53712411	55	1.00E-38	Bacteroides fragilis YCH46	putative hypoxanthine guanine phosphoribosyltransferase [Bacteroides fragilis YCH46] gb AAD40728.1 putative hypoxanthine guanine phosphoribosyltransferase [Bacteroides fragilis] db BAD47869.1 putative hypoxanthine guanine phosphoribosyltransferase [Bacteroides fragilis YCH46]				2.4.2.8
19009, 19010	48853835	59	1.00E-24	Cytophaga hutchinsonii	COG0563: Adenylate kinase and related kinases [Cytophaga hutchinsonii] transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_812706.1 transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_811980.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] ref NP_810669.1 transposase, invertase [Bacteroides thetaiotaomicron VPI- 5482] ref NP_810516.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] ref NP_809398.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO79845.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78900.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78174.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76863.1 transposase, invertase [Bacteroides thetaitaomicron VPI-5482] gb AAO76710.1 transposase [Bacteroides thetaitaomicron VPI-5482] gb AAO75592.1 transposase [Bacteroides thetaitaomicron VPI-5482]				2.7.4.3
1901, 1902	29350148	51	1.00E-31	Bacteroides thetaitaomicron VPI-5482	hypothetical protein Bd2807 [Bdellovibrio bacteriovorus HD100] emb CAE80590.1 conserved hypothetical protein [Bdellovibrio bacteriovorus HD100]				
19011, 19012	42524217	28	4.00E-07	Bdellovibrio bacteriovorus HD100	COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii]				
19015, 19016	48855561	55	1.00E-42	Cytophaga hutchinsonii	COG0612: Predicted Zn-dependent peptidases [Cytophaga hutchinsonii]				3.4.-.-
19017, 19018	48855398	27	4.00E-22	Cytophaga hutchinsonii	hypothetical protein WS0260 [Wolinella succinogenes DSM 1740] emb CAE09415.1 conserved hypothetical protein [Wolinella succinogenes]				
19021, 19022	34556700	45	4.00E-27	Wolinella succinogenes DSM 1740	COG5544: Predicted periplasmic lipoprotein [Cytophaga hutchinsonii]				
19023, 19024	48856547	44	3.00E-49	Cytophaga hutchinsonii	MGC82638 protein [Xenopus laevis]				
19025, 19026	49256557	54	1.00E-60	Xenopus laevis	COG1575: 1,4-dihydroxy-2-naphthoate octaprenyltransferase [Cytophaga hutchinsonii]				4.2.1.17
19027, 19028	48855770	42	6.00E-17	Cytophaga hutchinsonii					2.5.1.-

19029, 19030	42524558	42	1.00E-53	Bdellovibrio bacteriovorus HD100	hypothetical protein Bd3175 [Bdellovibrio bacteriovorus HD100] emb CAE80931.1 ptrB [Bdellovibrio bacteriovorus HD100]			3.4.21.8 3
1903, 1904	48854665	44	1.00E-39	Cytophaga hutchinsonii	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii]			
19031, 19032	AA13439 9	39	2.00E-23		Desc.Porphorymonas gingivalis protein PG63. Org: Porphorymonas gingivalis			
19033, 19034	46446972	70	1.00E-70	Parachlamydia sp. UWE25	probable 3-methyladenine-DNA glycosylase I [Parachlamydia sp. UWE25] emb CAF24062.1 probable 3-methyladenine-DNA glycosylase I [Parachlamydia sp. UWE25]			3.2.2.20
19035, 19036	48831629	42	2.00E-31	Magnetococcus sp. MC-1	COG0248: Exopolyphosphatase [Magnetococcus sp. MC-1]			3.6.1.11
19037, 19038	21242876	39	7.00E-36	Xanthomonas axonopodis pv. citri str. 306	two-component system regulatory protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM36994.1 two-component system regulatory protein [Xanthomonas axonopodis pv. citri str. 306]			
19039, 19040	48856046	38	1.00E-40	Cytophaga hutchinsonii	COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii]			
19045, 19046	52080825	33	3.00E-33	Bacillus licheniformis ATCC 14580	two-component sensor histidine kinase ResE [Bacillus licheniformis ATCC 14580] gb AAU23978.1 two-component sensor histidine kinase ResE [Bacillus licheniformis ATCC 14580] ref YP_092025.1 ResE1 [Bacillus licheniformis ATCC 14580] gb AAU41332.1 ResE1 [Bacillus licheniformis DSM 13]			2.7.3.-
19049, 19050	53711887	48	2.00E-34	Bacteroides fragilis YCH46	putative alpha-rhamnosidase [Bacteroides fragilis YCH46] db BAD47345.1 putative alpha-rhamnosidase [Bacteroides fragilis YCH46]			
1905, 1906	54294440	43	5.00E-39	Legionella pneumophila str. Lens	Legionella secretion system protein D [Legionella pneumophila str. Lens] emb CAH15749.1 Legionella secretion system protein D [Legionella pneumophila str. Lens]			
19057, 19058	48856412	57	5.00E-50	Cytophaga hutchinsonii	COG3604: Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains [Cytophaga hutchinsonii]			
19061, 19062	29346818	43	3.00E-42	Bacteroides thetalaotomicron VPI-5482	putative Tricorn-like protease [Bacteroides thetalaotomicron VPI-5482] gb AAO76515.1 putative Tricorn-like protease [Bacteroides thetalaotomicron VPI-5482]			3.4.21.-
19063, 19064	15603199	42	6.00E-42	Pasteurella multocida subsp. multocida str. Pm70	ApbE [Pasteurella multocida subsp. multocida str. Pm70] gb AAK03418.1 ApbE [Pasteurella multocida subsp. multocida str. Pm70]			

19065, 19066	29350005	57	3.00E-68	Bacteroides thetaiotaomicron VPI-5482	endopeptidase Clp ATP-binding chain B [Bacteroides thetaiotaomicron VPI-5482] sp Q89Y3 CLPB_BACTN Chaperone clpB gb AAO79702.1 endopeptidase Clp ATP-binding chain B [Bacteroides thetaiotaomicron VPI-5482]	Desc: Genomic fragment #36. Org: Moraxella catarrhalis	82	5.00E-10	
19067, 19068 19069, 19070	15894574 44 48856243	44 46	9.00E-16 3.00E-28	Clostridium acetobutylicum ATCC 824 Cytophaga hutchinsonii	Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog [Clostridium acetobutylicum ATCC 824] gb AAK79263.1 Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog [Clostridium acetobutylicum ATCC 824] pir D97059 membrane protein containing HD superfamily hydrolase domain, YQFF ortholog [imported] - Clostridium acetobutylicum				
19071, 19072	21674236	40	2.00E-34	Chlorobium tepidum TLS	COG1284: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
19073, 19074	52425551	39	4.00E-22	Mannheimia succiniciproducens MBEL55E	hypothetical protein CT1415 [Chlorobium tepidum TLS] gb AAM72643.1 conserved hypothetical protein [Chlorobium tepidum TLS]				
19075, 19076	34103421	49	5.00E-30	Chromobacterium violaceum ATCC 12472	RfaG protein [Mannheimia succiniciproducens MBEL55E] gb AAU38103.1 RfaG protein [Mannheimia succiniciproducens MBEL55E] probable methyltransferase [Chromobacterium violaceum ATCC 12472] ref NP_901781.1 probable methyltransferase [Chromobacterium violaceum ATCC 12472]			2.4.1.-	
19077, 19078 19079, 19080	52082575 48854173	33 29	1.00E-15 5.00E-11	Bacillus licheniformis ATCC 14580 Cytophaga hutchinsonii	hypothetical protein BL00270 [Bacillus licheniformis ATCC 14580] gb AAU25728.1 hypothetical protein BL00270 [Bacillus licheniformis ATCC 14580] ref YP_093799.1 hypothetical protein BL04293 [Bacillus licheniformis ATCC 14580] gb AAU43106.1 hypothetical protein BL04293 [Bacillus licheniformis DSM 13]				
19081, 19082 19083, 19084 19085, 19086 19087, 19088	29348873 48864132 9857170 48854793	31 30 24 58	1.00E-35 8.00E-12 9.00E-25 2.00E-91	Bacteroides thetaiotaomicron VPI-5482 Microbulbifer degradans 2-40 Streptomyces coelicolor A3(2) Cytophaga hutchinsonii	putative peptidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78570.1 putative peptidase [Bacteroides thetaiotaomicron VPI-5482] COG0582: Integrase [Microbulbifer degradans 2-40] hypothetical protein [Streptomyces coelicolor A3(2)] ref NP_628388.1 hypothetical protein SCO4213 [Streptomyces coelicolor A3(2)] COG1109: Phosphomannomutase [Cytophaga hutchinsonii]				5.4.2.8
19089, 19090	30018689	36	5.00E-22	Bacillus cereus ATCC 14579	Penicillin-binding protein [Bacillus cereus ATCC 14579] gb AAP07521.1 Penicillin-binding protein [Bacillus cereus ATCC 14579]				3.5.2.6

1909, 1910	42630962	30	3.00E-25	Haemophilus Influenzae R2866	COG3587: Restriction endonuclease [Haemophilus influenzae R2866]				3.1.21.5
19091, 19092				Bacteroides thetaiotaomicron	hypothetical protein BT0582 [Bacteroides thetaiotaomicron VPI-5482]				
	29345992	59	3.00E-30	VPI-5482	gblAAO75689.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
19095, 19096					two-component system sensor histidine kinase/response regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482]				
19095, 19096				Bacteroides thetaiotaomicron	gblAAO79216.1 two-component system sensor histidine kinase/response regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-
19097, 19098	29349519	30	2.00E-30	VPI-5482	hypothetical protein Avin02000281 [Azotobacter vinelandii]				
19097, 19098	53613162	29	2.00E-08	Azotobacter vinelandii	hypothetical SAM-dependent methyltransferase [Photobacterium profundum SS9] embjCAG22764.1 hypothetical SAM-dependent methyltransferase [Photobacterium profundum]				
19099, 19100	54302571	49	4.00E-34	Photobacterium profundum SS9	COG2114: Adenylate cyclase, family 3 (some proteins contain HAM/P domain) [Magnetococcus sp. MC-1]				
19101, 19102	48833211	35	2.00E-12	Magnetococcus sp. MC-1	COG0363: 6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase [Cytophaga hutchinsonii]				3.5.99.6
19103, 19104	48853763	48	1.00E-36	Cytophaga hutchinsonii	transcriptional repressor of sporulation and degradative enzymes production [Geobacillus kaustophilus HTA426] dbj BAD75999.1 transcriptional repressor of sporulation and degradative enzymes production [Geobacillus kaustophilus HTA426]				
19105, 19106	56420249	39	4.00E-35	Geobacillus kaustophilus HTA426	COG0302: GTP cyclohydrolase I [Cytophaga hutchinsonii]				3.5.4.16
19107, 19108	48854835	77	3.00E-45	Cytophaga hutchinsonii	type III restriction-modification system Styl.TI enzyme mod [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]				
				Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	gblAAV78249.1 type III restriction-modification system Styl.TI enzyme mod [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]				2.1.1.72
1911, 1912	56414486	33	6.00E-26	Bacteroides thetaiotaomicron	RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI- 5482] gblAAO77599.1 RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482]				
19113, 19114	29347902	30	2.00E-17	VPI-5482	SEC-independent protein translocase protein TATC [Bdellovibrio bacteriovorus HD100] embjCAE80315.1 SEC-independent protein translocase protein TATC [Bdellovibrio bacteriovorus HD100]				
19115, 19116	42523942	28	5.00E-11	Bdellovibrio bacteriovorus HD100	COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Rubrobacter xylanophilus DSM 9941]				
19119, 19120	45547643	32	5.00E-34	Rubrobacter xylanophilus DSM 9941	Desc: Putative glycosyltransferase, involved in cell wall biogenesis #1. Org: Pyrococcus abyssi				2.4.-.-
19121, 19122	AAB9631	41	3.00E-40						

19123, 19124	23117013	54	2.00E-51	Desulfotobacterium hafnense DCB-2	COG0266: Formamidopyrimidine-DNA glycosylase [Desulfotobacterium hafnense DCB-2]			3.2.2.23
1913, 1914	23127436	31	1.00E-17	Nostoc punctiforme PCC 73102	COG0465: ATP-dependent Zn proteases [Nostoc punctiforme PCC 73102]			2.7.1.-
19131, 19132	48861674	51	2.00E-35	Microbulbifer degradans 2-40	COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Microbulbifer degradans 2-40]			
19133, 19134	58459705	37	2.00E-18	Idiomarina loihlensis L2TR	Cation transport ATPase [Idiomarina loihlensis L2TR] gb AAV81437.1]			3.6.3.4
19139, 19140	21674082	67	6.00E-73	Chlorobium tepidum TLS	PhoH family protein [Chlorobium tepidum TLS] gb AAM72489.1] PhoH family protein [Chlorobium tepidum TLS]	Desc:Staphylococ- cus epidermidis ORF nucleic acid sequence SEQ ID NO:839. Org:Staphylococcus epidermidis	88 5.00E-10	
19141, 19142	42522964	43	8.00E-15	Bdellovibrio bacteriovorus HD100	transcriptional regulator, MarR family [Bdellovibrio bacteriovorus HD100] emb CAE79337.1] transcriptional regulator, MarR family [Bdellovibrio bacteriovorus HD100]			
19145, 19146	29346568	44	5.00E-23	Bacteroides thetaiotaomicron VPI-5482	Na+-translocating NADH-quinone reductase subunit [Bacteroides thetaiotaomicron VPI-5482] gb AAO76265.1] Na+-translocating NADH- quinone reductase subunit [Bacteroides thetaiotaomicron VPI-5482]			1.6.5.-
19147, 19148	26989028	46	3.00E-23	Pseudomonas putida KT2440	hypothetical protein PP2305 [Pseudomonas putida KT2440] gb AAN67918.1] conserved hypothetical protein [Pseudomonas putida KT2440]			3.4.21.-
19149, 19150	23013248	33	3.00E-26	Magnetospirillum magnetotacticum MS-1	COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1]			2.7.3.-
1915, 1916	48854041	35	2.00E-28	Cytophaga hutchinsonii	COG2808: Transcriptional regulator [Cytophaga hutchinsonii]			
19151, 19152	54401435	41	7.00E-29	Salmonella enterica subsp. salamae serovar Greenside	UDP-GlcNAc 4-epimerase [Salmonella enterica subsp. salamae serovar Greenside]			4.2.1.46
19155, 19156	48863906	46	1.00E-52	Microbulbifer degradans 2-40	hypothetical protein Mdeg02000268 [Microbulbifer degradans 2-40]			
19157, 19158	48853745	27	5.00E-17	Cytophaga hutchinsonii	hypothetical protein Chut02003380 [Cytophaga hutchinsonii]			

19159, 19160	28899839	48	3.00E-43	Vibrio parahaemolyticus RIMD 2210633	putative cyclohexadienyl dehydratase precursor signal peptide protein [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61328.1 putative cyclohexadienyl dehydratase precursor signal peptide protein [Vibrio parahaemolyticus]				4.2.-.-
19161, 19162	56677705	35	4.00E-17	Silicibacter pomeroiyi DSS-3	glutamine amidotransferase, class-I [Silicibacter pomeroiyi DSS-3] ref YP_166322.1 glutamine amidotransferase, class-I [Silicibacter pomeroiyi DSS-3]				
19165, 19166	34397542	32	1.00E-32	Porphyromonas gingivalis W83	transcriptional regulator, Crp family [Porphyromonas gingivalis W83] ref NP_905705.1 transcriptional regulator, Crp family [Porphyromonas gingivalis W83]				
19169, 19170	48855281	42	4.00E-28	Cytophaga hutchinsonii	COG0484: DnaJ-class molecular chaperone with C-terminal Zn finger domain [Cytophaga hutchinsonii]				
1917, 1918	48855210	49	3.00E-96	Cytophaga hutchinsonii	COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii]				
19173, 19174	57236797	39	1.00E-48	Flavobacterium johnsoniae	SprA [Flavobacterium johnsoniae]				
19175, 19176	48830838	73	6.00E-74	Magnetococcus sp. MC-1	COG1961: Site-specific recombinases, DNA invertase Pin homologs [Magnetococcus sp. MC-1]				
19177, 19178	40063063	27	1.00E-15	uncultured bacterium 560	transcriptional activator, putative, Baf family [uncultured bacterium 560] conserved hypothetical protein [Streptomyces coelicolor A3(2)]				6.3.4.15
19179, 19180	24418969	30	5.00E-18	Streptomyces coelicolor A3(2)	ref NP_733735.1 hypothetical protein SCO7509 [Streptomyces coelicolor A3(2)]				
19181, 19182	53712337	43	6.00E-25	Bacteroides fragilis YCH46	RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD47795.1 RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46]				
19183, 19184	48853549	40	7.00E-48	Cytophaga hutchinsonii	COG0277: FAD/FMN-containing dehydrogenases [Cytophaga hutchinsonii]				1.1.99.5
19185, 19186	53712491	33	3.00E-23	Bacteroides fragilis YCH46	putative nitrogen utilization substance protein [Bacteroides fragilis YCH46] dbj BAD47949.1 putative nitrogen utilization substance protein [Bacteroides fragilis YCH46]				
19189, 19190	27382463	36	9.00E-13	Bradyrhizobium japonicum USDA 110	hypothetical protein bll7352 [Bradyrhizobium japonicum USDA 110] dbj BAC52617.1 bll7352 [Bradyrhizobium japonicum USDA 110]				
19191, 19192	15678468	43	2.00E-22	Methanothermobac ter thermautotrophicus str. Delta H	sensory transduction regulatory protein [Methanothermobacter thermautotrophicus str. Delta H] gb AAB84946.1 sensory transduction regulatory protein [Methanothermobacter thermautotrophicus str. Delta H] pir E69157 sensory transduction regulatory protein - Methanobacterium thermautotrophicum (strain Delta H)				2.7.3.-

19193, 19194, 19195, 19196, 19197, 19198, 19199, 19200, 19201, 19202, 19203, 19204, 19205, 19206, 19207, 19208, 19209, 19210, 19211, 19212	16802462 52142333 29654094 56316003 50935741 2281663 23014263 23014263 51246929 48838416 48892140	42 28 28 40 27 62 47 42 48 36 27	8.00E-07 2.00E-13 8.00E-16 2.00E-47 1.00E-27 7.00E-36 7.00E-25 4.00E-32 5.00E-64 6.00E-35 6.00E-11	Listeria monocytogenes EGD-e Bacillus cereus ZK Coxiella burnetii RSA 493 Azoarcus sp. Ebn1 Oryza sativa (japonica cultivar- group) Flavobacterium johnsoniae Magnetospirillum magnetotacticum MS-1 Magnetospirillum magnetotacticum MS-1 Desulfotalea psychrophila LSV54 Methanosarcina barkeri str. fusaro Trichodesmium erythraeum IMS101	hypothetical protein Imo0418 [Listeria monocytogenes EGD-e] ref YP_013044.1 hypothetical protein LMO7365_0437 [Listeria monocytogenes str. 4b F2365] ref ZP_00234032.1 conserved hypothetical protein [Listeria monocytogenes str. 1/2a F6854] ref ZP_00230268.1 conserved hypothetical protein [Listeria monocytogenes str. 4b H7858] gb EAL09815.1 conserved hypothetical protein [Listeria monocytogenes str. 4b H7858] gb EAL06100.1 conserved hypothetical protein [Listeria monocytogenes str. 1/2a F6854] emb CAC98497.1 Imo0418 [Listeria monocytogenes] gb AAT03221.1 conserved hypothetical protein [Listeria monocytogenes str. 4b F2365] pir AC1127 hypothetical protein Imo0418 [Imported] - Listeria monocytogenes (strain EGD-e) possible DNA helicase [Bacillus cereus ZK] gb AAU17352.1 possible DNA helicase [Bacillus cereus ZK] hypothetical protein CBU0762 [Coxiella burnetii RSA 493] gb AAO90300.1 hypothetical protein [Coxiella burnetii RSA 493] DNA repair protein [Azoarcus sp. Ebn1] late embryogenesis abundant proteins-like [Oryza sativa (japonica cultivar- group)] dbj BAC83841.1 late embryogenesis abundant proteins-like [Oryza sativa (japonica cultivar-group)] gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding motility protein [Imported] - Flavobacterium johnsoniae COG0458: Carbamoylphosphate synthase large subunit (split gene in MJ) [Magnetospirillum magnetotacticum MS-1] COG0458: Carbamoylphosphate synthase large subunit (split gene in MJ) [Magnetospirillum magnetotacticum MS-1] probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSV54] emb CAG37806.1 probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSV54] COG1413: FOG: HEAT repeat [Methanosarcina barkeri str. fusaro] COG2866: Predicted carboxypeptidase [Trichodesmium erythraeum IMS101]			3.6.1.- 3.4.21.- 3.4.21.- 3.4.21.-
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19213, 19214	16078046	49	2.00E-47	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU09810 [Bacillus subtilis subsp. subtilis str. 168] emb CAA74443.1 hypothetical protein [Bacillus subtilis] emb CAB12820.1 yhaZ [Bacillus subtilis subsp. subtilis str. 168] pir D69820 hypothetical protein yhaZ - Bacillus subtilis				
19215, 19216	29346307	59	1.00E-73	Bacteroides thetaiotaomicron VPI-5482	chaperone protein htpG (heat shock protein htpG) [Bacteroides thetaiotaomicron VPI-5482] gb AAO76004.1 chaperone protein htpG (heat shock protein htpG) [Bacteroides thetaiotaomicron VPI-5482]	Bacteroides thetaiotaomicron VPI-5482, section 4 of 21 of the complete genome	88	4.00E-08	
19217, 19218	46135592	43	5.00E-24	Anabaena variabilis ATCC 29413	hypothetical protein Avar03001063 [Anabaena variabilis ATCC 29413] hypothetical protein LJ0432 [Lactobacillus johnsonii NCC 533]				
19221, 19222	42518527	36	2.00E-12	Lactobacillus johnsonii NCC 533	gb AAS08423.1 hypothetical protein LJ0432 [Lactobacillus johnsonii NCC 533]				
19225, 19226	52082597	41	3.00E-13	Bacillus licheniformis ATCC 14580	putative Type I restriction-modification system M subunit [Bacillus licheniformis ATCC 14580] gb AAU25750.1 putative Type I restriction- modification system M subunit [Bacillus licheniformis ATCC 14580] ref YP_093823.1 hypothetical protein BLI04318 [Bacillus licheniformis ATCC 14580] gb AAU43130.1 putative protein [Bacillus licheniformis DSM 13] COG0286: Type I restriction-modification system methyltransferase subunit [Lactobacillus gasser]			2.1.1.72	
19227, 19228	23002416	64	1.00E-64	Lactobacillus gasser				2.1.1.72	
19229, 19230	46120266	36	2.00E-24	Crocospaera watsonii WH 8501	COG1051: ADP-ribose pyrophosphatase [Crocospaera watsonii WH 8501] COG5000: Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation [Cytophaga hutchinsonii]				
1923, 1924	48855461	36	4.00E-37	Cytophaga hutchinsonii				2.7.3.-	
19235, 19236	53712881	27	7.00E-17	Bacteroides fragilis YCH46	hypothetical protein BF1590 [Bacteroides fragilis YCH46] dbj BAD48339.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
19237, 19238	29346555	59	5.00E-64	Bacteroides thetaiotaomicron VPI-5482	glucose-inhibited division protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76252.1 glucose-inhibited division protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A8M2 GIDB_BACTN Methyltransferase gidB (Glucose inhibited division protein B)				
19241, 19242	47566169	47	8.00E-31	Bacillus cereus G9241	aldohyde dehydrogenase [Bacillus cereus G9241] gb EAL15053.1 aldohyde dehydrogenase [Bacillus cereus G9241] PUTATIVE SUGAR EPIMERASE/DEHYDRATASE [Wolinnella succinogenes DSM 1740] emb CAE09208.1 PUTATIVE SUGAR EPIMERASE/DEHYDRATASE [Wolinnella succinogenes]			1.2.1.3	4.2.1.-
19243, 19244	34556493	72	9.00E-69	Wolinnella succinogenes DSM 1740					

19245, 19246	56460623	44	4.00E-31	Idiomarina	ABC-type transport system, involved in lipoprotein release, ATPase component [Idiomarina loihiensis L2TR] gb AAV82355.1 ABC-type transport system, involved in lipoprotein release, ATPase component [Idiomarina loihiensis L2TR]	Bartonella quintana str. Toulouse, complete genome	88	1.00E-06	1.8.-.-
1925, 19251, 19252	48855461	23	7.00E-10	Cytophaga hutchinsonii	COG5000: Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation [Cytophaga hutchinsonii]				
19252	48854759	61	4.00E-38	Cytophaga hutchinsonii	COG0604: NADPH:quinone reductase and related Zn-dependent oxidoreductases [Cytophaga hutchinsonii]				
19253, 19254	29347521	57	8.00E-50	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT2111 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77218.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
19255, 19256	27464468	60	6.00E-38	Enterobacter sp. RFL1396	DNA methyltransferase [Enterobacter sp. RFL1396] ref NP_862209.1 DNA methyltransferase [Enterobacter sp. RFL1396]				2.1.1.72
19257, 19258	37520798	49	2.00E-21	Gloeobacter violaceus PCC 7421	hypothetical protein glr1229 [Gloeobacter violaceus PCC 7421] dbj BAC89170.1 glr1229 [Gloeobacter violaceus PCC 7421]				
19259, 19260	33862068	44	2.00E-71	Prochlorococcus marinus subsp. pastoris str. CCMP1986	Ferredoxin-dependent glutamate synthase, Fd-GOGAT [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19971.1 Ferredoxin-dependent glutamate synthase, Fd-GOGAT [Prochlorococcus marinus subsp. pastoris str. CCMP1986]				1.4.7.1
19261, 19262	48847259	29	7.00E-11	Geobacter metallireducens GS-15	hypothetical protein Gmet0200333 [Geobacter metallireducens GS-15]				
19265, 19266	29349385	29	9.00E-11	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3977 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79082.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
19267, 19268	48853686	38	3.00E-23	Cytophaga hutchinsonii	COG1186: Protein chain release factor B [Cytophaga hutchinsonii]				
19275, 19276	53711522	54	1.00E-60	Bacteroides fragilis YCH46	ribonuclease H-related protein [Bacteroides fragilis YCH46] dbj BAD46980.1 ribonuclease H-related protein [Bacteroides fragilis YCH46]				3.1.26.4
19283, 19284	53714264	44	2.00E-72	Bacteroides fragilis YCH46	folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 folypolyglutamate synthase [Bacteroides fragilis YCH46]				6.3.2.17
19285, 19286	53714264	34	6.00E-38	Bacteroides fragilis YCH46	folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 folypolyglutamate synthase [Bacteroides fragilis YCH46]				6.3.2.17
19289, 19290	48856755	66	5.00E-68	Cytophaga hutchinsonii	COG0139: Phosphoribosyl-AMP cyclohydrolase [Cytophaga hutchinsonii]				3.5.4.19
1929, 1930	48855800	60	3.00E-50	Cytophaga hutchinsonii	COG0688: Phosphatidylserine decarboxylase [Cytophaga hutchinsonii]				4.1.1.65

19295, 19296	42528141	48	3.00E-33	Treponema denticola ATCC 35405	Fic family protein [Treponema denticola ATCC 35405] gb AAS13158.1 Fic family protein [Treponema denticola ATCC 35405]				
19297, 19298	32262994	41	4.00E-15	Helicobacter hepaticus ATCC 51449	putative endonuclease [Helicobacter hepaticus ATCC 51449] ref NP_860974.1 putative endonuclease [Helicobacter hepaticus ATCC 51449]				3.1.21.-
19299, 19300	1695686	53	8.00E-62	Geobacillus stearothermophilus	pyruvate carboxylase [Geobacillus stearothermophilus]				6.4.1.1
193, 194	32414055	29	1.00E-11	Neurospora crassa	hypothetical protein [Neurospora crassa] gb EAA28210.1 hypothetical protein [Neurospora crassa]				
					atp-dependent clip protease, atp-binding subunit clip [Bacillus anthracis str. 'Ames Ancestor'] ref YP_085795.1 ATP-dependent Clip protease, ATP- binding subunit [Bacillus cereus ZK] gb AAU16053.1 ATP-dependent Clip protease, ATP-binding subunit [Bacillus cereus ZK] ref YP_038522.1 ATP- dependent Clip protease, ATP-binding subunit [Bacillus thuringiensis serovar konkukian str. 97-27] ref YP_030616.1 ATP-dependent Clip protease, ATP- binding subunit ClipX [Bacillus anthracis str. Sterne] ref NP_980856.1 ATP- dependent Clip protease, ATP-binding subunit ClipX [Bacillus cereus ATCC 10987] ref NP_846917.1 ATP-dependent Clip protease, ATP-binding subunit ClipX [Bacillus anthracis str. Ames] ref NP_658503.1 AAA, ATPase family associated with various cellular activities (AAA) [Bacillus anthracis str. A2012] gb AAP28403.1 ATP-dependent Clip protease, ATP-binding subunit ClipX [Bacillus anthracis str. Ames] gb AAT63717.1 ATP-dependent Clip protease, ATP-binding subunit [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAT33827.1 ATP-dependent Clip protease, ATP-binding subunit ClipX [Bacillus anthracis str. 'Ames Ancestor'] gb AAT56667.1 ATP-dependent			81 1.00E-11	
19301, 19302	47530003	65	1.00E-107	Bacillus anthracis str. 'Ames Ancestor'	Oceanobacillus lheyensis HTE831 genomic DNA, section 8/13				
19303, 19304	34762740	37	1.00E-56	Fusobacterium nucleatum subsp. vincentii ATCC 49256	VaiY-tRNA synthetase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24670.1 VaiY-tRNA synthetase [Fusobacterium nucleatum subsp. vincentii ATCC 49256]	Desc:Listeria innocua DNA sequence #684. Org:Listeria innocua		95 4.00E-08 6.1.1.9	
19305, 19306	40067365	58	3.00E-43	Pasteurella multocida	hypothetical protein [Pasteurella multocida]	Bacteriophage EJ-1 proviral DNA, complete genome		91 4.00E-07	
1931, 1932	48864299	35	2.00E-14	Microbulifer degradans 2-40	COG0784: FOG: CheY-like receiver [Microbulifer degradans 2-40]				2.7.3.-
19311, 19312	29349412	55	1.00E-43	Bacteroides thetaiotaomicron VPI-5482	lipid-A-disaccharide synthase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79109.1 lipid-A-disaccharide synthase [Bacteroides thetaiotaomicron VPI-5482]				2.4.1.18 2

19319,	56675038	39	2.00E-13	uncultured bacterium	cellulase [uncultured bacterium]				
19320				bacterium					
19321,				Psychrobacter sp.					
19322	52853726	32	4.00E-26	273-4	COG1479: Uncharacterized conserved protein [Psychrobacter sp. 273-4]				
19325,				Bacteroides	BatD, conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO7601.1 BatD, conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
19326	29346314	32	2.00E-30	thetaiotaomicron VPI-5482					
19327,				Photobacterium	hypothetical protein PBRB0725 [Photobacterium profundum SS9]				
19328	54302404	41	2.00E-15	profundum SS9	emb CAG22597.1 hypothetical protein [Photobacterium profundum]				
					lipoprotein releasing system ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76745.1 lipoprotein releasing system ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482]				
1933,				Bacteroides	sp Q8A1M1 IOLD_BACTN Lipoprotein releasing system ATP-binding protein IOLD				1.8.-
1934	29349048	60	5.00E-27	VPI-5482					
19331,				Methanosarcina	ATPase involved in DNA repair [Methanosarcina mazei Go1]				
19332	21227768	34	9.00E-21	mazei Go1	gb AAM31362.1 ATPase involved in DNA repair [Methanosarcina mazei Goe1]				
19333,				Methanosarcina	magnesium Mg(2+)/cobalt Co(2+) transport protein [Methanosarcina acetivorans C2A] gb AAM05128.1 magnesium Mg(2+)/cobalt Co(2+) transport protein [Methanosarcina acetivorans str. C2A]				
19334	20090573	39	1.00E-30	acetivorans C2A					
						Desc:Enterococcus faecalis DNA for cellular proliferation protein #405.			
19335,						Org:Enterococcus faecalis	91	6.00E-07	1.8.-
19336	48856262	70	2.00E-94	Cytophaga hutchinsonii	COG1134: ABC-type polysaccharide/polyol phosphate transport system, ATPase component [Cytophaga hutchinsonii]				
19337,				Cytophaga	COG1682: ABC-type polysaccharide/polyol phosphate export systems, permease component [Cytophaga hutchinsonii]				
19338	48856261	38	1.00E-10	hutchinsonii					
19339,				Ralstonia					
19340	48769421	35	4.00E-26	metallidurans CH34	COG1510: Predicted transcriptional regulators [Ralstonia metallidurans CH34]				
19341,									
19342	21227769	31	6.00E-26	Methanosarcina mazei Go1	type I restriction-modification system specificity subunit [Methanosarcina mazei Go1] gb AAM31363.1 type I restriction-modification system specificity subunit [Methanosarcina mazei Goe1]				3.1.21.3
19345,				Cytophaga	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]				
19346	48853597	69	1.00E-91	hutchinsonii					2.4.1.83
19349,				Geobacter	PPIC-type PPIASE domain protein [Geobacter sulfurreducens PCA]				
19350	39995127	31	4.00E-09	sulfurreducens PCA	gb AAR33351.1 PPIC-type PPIASE domain protein [Geobacter sulfurreducens PCA]				5.2.1.8

1935, 1936	53712402	62	3.00E-64	Bacteroides fragilis YCH46	putative undecaprenyl-phosphate glycosyl-1-phosphate transferase [Bacteroides fragilis YCH46] gb AAD58746.1 putative undecaprenyl- phosphate glycosyl-1-phosphate transferase [Bacteroides fragilis] dbj BAD47860.1 putative undecaprenyl-phosphate glycosyl-1-phosphate transferase [Bacteroides fragilis YCH46]	2.4.-
19351, 19352	33599115	39	2.00E-24	Bordetella bronchiseptica RB50	putative asparagine synthetase [Bordetella bronchiseptica RB50] emb CAE30624.1 putative asparagine synthetase [Bordetella bronchiseptica RB50]	6.3.5.4
19353, 19354	29654159	50	1.00E-45	Coxiella burnetii RSA 493	asparagine synthetase B, glutamine-hydrolyzing [Coxiella burnetii RSA 493] gb AAO90365.1 asparagine synthetase B, glutamine-hydrolyzing [Coxiella burnetii RSA 493]	6.3.5.4
19355, 19356	31195869	42	6.00E-35	Anopheles gambiae	ENSANGP0000000393 [Anopheles gambiae]	
19357, 19358	4854542	41	3.00E-44	Cytophaga hutchinsonii	COG1748: Saccharopine dehydrogenase and related proteins [Cytophaga hutchinsonii]	1.5.1.7
19361, 19362	53711775	46	6.00E-58	Bacteroides fragilis YCH46	glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD47233.1 glycosyltransferase [Bacteroides fragilis YCH46]	
19365, 19366	53686749	35	7.00E-11	Nostoc punctiforme PCC 73102	COG0187: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit [Nostoc punctiforme PCC 73102]	
19367, 19368	56543835	33	4.00E-23	Zymomonas mobilis subsp. mobilis ZM4	conserved hypothetical protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_163100.1 hypothetical protein ZMO1365 [Zymomonas mobilis subsp. mobilis ZM4]	2.7.3.-
19369, 19370	45658787	24	6.00E-13	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_710808.1 Putative glycosyl transferase [Leptospira interrogans serovar Lai str. 56601] gb AAN47826.1 Putative glycosyl transferase [Leptospira interrogans serovar lai str. 56601] gb AAS71510.1 glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]	
19371, 19372	29349086	24	1.00E-19	Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482] gb AAO78783.1 two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482]	2.7.3.-
19373, 19374	34397026	49	3.00E-52	Porphyrromonas gingivalis W83	conserved hypothetical protein [Porphyrromonas gingivalis W83] ref NP_905191.1 hypothetical protein PG0960 [Porphyrromonas gingivalis W83] sp Q7MVS9 TRMB_PORGI tRNA (guanine-N(7)-methyltransferase (tRNA(m7G46)-methyltransferase)	2.1.1.-

19375, 19376	16078053	46	2.00E-61	168	Bacillus subtilis subsp. subtilis str.	hypothetical protein BSU09890 [Bacillus subtilis subsp. subtilis str. 168] emb CAA74424.1 Hypothetical protein [Bacillus subtilis] emb CAB12829.1 yhaQ [Bacillus subtilis subsp. subtilis str. 168] pir C69819 ABC transporter (ATP-binding protein) homolog yhaQ - Bacillus subtilis			3.6.3.33
19377, 19378	48855712	43	1.00E-45	hutchinsonii	Cytophaga hutchinsonii	hypothetical protein Chut02000916 [Cytophaga hutchinsonii]			
19383, 19384	53714123	74	2.00E-59	YCH46	Bacteroides fragilis YCH46	hypothetical protein BF2831 [Bacteroides fragilis YCH46] dbj BAD49581.1 hypothetical protein [Bacteroides fragilis YCH46]			
19385, 19386	48854490	29	2.00E-08	hutchinsonii	Cytophaga hutchinsonii	hypothetical protein Chut02002689 [Cytophaga hutchinsonii]			
1939, 1940	21673557	44	1.00E-46	tepidum TLS	Chlorobium tepidum TLS	glucose-1-phosphate thymidyltransferase, putative [Chlorobium tepidum TLS] gb AAM71964.1 glucose-1-phosphate thymidyltransferase, putative [Chlorobium tepidum TLS]			2.7.7.24
19391, 19392	52853852	36	6.00E-31	273-4	Psychrobacter sp.	COG0442: Prollyl-tRNA synthetase [Psychrobacter sp. 273-4]			
19393, 19394	42524139	41	1.00E-15	HD100	Bdellovibrio bacteriovorus HD100	probable HspC2 heat shock protein [Bdellovibrio bacteriovorus HD100] emb CAE80512.1 probable HspC2 heat shock protein [Bdellovibrio bacteriovorus HD100]			
19395, 19396	56675038	44	2.00E-17	bacterium	uncultured bacterium	cellulase [uncultured bacterium]			
19397, 19398	48856840	44	4.00E-18	hutchinsonii	Cytophaga hutchinsonii	COG1396: Predicted transcriptional regulators [Cytophaga hutchinsonii]			
19399, 19400	48859701	44	5.00E-17	ATCC 27405	Clostridium thermocellum ATCC 27405	COG1162: Predicted GTPases [Clostridium thermocellum ATCC 27405]			3.6.1.-
19401, 19402	AAB9608	42	3.00E-51			Desc:Putative P. abyssi alpha-amylase. Org:Pyrococcus abyssi			3.2.1.1
19403, 19404	48833211	39	8.00E-36	MC-1	Magnetococcus sp. MC-1	COG2114: Adenyate cyclase, family 3 (some proteins contain HAMP domain) [Magnetococcus sp. MC-1]			4.6.1.1
19405, 19406	29345965	56	3.00E-84	VPI-5482	Bacteroides thetaiotaomicron VPI-5482	amidophosphoribosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75662.1 amidophosphoribosyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.4.2.14
19407, 19408	48855017	51	1.00E-63	hutchinsonii	Cytophaga hutchinsonii	COG0501: Zn-dependent protease with chaperone function [Cytophaga hutchinsonii]			3.4.-.-
19409, 19410	29347119	36	7.00E-45	VPI-5482	Bacteroides thetaiotaomicron VPI-5482	putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76816.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.4.1.-
19411, 19412	31194819	52	5.00E-74	gambiae	Anopheles gambiae	ENSANGP00000002020 [Anopheles gambiae]			

19413, 19414	48854902	30	6.00E-28	Cytophaga hutchinsonii	COG0845: Membrane-fusion protein [Cytophaga hutchinsonii]			
19415, 19416	30249805	28	2.00E-10	Nitrosomonas europaea ATCC 19718	hypothetical protein NE1853 [Nitrosomonas europaea ATCC 19718] emb CAD85764.1 hypothetical protein [Nitrosomonas europaea ATCC 19718]			
19417, 19418	29347660	58	2.00E-38	Bacteroides thetaiotaomicron VPI-5482	putative GTPase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77357.1 putative GTPase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A5I9 EGC1_BACTN Probable GTPase engC protein 1 type I restriction enzyme m protein [Mycoplasma mobile 163K] gb AAAT27772.1 type I restriction enzyme m protein [Mycoplasma mobile 163K]	Oceanobacillus theysensis HTE831 genomic DNA, section 6/13	91	1.00E-06 3.6.1.-
19419, 19420	47459121	27	4.00E-08	Mycoplasma mobile 163K				
19423, 19424	48854772	33	2.00E-23	Cytophaga hutchinsonii	COG2234: Predicted aminopeptidases [Cytophaga hutchinsonii]			3.4.17.2 1
19425, 19426	24373489	39	5.00E-24	Shewanella oneidensis MR-1	HlyD family secretion protein [Shewanella oneidensis MR-1] gb AAN54976.1 HlyD family secretion protein [Shewanella oneidensis MR-1] N-acetylornithine aminotransferase [Synecococcus elongatus PCC 6301] dbj BAD79656.1 N-acetylornithine aminotransferase [Synecococcus elongatus PCC 6301] ref ZP_00351244.1 COG0161: Adenosylmethionine-8-amino-7-oxonanoate aminotransferase [Synecococcus elongatus PCC 6301] 7942]			2.6.1.62
19427, 19428	56751475	47	1.00E-38	Synechococcus elongatus PCC 6301				
19429, 19430	48846624	32	5.00E-24	Geobacter metallireducens GS-15	COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Geobacter metallireducens GS-15] hypothetical protein, probably cold-shock inducible [Desulfotalea psychrophila LSV54] emb CAG37151.1 hypothetical protein, probably cold-shock inducible [Desulfotalea psychrophila LSV54]			3.2.1.8
19431, 19432	51246274	33	1.00E-17	Desulfotalea psychrophila LSV54	type I restriction-modification system, S subunit [Pseudomonas putida KT2440] gb AAN70314.1 type I restriction-modification system, S subunit [Pseudomonas putida KT2440]			3.1.21.3
19433, 19434	26991425	33	4.00E-29	Pseudomonas putida KT2440	putative aldose reductase [Rhodopseudomonas palustris CGA009] emb CAE29738.1 putative aldose reductase [Rhodopseudomonas palustris CGA009]			1.-.-.-
19435, 19436	39937357	49	2.00E-54	Rhodopseudomona s palustris CGA009	FOG: CheY-like receiver [Vibrio vulnificus CMCP6] gb AAO07892.1 FOG: CheY-like receiver [Vibrio vulnificus CMCP6]			2.7.3.-
19439, 19440	27367375	53	3.00E-62	Vibrio vulnificus CMCP6				
19441, 19442	45655974	41	4.00E-19	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	hypothetical protein LIC10060 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS68697.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			2.7.3.-

19443, 19444, 19445, 19446	20808554 31195869	31 41	2.00E-29 1.00E-19	Thermoanaerobacter tengcongensis MB4 Anopheles gambiae	predicted sugar kinase [Thermoanaerobacter tengcongensis MB4] ENSANGP00000000393 [Anopheles gambiae]			
19447, 19448	53713710	53	5.00E-37	Bacteroides fragilis YCH46	conserved hypothetical protein Bata [Bacteroides fragilis YCH46] gb AAD30858.1 Bata [Bacteroides fragilis] db BAD49168.1 conserved hypothetical protein Bata [Bacteroides fragilis YCH46]			
1945, 1946	42527338	50	3.00E-55	Treponema denticola ATCC 35405	hypothetical protein TDE1832 [Treponema denticola ATCC 35405] ref NP_972400.1 hypothetical protein TDE1796 [Treponema denticola ATCC 35405] gb AAS12347.1 conserved hypothetical protein [Treponema denticola ATCC 35405] gb AAS12311.1 conserved hypothetical protein [Treponema denticola ATCC 35405]			
19457, 19458	15893072	58	9.00E-36	EC:4.2.99.18	endonuclease III [EC:4.2.99.18] [Rickettsia conorii str. Malish 7] gb AAL03687.1 endonuclease III [EC:4.2.99.18] [Rickettsia conorii str. Malish 7] pir E97843 DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) - Rickettsia conorii (strain Malish 7)			4.2.99.18
19461, 19462	56750775	34	1.00E-12	Synechococcus elongatus PCC 6301	hypothetical protein syc0766_c [Synechococcus elongatus PCC 6301] db BAD78956.1 hypothetical protein [Synechococcus elongatus PCC 6301]			3.1.3.5
19469, 19470 19471, 19472	47228040 28274156	28 62	7.00E-19 1.00E-42	Tetraodon nigroviridis Tannerella forsythensis	unnamed protein product [Tetraodon nigroviridis] GlyA [Tannerella forsythensis]			5.1.1.-
19473, 19474 19475, 19476 19477, 19478	34397184 48856857 56675038	36 33 27	4.00E-36 7.00E-12 8.00E-16	Porphyromonas gingivalis W83 Cytophaga hutchinsonii uncultured bacterium	glycosyl transferase, group 2 family protein [Porphyromonas gingivalis W83] ref NP_905348.1 glycosyl transferase, group 2 family protein [Porphyromonas gingivalis W83] hypothetical protein Chut02000824 [Cytophaga hutchinsonii]			2.1.2.1
19481, 19482	48853984	38	4.00E-22	Cytophaga hutchinsonii	cellulase [uncultured bacterium] COG1197: Transcription-repair coupling factor (superfamily II helicase)			
19483, 19484 19485, 19486	39997412 52853726	34 33	7.00E-35 9.00E-27	Geobacter sulfurreducens PCA Psychrobacter sp. 273-4	sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] gb AAR35690.1 sensory box histidine kinase/response regulator [Geobacter sulfurreducens PCA] COG1479: Uncharacterized conserved protein [Psychrobacter sp. 273-4]			2.7.3.-
19487, 19488	52425668	34	6.00E-40	Mannheimia succiniciproducens MBEL55E	LysC protein [Mannheimia succiniciproducens MBEL55E] gb AAU38220.1 LysC protein [Mannheimia succiniciproducens MBEL55E]			2.7.2.4

19489, 19490	45524150	59	2.00E-95	Crocospaera watsonii WH 8501	COG0674: Pyruvate:ferredoxin oxidoreductase and related 2-oxoacid:ferredoxin oxidoreductases, alpha subunit [Crocospaera watsonii WH 8501]			1.2.7.1
1949, 1950	53795203	44	5.00E-38	Chloroflexus aurantiacus	COG1680: Beta-lactamase class C and other penicillin binding proteins [Chloroflexus aurantiacus]			3.5.2.6
19491, 19492	20808779	33	5.00E-16	Thermoanaerobacter tengcongensis MB4	Transcriptional regulator [Thermoanaerobacter tengcongensis MB4]			2.7.1.2
195, 196	48854506	45	2.00E-26	Cytophaga hutchinsonii	hypothetical protein Chut02002705 [Cytophaga hutchinsonii]			3.6.1.-
19501, 19502	48863156	44	4.00E-22	Microbulbifer degradans 2-40	COG4067: Uncharacterized protein conserved in archaea [Microbulbifer degradans 2-40]			
19503, 19504	54032693	33	3.00E-09	Polaromonas sp. JS666	COG3616: Predicted amino acid aldolase or racemase [Polaromonas sp. JS666]			
19507, 19508	34397138	40	5.00E-15	Porphyrromonas gingivalis W83	DNA-binding response regulator RprY [Porphyrromonas gingivalis W83]			
19509, 19510	48855901	53	4.00E-80	Cytophaga hutchinsonii	COG1482: Phosphomannose isomerase [Cytophaga hutchinsonii]			5.3.1.8
1951, 1952	45659189	52	5.00E-89	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714399.1 CysC; CysN [Leptospira interrogans serovar Lai str. 56601] gb AA51417.1 CysN; CysC [Leptospira interrogans serovar lai str. 56601] gb AAS71912.1 sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			2.7.7.4
19511, 19512					Desc:DNA encoding novel human diagnostic protein #27879. Org:Homo sapiens	94	3.00E-14	
19513, 19514	42527309	49	3.00E-17	Treponema denticola ATCC 35405	hypothetical protein TDE1803 [Treponema denticola ATCC 35405] gb AAS12318.1 conserved hypothetical protein [Treponema denticola ATCC 35405]			
19515, 19516	29349133	33	1.00E-36	Bacteroides thetaiotaomicron VPI-5482	putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO78830.1 putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482]			
19517, 19518	24213772	43	1.00E-39	Leptospira interrogans serovar Lai str. 56601	hypothetical protein LA1072 [Leptospira interrogans serovar Lai str. 56601] gb AA48271.1 unknown protein [Leptospira interrogans serovar lai str. 56601]			

19523,	AAU6761	27	2.00E-22			Desc:Propionibacterium acnes immunogenic protein #28510.			
19524	4			Microbulbifer		Org:Propionibacterium acnes			
19527,				degradans 2-40		COG2951: Membrane-bound lytic murein transglycosylase B [Microbulbifer			
19528	48863961	55	2.00E-63			degradans 2-40]			3.2.1.-
19529,				Wolinella		hypothetical protein WS2184 [Wolinella succinogenes DSM 1740]			
19530	34558460	53	2.00E-81	1740		emb CAE11175.1 CONSERVED HYPOTHETICAL PROTEIN [Wolinella			
				succinogenes]					
1953,				Yersinia		possible restriction modification enzyme [Yersinia pseudotuberculosis IP			
1954	51598166	39	4.00E-20	IP 32953		32953] emb CAH23119.1 possible restriction modification enzyme [Yersinia			
				pseudotuberculosis		pseudotuberculosis IP 32953]			3.1.21.3
19531,				Rhodopseudomonas		possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009]			
19532	39936881	49	4.00E-40	s palustris CGA009		emb CAE29361.1 possible ADP-heptose synthase [Rhodopseudomonas			
19535,				Cytophaga		palustris CGA009]			2.7.7.39
19536	48854159	26	2.00E-09	hutchinsonii		COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase			
19539,				superfamily) [Cytophaga hutchinsonii]					3.1.1.24
19540	34397427	31	8.00E-28	Porphyromonas		ATPase, putative [Porphyromonas gingivalis W83] ref NP_905590.1			
				gingivalis W83		ATPase, putative [Porphyromonas gingivalis W83]			
19541,				Bacteroides		hypothetical protein BT0083 [Bacteroides thetaiotaomicron VPI-5482]			
19542	29345493	37	2.00E-21	thetataomicron		gb AAO75190.1 conserved hypothetical protein [Bacteroides			
				VPI-5482		thetataomicron VPI-5482]			
19543,				Bacteroides fragilis		putative glycosyltransferase [Bacteroides fragilis YCH46] db BAD49674.1			
19544	53714216	38	2.00E-25	YCH46		putative glycosyltransferase [Bacteroides fragilis YCH46]			
19545,				Cytophaga		COG0768: Cell division protein FtsI/penicillin-binding protein 2 [Cytophaga			2.3.2.-
19546	48854578	41	8.00E-55	hutchinsonii		hutchinsonii]			
19547,				Cytophaga		COG4365: Uncharacterized protein conserved in bacteria [Cytophaga			
19548	48856112	40	2.00E-62	hutchinsonii		hutchinsonii]			
19549,				Geobacillus		cystathionine beta-lyase [Geobacillus kaustophilus HTA426]			
19550	56419402	42	8.00E-57	kaustophilus		db BAD75152.1 cystathionine beta-lyase [Geobacillus kaustophilus			4.2.99.9
				HTA426		HTA426]			
19551,				Microbulbifer		COG2972: Predicted signal transduction protein with a C-terminal ATPase			
19552	48862505	40	4.00E-35	degradans 2-40		domain [Microbulbifer degradans 2-40]			2.7.3.-
19553,	ABB8477					Desc:DNA polymerase III holoenzyme delta subunit related protein SEQ			
19554	1	34	3.00E-39			ID:144. Org: Cytophaga hutchinsonii			2.7.7.7
19555,				Cytophaga		COG0793: Periplasmic protease [Cytophaga hutchinsonii]			3.4.21.-
19556	48853807	47	6.00E-70	hutchinsonii					
				Bacteroides					
19561,				thetataomicron		Ribonuclease G [Bacteroides thetaiotaomicron VPI-5482] gb AAO76607.1			
19562	29346910	52	1.00E-32	VPI-5482		Ribonuclease G [Bacteroides thetaiotaomicron VPI-5482]			3.1.4.-
19563,				Chryseobacterium		PI-repressible alkaline phosphatase PafA [Chryseobacterium			
19564	8886019	51	3.00E-55	meningosepticum		meningosepticum]			

19569, 19570	19704590	43	4.00E-29	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	NagD protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95451.1 NagD protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]				3.1.3.41
1957, 1958	45508953	41	3.00E-19	Anabaena variabilis ATCC 29413	COG4636: Uncharacterized protein conserved in cyanobacteria [Anabaena variabilis ATCC 29413]				
19573, 19574	33596386	33	1.00E-07	Bordetella parapertussis 12822	putative lipoprotein [Bordetella parapertussis 12822] emb CAE37057.1 putative lipoprotein [Bordetella parapertussis]				
19575, 19576	32474694	30	6.00E-11	Rhodopirellula baltica SH 1	probable penicillin resistance regulatory protein [Rhodopirellula baltica SH 1] emb CAD75235.1 probable penicillin resistance regulatory protein [Pirellula sp.]				
19579, 19580	46141189	43	6.00E-44	Psychrobacter sp. 273-4	hypothetical protein Psc03002392 [Psychrobacter sp. 273-4]				
19583, 19584	48854401	49	7.00E-41	Cytophaga hutchinsonii	COG1475: Predicted transcriptional regulators [Cytophaga hutchinsonii]				
19585, 19586	52853548	29	8.00E-10	Psychrobacter sp. 273-4	COG0668: Small-conductance mechanosensitive channel [Psychrobacter sp. 273-4]				
1959, 1960	21228318	42	4.00E-21	Methanosarcina mazel Go1	Glucose-1-phosphate thymidyltransferase [Methanosarcina mazel Go1] gb AAM31912.1 Glucose-1-phosphate thymidyltransferase [Methanosarcina mazel Goe1]				2.7.7.24
19591, 19592	27382256	42	1.00E-22	Bradyrhizobium japonicum USDA 110	hypothetical protein bli7145 [Bradyrhizobium japonicum USDA 110] dbj BAC52410.1 bli7145 [Bradyrhizobium japonicum USDA 110]				
19595, 19596	9947830	68	9.00E-94	Pseudomonas aeruginosa PAO1	methionine synthase [Pseudomonas aeruginosa PAO1] ref NP_250534.1 methionine synthase [Pseudomonas aeruginosa PAO1] pir E83415 methionine synthase PA1843 [imported] - Pseudomonas aeruginosa (strain PAO1)	Vibrio fischeri gene for cobalamin- dependent methionine synthase, Na ⁺ /H ⁺ antiporter and aspartokinase III, partial and complete cds	82	1.00E-11	2.1.1.13
19603, 19604	53714398	27	9.00E-26	Bacteroides fragilis YCH46	putative patatin-like phospholipase [Bacteroides fragilis YCH46] dbj BAD49856.1 putative patatin-like phospholipase [Bacteroides fragilis YCH46]				3.4.21.-
19605, 19606	53712844	46	4.00E-30	Bacteroides fragilis YCH46	ribonuclease G [Bacteroides fragilis YCH46] dbj BAD48302.1 ribonuclease G [Bacteroides fragilis YCH46]				3.1.4.-

19607, 19608	53712144	37	1.00E-10	Bacteroides fragilis YCH46	hypothetical protein BF0851 [Bacteroides fragilis YCH46] dbj BAD47602.1 hypothetical protein [Bacteroides fragilis YCH46]			
19609, 19610	18310494	24	2.00E-16	Clostridium perfringens str. 13	two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] dbj BAB81218.1 two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13]			
1961, 1962	53714371	36	4.00E-29	Bacteroides fragilis YCH46	putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] dbj BAD49829.1 putative ATPase involved in DNA repair [Bacteroides fragilis YCH46]			
19611, 19612	52079413	34	2.00E-18	Bacillus licheniformis ATCC 14580	putative transcriptional regulator [Bacillus licheniformis ATCC 14580] gb AAU22566.1 putative transcriptional regulator [Bacillus licheniformis ATCC 14580] ref YP_090602.1 YncZ [Bacillus licheniformis ATCC 14580] gb AAU39909.1 YncZ [Bacillus licheniformis DSM 13]			
19615, 19616	53712519	36	3.00E-38	Bacteroides fragilis YCH46	hypothetical protein BF1227 [Bacteroides fragilis YCH46] dbj BAD47977.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
19617, 19618	48856396	46	2.00E-22	Cytophaga hutchinsonii	COG1579: Zn-ribbon protein, possibly nucleic acid-binding [Cytophaga hutchinsonii]			
19619, 19620	53715653	27	4.00E-12	Bacteroides fragilis YCH46	hypothetical protein BF4373 [Bacteroides fragilis YCH46] dbj BAD51111.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
19621, 19622	29350071	30	1.00E-13	Bacteroides thetataoimicron VPI-5482	two-component system sensor histidine kinase/response [Bacteroides thetataoimicron VPI-5482] gb AAO79768.1 two-component system sensor histidine kinase/response [Bacteroides thetataoimicron VPI-5482]			2.7.3.-
19625, 19626	31194451	62	4.00E-93	Anopheles gambiae	ENSANGP00000015516 [Anopheles gambiae]			3.4.21.-
19627, 19628	48853783	38	2.00E-27	Cytophaga hutchinsonii	COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii]			2.7.7.7
19629, 19630	48854335	52	1.00E-29	Cytophaga hutchinsonii	COG3762: Predicted membrane protein [Cytophaga hutchinsonii]			
1963, 1964	28211857	27	8.00E-15	Clostridium tetani E88	glycosyl transferase [Clostridium tetani E88] gb AAO36738.1 glycosyl transferase [Clostridium tetani E88]			2.4.1.-
19631, 19632	56459804	29	3.00E-33	Idiomarina loihensis L2TR	Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihensis L2TR] gb AAV81536.1 Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihensis L2TR]			
19633, 19634	48853480	47	2.00E-19	Cytophaga hutchinsonii	COG1187: 16S rRNA uridine-516 pseudouridylation synthase and related pseudouridylation synthases [Cytophaga hutchinsonii]			4.2.1.70

19635, 19636	52842257	29	1.00E-13	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	mevalonate diphosphate decarboxylase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]				4.1.1.33
19639, 19640	29349999	38	1.00E-48	Bacteroides thetaiotaomicron VPI-5482	putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79696.1 putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482]				
19641, 19642	48892769	26	1.00E-12	Trichodesmium erythraeum IMS101	COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101]				
19643, 19644	48854025	51	4.00E-19	Cytophaga hutchinsonii	hypothetical protein Chut02003116 [Cytophaga hutchinsonii]				
19645, 19646	32475496	42	9.00E-55	Rhodopirellula baltica SH 1	chloromuconate cycloisomerase YkfB1 [Rhodopirellula baltica SH 1] emb CAD75867.1 chloromuconate cycloisomerase YkfB1 [Pirellula sp.]				5.5.-.-
1965, 1966	17230329	35	4.00E-17	Nostoc sp. PCC 7120	glycosyltransferase [Nostoc sp. PCC 7120] pir AF2160 glycosyltransferase alr2837 [imported] - Nostoc sp. (strain PCC 7120) db BAB74536.1 glycosyltransferase [Nostoc sp. PCC 7120]				2.-.-.-
19651, 19652	45657936	53	6.00E-23	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	response regulator [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70659.1 response regulator [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				
19653, 19654	21674101	51	1.00E-36	Chlorobium tepidum TLS	peptide methionine sulfoxide reductase [Chlorobium tepidum TLS] gb AAM72508.1 peptide methionine sulfoxide reductase [Chlorobium tepidum TLS]				1.8.4.6
19655, 19656	48853937	65	1.00E-110	Cytophaga hutchinsonii	COG0482: Predicted tRNA(5-methylaminomethyl-2-thiouridylylate) methyltransferase, contains the PP-loop ATPase domain [Cytophaga hutchinsonii]				2.1.1.61
19659, 19660	48853990	24	5.00E-15	Cytophaga hutchinsonii	COG1196: Chromosome segregation ATPases [Cytophaga hutchinsonii]				
19661, 19662	23125186	34	2.00E-16	Nostoc punctiforme PCC 73102	hypothetical protein Npun02006402 [Nostoc punctiforme PCC 73102]				
19663, 19664	51892061	38	2.00E-34	Symbiobacterium thermophilum IAM 14863	two-component response regulator [Symbiobacterium thermophilum IAM 14863] db JBAD39908.1 two-component response regulator [Symbiobacterium thermophilum IAM 14863]				3.1.1.61
19665, 19666	53613391	22	7.00E-12	Azotobacter vinelandii	COG1357: Uncharacterized low-complexity proteins [Azotobacter vinelandii]				

19667,	48856618	40	2.00E-14	Cytophaga hutchinsonii	COG1562: Phytoene/squalene synthetase [Cytophaga hutchinsonii]			
19668					COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii]			
19669,	48853984	33	9.00E-21	Cytophaga hutchinsonii				
19670								
1967,	53685350	31	2.00E-12	Desulfotobacterium hafniense DCB-2	COG0535: Predicted Fe-S oxidoreductases [Desulfotobacterium hafniense DCB-2]			
1968					hypothetical protein al12423 [Nostoc sp. PCC 7120] pir AH2108 hypothetical protein al12423 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB74122.1]			
19671,	17229915	27	2.00E-15	Nostoc sp. PCC 7120	al12423 [Nostoc sp. PCC 7120]			2.7.3.-
19672								
19673,				Geobacillus kaustophilus HTA426	formiminoglutamase [Geobacillus kaustophilus HTA426] dbj BAD75650.1 formiminoglutamase [Geobacillus kaustophilus HTA426]			3.5.3.8
19674	56419900	41	4.00E-38		COG0382: 4-hydroxybenzoate polyprenyltransferase and related prenyltransferases [Cytophaga hutchinsonii]			2.5.1.-
19675,	48856973	32	6.00E-17	Cytophaga hutchinsonii	conserved hypothetical protein with rhodanese domain [Bacillus licheniformis ATCC 14580] gb AAU25028.1 conserved hypothetical protein with rhodanese domain [Bacillus licheniformis ATCC 14580] ref YP_093092.1 YbfQ [Bacillus licheniformis ATCC 14580] gb AAU42399.1 YbfQ [Bacillus licheniformis DSM 13]			
19676								
19677,	52081875	47	9.00E-68	Bacillus licheniformis ATCC 14580				
19678								
19679,								
19680	48837393	40	6.00E-39	Thermobifida fusca	COG1321: Mn-dependent transcriptional regulator [Thermobifida fusca]			
19681,				Chlorobium tepidum TLS	CBS domain protein [Chlorobium tepidum TLS] gb AAM72271.1 CBS domain protein [Chlorobium tepidum TLS]			
19682	21673884	34	4.00E-15		DNA polymerase II, epsilon subunit [Chlorobium tepidum TLS]			
19683,				Chlorobium tepidum TLS	gb AAM72272.1 DNA polymerase III, epsilon subunit [Chlorobium tepidum TLS]			2.7.7.7
19684	21673865	35	1.00E-24					
19687,				Bacteroides fragilis YCH46	hypothetical protein BF2616 [Bacteroides fragilis YCH46] dbj BAD49366.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
19688	53713908	65	2.00E-35					
1969,				Methanosarcina barkeri str. fusaro	COG0732: Restriction endonuclease S subunits [Methanosarcina barkeri str. fusaro]			95 1.00E-54 3.1.21.3
1970	48839273	62	1.00E-54		Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog [Clostridium acetobutylicum ATCC 824] gb AAK79263.1 Membrane protein containing HD superfamily hydrolase domain, YQFF ortholog [Clostridium acetobutylicum ATCC 824] pir D97059 membrane protein containing HD superfamily hydrolase domain, YQFF ortholog [imported] - Clostridium acetobutylicum			
19693,								
19694	15894574	41	5.00E-38	Clostridium acetobutylicum ATCC 824				

19695, 19696	ABP3834 7	43	1.00E-14			Desc:Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3192. Org:Staphylococcus epidermidis				
19697, 19698	27364115	45	9.00E-21	Vibrio vulnificus CMCP6		hypothetical protein VV10658 [Vibrio vulnificus CMCP6] gb AAO09170.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6]				
19699, 19700	29345776	27	7.00E-21	Bacteroides thetaiotaomicron VPI-5482		two-component system sensor histidine kinase/response regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482] gb AAO75473.1 two-component system sensor histidine kinase/response regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-
19701, 19702	29348012	47	3.00E-24	Bacteroides thetaiotaomicron VPI-5482		putative maturase/reverse transcriptase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77709.1 putative maturase/reverse transcriptase [Bacteroides thetaiotaomicron VPI-5482]				
19707, 19708	34556775	71	5.00E-99	Wolinella succinogenes DSM 1740		UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09490.1 UTP-GLUCOSE-1-PHOSPHATE URIDYLTRANSFERASE [Wolinella succinogenes]	Helicobacter hepaticus ATCC 51449 section 2 of 6 of the complete genome	81	6.00E-07	2.7.7.9
19709, 19710	34397507	36	1.00E-19	Porphyromonas gingivalis W83		hypothetical protein PG1529 [Porphyromonas gingivalis W83] ref NP_905670.1 hypothetical protein PG1529 [Porphyromonas gingivalis W83]				
1971, 1972	48838982	67	2.00E-67	Methanosarcina barkeri str. fusaro		COG2043: Uncharacterized protein conserved in archaea [Methanosarcina barkeri str. fusaro]				
19711, 19712	15617468	26	8.00E-09	Lactococcus lactis		putative IS-like element [Lactococcus lactis] gb AAL02009.1 putative IS-like element [Lactococcus lactis] pir SS3879 hypothetical protein 1 (insertion sequence-like element) - Lactococcus lactis subsp. lactis biovar diacetylactis gb AAB33915.1 Bacillus stearothermophilus putative IS-like element homolog [Lactococcus lactis]				
19713, 19714	21672971	55	2.00E-65	Chlorobium tepidum TLS		glucosamine-fructose-6-phosphate aminotransferase [Chlorobium tepidum TLS] gb AAM71378.1 glucosamine-fructose-6-phosphate aminotransferase [Chlorobium tepidum TLS] sp Q8KG38 GLMS_CHL TE Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase)				2.6.1.16
19715, 19716	17229771	29	3.00E-07	Nostoc sp. PCC 7120		two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] pir AH2090 two-component hybrid sensor and regulator alr2279 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73978.1 two-component hybrid sensor and regulator [Nostoc sp. PCC 7120]				
19719, 19720	48787144	26	2.00E-11	Burkholderia fungorum LB400		hypothetical protein Bcep02001927 [Burkholderia fungorum LB400]				

19723, 19724	48853434	67	6.00E-61	Cytophaga hutchinsonii		COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii]	Chromobacterium violaceum ATCC 12472 section. 15 of 16 of the complete genome	89	4.00E-07	2.7.7.24
19725, 19726	29345936	52	3.00E-68	Bacteroides thetaiotaomicron VPI-5482		L-asparaginase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75633.1 L-asparaginase [Bacteroides thetaiotaomicron VPI-5482]				3.5.1.1
19729, 19730	19068097	50	3.00E-51	Bacteroides fragilis Rubrobacter xylanophilus DSM 9941		unknown [Bacteroides fragilis]				
1973, 1974	45547683	28	2.00E-16			COG2802: Uncharacterized protein, similar to the N-terminal domain of Lon protease [Rubrobacter xylanophilus DSM 9941]				3.4.21.5 3
19731, 19732	48856913	52	3.00E-63	Cytophaga hutchinsonii		COG0647: Predicted sugar phosphatases of the HAD superfamily [Cytophaga hutchinsonii]				3.1.3.41
19733, 19734	34557000	58	3.00E-64	Wolinella succinogenes DSM 1740		UDP-GLUCOSE DEHYDROGENASE [Wolinella succinogenes DSM 1740] emb CAE09715.1 UDP-GLUCOSE DEHYDROGENASE [Wolinella succinogenes]				1.1.1.22
19735, 19736	53712881	26	1.00E-16	Bacteroides fragilis YCH46		hypothetical protein BF1590 [Bacteroides fragilis YCH46] dbj BAD48339.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
19737, 19738	29346555	59	5.00E-64	Bacteroides thetaiotaomicron VPI-5482		glucose-inhibited division protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76252.1 glucose-inhibited division protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A8M2 GIDB_BACTN Methyltransferase gidB (Glucose inhibited division protein B)				
19739, 19740	48853433	42	2.00E-53	Cytophaga hutchinsonii		COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] hypothetical protein LIC20117 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714691.1 conserved hypothetical protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51706.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS72145.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				
19743, 19744	45655699	34	6.00E-25	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130		COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Mesorhizobium sp. BNC1]				
19749, 19750	45682916	32	7.00E-28	Mesorhizobium sp. BNC1		COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Cytophaga hutchinsonii]				1.8.-.-
1975, 1976	48856435	71	2.00E-78	Cytophaga hutchinsonii						

19751, 19752	48854648	80	4.00E-72	Cytophaga hutchinsonii	COG0059: Ketol-acid reductoisomerase [Cytophaga hutchinsonii]	Desc:Haemophilus influenzae DNA for cellular proliferation protein #127. Org:Haemophilus influenzae	85	2.00E-09	1.1.1.86
19753, 19754	29027481	62	4.00E-82	Aster yellows phytoplasma	threonine dehydratase [Aster yellows phytoplasma] related to 2-oxoglutarate synthase, subunit KorA [Desulfotalea psychrophila LSv54] emb CAG35621.1 related to 2-oxoglutarate synthase, subunit KorA [Desulfotalea psychrophila LSv54]	Streptococcus mutans UA159 section 21 of 185 of the complete genome	93	3.00E-08	4.2.1.16
19759, 19760	51244744	55	3.00E-66	Desulfotalea psychrophila LSv54					1.2.7.3
19763, 19764	23126889	48	7.00E-45	Nostoc punctiforme PCC 73102	COG3899: Predicted ATPase [Nostoc punctiforme PCC 73102]				2.7.3.-
19765, 19766	14030779	35	6.00E-29	Mus musculus	ectonucleotide pyrophosphatase/phosphodiesterase 5 [Mus musculus] pir A59390 probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) 5 - mouse gb AAG49143.1 putative nucleotide pyrophosphatase/phosphodiesterase; NPP5 [Mus musculus] putative helicase [Synecococcus elongatus PCC 6301] dbj BAD78996.1 putative helicase [Synecococcus elongatus PCC 6301] ref ZP_00163885.1 COG1061: DNA or RNA helicases of superfamily II [Synecococcus elongatus PCC 7942]			3.1.4.1	
19767, 19768	56750815	29	1.00E-08	Synechococcus elongatus PCC 6301					
19771, 19772	53713904	68	5.00E-89	Bacteroides fragilis YCH46	excinuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46]				1.8.-
19773, 19774	21226750	25	7.00E-07	Methanosarcina mazel Go1	glycosyltransferase [Methanosarcina mazel Go1] gb AAM30344.1 glycosyltransferase [Methanosarcina mazel Go1]				2.4.1.-
19775, 19776	56460818	50	2.00E-65	Idiomarina lohiensis L2TR	Secreted enzyme, contains two amidohydrolase related domains [Idiomarina lohiensis L2TR] gb AAV82550.1 Secreted enzyme, contains two amidohydrolase related domains [Idiomarina lohiensis L2TR]				3.5.1.5
19777, 19778	38044083	38	4.00E-25	Helicobacter pylori Clostridium thermocellum	restriction endonuclease [Helicobacter pylori]				
19781, 19782	48858283	67	2.00E-99	ATCC 27405	COG2304: Uncharacterized protein containing a von Willebrand factor type A (VWA) domain [Clostridium thermocellum ATCC 27405]				

19787,	38044083	32	1.00E-24	Helicobacter pylori	restriction endonuclease [Helicobacter pylori]				
19788				Cytophaga	COG0769: UDP-N-acetylmutamyl tripeptide synthase [Cytophaga				
19789,	48854577	56	7.00E-83	hutchinsonii	hutchinsonii]				6.3.2.13
19790									
1979,					hypothetical replication factor C small subunit [Sulfolobus tokodaii str. 7]				
1980	15920690	46	4.00E-69	Sulfolobus tokodaii str. 7	spiQ975D3[RFC5_SULO Replication factor C small subunit (RFC small subunit) (Clamp loader small subunit) dbj BAB65468.1 327aa long				2.7.7.7
19791,					hypothetical replication factor C small subunit [Sulfolobus tokodaii str. 7]				
19792	48854578	43	9.00E-41	Cytophaga hutchinsonii	COG0768: Cell division protein Fis/penicillin-binding protein 2 [Cytophaga hutchinsonii]				2.3.2.-
19793,				Cytophaga					
19794	48856707	45	8.00E-31	hutchinsonii	COG1300: Uncharacterized membrane protein [Cytophaga hutchinsonii]				
19797,					predicted protein [Neurospora crassa] emb CAD70330.1 putative protein				
19798	32404060	27	1.00E-08	Neurospora crassa	gb EAA27596.1 predicted protein [Neurospora crassa]				
19799,					two-component response regulator [Nostoc sp. PCC 7120] dbj BAB75465.1				
19800	17231258	45	3.00E-29	Nostoc sp. PCC 7120	two-component response regulator [Nostoc sp. PCC 7120] pir AG2276 two-component response regulator all3766 [imported] - Nostoc sp. (strain PCC 7120)				2.7.3.-
19801,				Silicibacter	hypothetical protein SPOA0125 [Silicibacter pomeroyi] DSS-3				
19802	56708912	28	7.00E-13	pomeroyi DSS-3	gb AAV97262.1 hypothetical protein SPOA0125 [Silicibacter pomeroyi] DSS-3				
19805,				Geobacter	hypothetical protein GSU1169 [Geobacter sulfurreducens PCA]				
19806	39996271	40	7.00E-30	sulfurreducens PCA	gb AAR34545.1 hypothetical protein GSU1169 [Geobacter sulfurreducens PCA]				
19811,				uncultured marine gamma	predicted 3-oxoacyl-ACP synthase [uncultured marine gamma				
19812	45644726	37	1.00E-25	proteobacterium EBAC20E09	proteobacterium EBAC20E09]				2.3.1.41
19813,					conserved hypothetical protein [Campylobacter coli RM2228]				
19814	57169064	32	3.00E-33	Campylobacter coli RM2228	gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228]				
19815,				Cytophaga	COG1331: Highly conserved protein containing a thioredoxin domain				
19816	48854435	49	7.00E-53	hutchinsonii	[Cytophaga hutchinsonii]				2.7.4.9
19817,					hypothetical short chain dehydrogenase [Photobacterium profundum SS9]				
19818	54309391	58	1.00E-81	Photobacterium profundum SS9	emb CAG20609.1 hypothetical short chain dehydrogenase [Photobacterium profundum]				1.2.1.31
19819,				Shewanella	membrane protein, putative [Shewanella oneidensis MR-1] gb AAN54805.1				
19820	24373318	35	6.00E-35	oneidensis MR-1	membrane protein, putative [Shewanella oneidensis MR-1]				

19821, 19822	21675068	43	9.00E-72	Chlorobium tepidum TLS	ribonuclease G [Chlorobium tepidum TLS]				3.1.4.-
19823, 19824	29346171	33	6.00E-15	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0761 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75868.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
19825, 19826	50120667	35	2.00E-11	Erwinia carotovora subsp. atroseptica SCRI1043	hypothetical protein ECA1734 [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG74639.1 conserved hypothetical protein [Erwinia carotovora subsp. atroseptica SCRI1043]				
19827, 19828	48834834	53	1.00E-61	Thermobifida fusca	COG1611: Predicted Rossmann fold nucleotide-binding protein [Thermobifida fusca]				1.1.1.85
1983, 1984	15922432	26	2.00E-12	Sulfolobus tokodaii str. 7	hypothetical protein ST2106 [Sulfolobus tokodaii str. 7] dbj BAB67210.1 495aa long conserved hypothetical protein [Sulfolobus tokodaii str. 7]				
19831, 19832	48853849	30	2.00E-10	Cytophaga hutchinsonii	COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii]				
19835, 19836	34397507	32	6.00E-28	Porphyromonas gingivalis W83	hypothetical protein PG1529 [Porphyromonas gingivalis W83] ref NP_905670.1 hypothetical protein PG1529 [Porphyromonas gingivalis W83]				
19837, 19838	47565344	38	2.00E-50	Bacillus cereus G9241	hypothetical protein protein [Bacillus cereus G9241] gb EAL16024.1 hypothetical protein protein [Bacillus cereus G9241]				
19841, 19842	56459804	32	1.00E-36	Idiomarina loihlensis L2TR	Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihlensis L2TR] protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihlensis L2TR]				
19843, 19844	32476735	28	6.00E-10	Rhodopirellula baltica SH 1	probable serine/threonine protein kinase [Rhodopirellula baltica SH 1] emb CAD77107.1 probable serine/threonine protein kinase [Pirellula sp.]				2.7.1.-
19847, 19848	48854120	34	8.00E-12	Cytophaga hutchinsonii	COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii]				6.2.1.3
19849, 19850	37525769	41	1.00E-31	Photorhabdus luminescens subsp. laumondii TTO1	hypothetical protein plu1836 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE14129.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1]				
1985, 1986	46199730	40	4.00E-20	Thermus thermophilus HB27	hypothetical protein TTC1428 [Thermus thermophilus HB27] gb AAS81770.1 hypothetical protein TTC1428 [Thermus thermophilus HB27]				

19855, 19856	AAV7437 7	38	3.00E-08				Desc:Neisseria gonorrhoeae ORF 073 protein sequence SEQ ID NO:230. Org:Neisseria gonorrhoeae	Anopheles gambiae ENSANGP000000000 0381 (ENSANGG000000000 00361) mRNA, partial cds	87	4.00E-10	
19857, 19858	46188929	42	8.00E-23		Pseudomonas syringae pv. syringae B728a		COG0702: Predicted nucleoside-diphosphate-sugar epimerases [Pseudomonas syringae pv. syringae B728a]				
19859, 19860	28899147	33	1.00E-31		Vibrio parahaemolyticus RIMD 2210633		exodeoxyribonuclease V, 67 kDa subunit [Vibrio parahaemolyticus RIMD 2210633] dbj BAC60636.1 exodeoxyribonuclease V, 67 kDa subunit [Vibrio parahaemolyticus]			3.1.1.15	
19861, 19862	32330663	29	4.00E-13		Solenopsis invicta		glutathione S-transferase [Solenopsis invicta]			2.5.1.18	
19863, 19864	20808758	47	6.00E-43		Thermoanaerobacter tengcongensis MB4		Hypoxanthine-guanine phosphoribosyltransferase [Thermoanaerobacter tengcongensis MB4] gb AAM25533.1 Hypoxanthine-guanine phosphoribosyltransferase [Thermoanaerobacter tengcongensis MB4]			2.4.2.8	
19869, 19870	29349247	60	6.00E-60		Bacteroides thetaiotaomicron VPI-5482		ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78944.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482]			1.8.-.-	
19871, 19872	23100131	34	1.00E-26		Oceanobacillus lheyensis HTE831		hypothetical protein OB2676 [Oceanobacillus lheyensis HTE831] dbj BAC14632.1 hypothetical conserved protein [Oceanobacillus lheyensis HTE831]			6.3.4.6	
19875, 19876	44894463	35	1.00E-17		Bacillus thuringiensis		putative transposase [Bacillus thuringiensis] gb AAL86920.1 putative transposase [Bacillus thuringiensis]				
19877, 19878	24214680	38	3.00E-26		Leptospira interrogans serovar Lai str. 56601		hypothetical protein LA1980 [Leptospira interrogans serovar Lai str. 56601] gb AAN49179.1 hypothetical protein [Leptospira interrogans serovar lai str. 56601]				
19881, 19882	34557504	63	1.00E-97		Wolinella sucinogenes DSM 1740		HSDR PROTEIN PROBABLE TYPE I RESTRICTION ENZYME RESTRICTIONCHAIN [Wolinella sucinogenes DSM 1740] emb CAE10219.1 HSDR PROTEIN PROBABLE TYPE I RESTRICTION ENZYME RESTRICTIONCHAIN [Wolinella sucinogenes]	Nostoc sp. PCC 7120 DNA, complete genome	84	4.00E-08	3.1.21.3
19889, 19890	52632010	40	2.00E-23		uncultured archaeon GZfos12E1		conserved hypothetical protein [uncultured archaeon GZfos12E1]				
19891, 19892	52008727	37	7.00E-30		Silicibacter sp. TM1040		COG0262: Dihydrofolate reductase [Silicibacter sp. TM1040]			3.4.24.-	

19893, 19894	51244744	58	2.00E-68	Desulfotalea psychrophila LSV54	related to 2-oxoglutarate synthase, subunit KorA [Desulfotalea psychrophila LSV54] emb CAG35621.1 related to 2-oxoglutarate synthase, subunit KorA [Desulfotalea psychrophila LSV54]				1.2.7.3
19895, 19896	34397542	37	1.00E-34	Porphyromonas gingivalis W83	transcriptional regulator, Crp family [Porphyromonas gingivalis W83] ref NP_005705.1 transcriptional regulator, Crp family [Porphyromonas gingivalis W83]				
19897, 19898	15606303	51	3.00E-76	Aquifex aeolicus VF5	long-chain-fatty-acid CoA ligase [Aquifex aeolicus VF5] gb AAC07072.1 long-chain-fatty-acid CoA ligase [Aquifex aeolicus VF5] pir D70386 probable polyketide synthetase [similarity] - Aquifex aeolicus				6.2.1.3
19899, 19900	34763672	41	2.00E-28	Fusobacterium nucleatum subsp. vincentii ATCC 49256	Long-chain-fatty-acid-CoA ligase [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA23796.1 Long-chain-fatty-acid-CoA ligase [Fusobacterium nucleatum subsp. vincentii ATCC 49256]				6.2.1.3
199, 200	48854665	44	1.00E-39	Cytophaga hutchinsonii	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii]				
19901, 19902	53712448	32	7.00E-20	Bacteroides fragilis YCH46	hypothetical protein BF1156 [Bacteroides fragilis YCH46] dbj BAD47906.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
19903, 19904	29346729	35	9.00E-17	Bacteroides thetaiotaomicron VPI-5482	two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO76426.1 two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482]				
19907, 19908	56678876	32	2.00E-28	Silicibacter pomeroi DSS-3	hypothetical protein SPO2278 [Silicibacter pomeroi DSS-3] ref YP_167502.1 hypothetical protein SPO2278 [Silicibacter pomeroi DSS-3]				
19913, 19914	48855430	31	8.00E-38	Cytophaga hutchinsonii	hypothetical protein Chut02001765 [Cytophaga hutchinsonii]				
19917, 19918	53711756	25	6.00E-09	Bacteroides fragilis YCH46	hypothetical protein BF0465 [Bacteroides fragilis YCH46] dbj BAD47214.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
19921, 19922	24374550	29	5.00E-18	Shewanella oneidensis MR-1	hypothetical protein SO3025 [Shewanella oneidensis MR-1] gb AAN56037.1 conserved hypothetical protein [Shewanella oneidensis MR-1]				
1993, 1994	37526903	28	5.00E-16	Photorhabdus luminescens subsp. laumondii TTO1	hypothetical protein plu3015 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15389.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1]				2.4.1.16 6

19931, 19932	53712348	33	8.00E-15	Bacteroides fragilis YCH46	putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD47806.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46]			
19937, 19938	16126741	37	5.00E-34	Caulobacter crescentus CB15	peptidase M20/M25/M40 family protein [Caulobacter crescentus CB15] gb AAK24473.1 peptidase M20/M25/M40 family protein [Caulobacter crescentus CB15] pir [E87559] peptidase M20/M25/M40 family protein [Imported] - Caulobacter crescentus			
19939, 19940	48855337	53	2.00E-62	Cytophaga hutchinsonii	COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii]			
19943, 19944	48854288	41	7.00E-32	Cytophaga hutchinsonii	COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii]			
19945, 19946	48854286	29	4.00E-10	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]			
19947, 19948	48856513	57	2.00E-29	Cytophaga hutchinsonii	COG0307: Riboflavin synthase alpha chain [Cytophaga hutchinsonii]			2.5.1.9
19949, 19950	56544347	45	1.00E-24	Zymomonas mobilis subsp. mobilis ZM4	glutamine cyclotransferase [Zymomonas mobilis subsp. mobilis ZM4] ref YP_163612.1 glutamine cyclotransferase [Zymomonas mobilis subsp. mobilis ZM4]			
1995, 1996	53713033	59	1.00E-114	Bacteroides fragilis YCH46	ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] dbj BAD48491.1 ABC transporter ATP-binding protein [Bacteroides fragilis YCH46]			
19951, 19952	17934032	44	1.00E-28	Agrobacterium tumefaciens str. C58	two component sensor kinase [Agrobacterium tumefaciens str. C58] gb AAL41138.1 two component sensor kinase [Agrobacterium tumefaciens str. C58] pir [AD2590] two component sensor kinase dctB [Imported] - Agrobacterium tumefaciens (strain C58, Dupont)			2.7.3.-
19957, 19958	29347086	44	8.00E-24	Bacteroides thetaiotaomicron VPI-5482	Maf protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76783.1 Maf protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A749 YG76_BACTN Maf-like protein BT1676			
19959, 19960	48855136	58	7.00E-62	Cytophaga hutchinsonii	COG0118: Glutamine amidotransferase [Cytophaga hutchinsonii]			2.4.2.-
19961, 19962	29345612	51	3.00E-52	Bacteroides thetaiotaomicron VPI-5482	histidinol-phosphate aminotransferase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO75309.1 histidinol-phosphate aminotransferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8ABA8 HIS8_BACTN Histidinol-phosphate aminotransferase [imidazole acetol-phosphate transaminase]			2.6.1.9
19967, 19968	12024595	63	2.00E-63	Flavobacterium johnsoniae	GldE [Flavobacterium johnsoniae]			
19969, 19970	39937015	67	4.00E-52	Rhodopseudomonas palustris CGA009	thioredoxin reductase [Rhodopseudomonas palustris CGA009] emb CAE29395.1 thioredoxin reductase [Rhodopseudomonas palustris CGA009]			1.6.4.5

1997, 1998	56963167	26	2.00E-08	Bacillus clausii KSM-K16	penicillin-binding protein 4 [Bacillus clausii KSM-K16] dbj BAD63934.1 penicillin-binding protein 4 [Bacillus clausii KSM-K16]				
19973, 19974	21674329	68	6.00E-31	Chlorobium tepidum TLS	CAAX prenyl protease 1, putative [Chlorobium tepidum TLS] gb AAM72736.1 CAAX prenyl protease 1, putative [Chlorobium tepidum TLS]				3.4.24.-
19975, 19976	15899493	31	7.00E-11	Sulfolobus solfataricus P2	hypothetical protein SSO2778 [Sulfolobus solfataricus P2] gb AAK42888.1 Conserved hypothetical protein [Sulfolobus solfataricus P2] pir A90454 conserved hypothetical protein [imported] - Sulfolobus solfataricus				
19977, 19978	56707657	63	1.00E-58	Francisella tularensis subsp. tularensis Schu 4	hypothetical protein FT10522 [Francisella tularensis subsp. tularensis Schu 4] emb CAG45155.1 conserved hypothetical protein [Francisella tularensis subsp. tularensis]				2.1.1.72
19979, 19980	53796853	41	8.00E-37	Chloroflexus aurantiacus	COG0210: Superfamily I DNA and RNA helicases [Chloroflexus aurantiacus]				3.6.1.-
19981, 19982	21243533	31	4.00E-23	Xanthomonas axonopodis pv. citri str. 306	beta-lactamase [Xanthomonas axonopodis pv. citri str. 306] gb AAM37651.1 beta-lactamase [Xanthomonas axonopodis pv. citri str. 306]				
19983, 19984	48855481	34	5.00E-29	Cytophaga hutchinsonii	hypothetical protein Chut02001820 [Cytophaga hutchinsonii] putative protoporphyrinogen oxidase [Bacteroides fragilis YCH46]				
19987, 19988	53711799	51	1.00E-21	Bacteroides fragilis YCH46	dbj BAD47257.1 putative protoporphyrinogen oxidase [Bacteroides fragilis YCH46]				2.1.1.-
19989, 19990	52008034	33	1.00E-18	Thiobacillus denitrificans ATCC 25259	COG2202: FOG: PAS/PAC domain [Thiobacillus denitrificans ATCC 25259]				2.7.3.-
1999, 2000	AAR0646 4	87	1.00E-97		Desc:Pancreatic islet cell antigen (ICA) encoding cDNA (clone ICA-302). Org:Homo sapiens			80	2.00E-50 2.7.7.8
19991, 19992	57240784	50	7.00E-44	Campylobacter lari RM2100	Desc:Derived protein from clone ICA302 (ATCC 40551). Org:Homo sapiens conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55177.1 conserved hypothetical protein [Campylobacter lari RM2100]				3.4.13.9
19993, 19994	29347851	27	5.00E-12	Bacteroides thetaiotaomicron VPI-5482	putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77548.1 putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides thetaiotaomicron VPI-5482]				3.1.3.5

19997, 19998	15884727	36	1.00E-18	Clostridium acetobutylicum ATCC 824	tetracycline resistance protein, tetQ family, GTPase [Clostridium acetobutylicum ATCC 824] gb AAK79416.1 tetracycline resistance protein, tetQ family, GTPase [Clostridium acetobutylicum ATCC 824] pir E97078 tetracycline resistance protein, tetQ family, GTPase [imported] - Clostridium acetobutylicum			3.6.1.48
19999, 20000	23014264	44	1.00E-43	Magnetospirillum magnetotacticum MS-1	COG0019: Diaminopimelate decarboxylase [Magnetospirillum magnetotacticum MS-1]			4.1.1.20
20003, 20004	13488054	29	3.00E-11	Mesorhizobium loti MAFF303099	hypothetical protein ml9010 [Mesorhizobium loti MAFF303099] dbj BAB54441.1 ml9010 [Mesorhizobium loti MAFF303099]			4.2.1.79
20009, 20010	53799012	31	1.00E-13	Chloroflexus aurantiacus	COG2936: Predicted acyl esterases [Chloroflexus aurantiacus]			
2001, 2002	52548759	51	3.00E-69	uncultured archaeon GZfos18F2	putative glycosyl transferase [uncultured archaeon GZfos18F2]			2.---
20013, 20014	48853712	59	6.00E-56	Cytophaga hutchinsonii	COG0845: Membrane-fusion protein [Cytophaga hutchinsonii]			
20015, 20016	48856025	35	5.00E-20	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]			
20017, 20018	48846974	47	2.00E-19	Geobacter metallireducens GS-15	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Geobacter metallireducens GS-15]			2.7.3.-
20019, 20020	20807152	43	2.00E-34	Thermoanaerobact er tengcongensis MB4	UDP-N-acetylglucosamine 2-epimerase [Thermoanaerobacter tengcongensis MB4] gb AAM23927.1 UDP-N-acetylglucosamine 2- epimerase [Thermoanaerobacter tengcongensis MB4]			5.1.3.14
20021, 20022	47526988	33	2.00E-11	Bacillus anthracis str. 'Ames Ancestor'	tpg/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] ref YP_027843.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne] ref NP_844138.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAP25624.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAT30812.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] gb AAT53894.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne]			
20025, 20026	34558474	40	2.00E-48	Wolfinella succinogenes DSM 1740	hypothetical protein WS2199 [Wolfinella succinogenes DSM 1740] emb CAE11189.1 conserved hypothetical protein [Wolfinella succinogenes]			
20027, 20028	55540738	23	2.00E-07	Flavobacterium columnare	Fjo24 [Flavobacterium columnare]			

20029, 20030	16077248	38	1.00E-30	168	Bacillus subtilis subsp. subtilis str.	DNA-3-methyladenine glycosylase [Bacillus subtilis str. 168] emb CAB11956.1 DNA-3-methyladenine glycosylase [Bacillus subtilis subsp. subtilis str. 168] pir E69584 3-methyladenine DNA glycosylase (EC 3.2.2.-) - Bacillus subtilis sp P37878 3MGA_BACSU DNA-3-methyladenine glycosylase (3-methyladenine-DNA glycosidase) dbj BAA03361.1 3-methyladenine DNA glycosylase [Bacillus subtilis] dbj BAA33073.1 3-METHYLADEININE DNA GLYCOSYLASE [Bacillus subtilis]	3.2.2.21		
2003, 2004	29347199	27	2.00E-13	VPI-5482	Bacteroides thetataomicron	aminopeptidase C (bleomycin hydrolase) [Bacteroides thetataomicron VPI-5482] gb AAO76896.1 aminopeptidase C (bleomycin hydrolase) [Bacteroides thetataomicron VPI-5482]			
20031, 20032	21672847	46	3.00E-45	tepidum TLS	Chlorobium	Oxa1/60 kDa IMP family protein [Chlorobium tepidum TLS] gb AAM71254.1 Oxa1/60 kDa IMP family protein [Chlorobium tepidum TLS]			
20033, 20034	21885294	44	7.00E-43	Vibrio cholerae		putative histidine kinase [Vibrio cholerae]	2.7.3.-		
20035, 20036	48853472	32	1.00E-23	hutchinsonii	Cytophaga	hypothetical protein Chut02003804 [Cytophaga hutchinsonii]			
20037, 20038	23127700	36	2.00E-42	PCC 73102	Nostoc punctiforme	COG1357: Uncharacterized low-complexity proteins [Nostoc punctiforme PCC 73102]			
20039, 20040	15894108	33	8.00E-09	ATCC 824	Clostridium acetobutylicum	Transcriptional regulator (TetR/AcrR family) [Clostridium acetobutylicum ATCC 824] gb AAK78797.1 Transcriptional regulator (TetR/AcrR family) [Clostridium acetobutylicum ATCC 824] pir B97001 transcription regulator (TetR/AcrR family) [Imported] - Clostridium acetobutylicum			
20043, 20044	34397911	28	3.00E-13	gingivalis W83	Porphyromonas	signal peptidase I [Porphyromonas gingivalis W83] ref NP_906073.1 signal peptidase I [Porphyromonas gingivalis W83]			
20045, 20046	20091299	25	3.00E-08	acetivorans C2A	Methanosarcina	hypothetical protein MA2468 [Methanosarcina acetivorans C2A] gb AAM05854.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A]			
20047, 20048	48856576	32	4.00E-24	hutchinsonii	Cytophaga	COG1071: Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, alpha subunit [Cytophaga hutchinsonii]			
20049, 20050	40062939	30	4.00E-29	bacterium 443	uncultured	DNA polymerase IV [uncultured bacterium 443]	2.7.7.7		
2005, 2006	53714487	56	3.00E-44	YCH46	Bacteroides fragilis	SsrA-binding protein [Bacteroides fragilis YCH46] dbj BAD49945.1 SsrA-binding protein [Bacteroides fragilis YCH46]			

20051, 20052	21229991	39	1.00E-16	Xanthomonas campestris pv. campestris str. ATCC 33913	hypothetical protein XCC0516 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM39832.1 conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913]				
20053, 20054	34397363	35	2.00E-14	Porphyromonas gingivalis W83	ref NP_905527.1 hypothetical protein PG1362 [Porphyromonas gingivalis W83]				
20055, 20056	23474790	41	2.00E-17	Desulfovibrio desulfuricans G20	COG1157: Flagellar biosynthesis/type III secretory pathway ATPase [Desulfovibrio desulfuricans G20]				
20057, 20058	32473614	33	1.00E-27	Rhodopirellula baltica SH 1	D-amino acid dehydrogenase, small chain [Rhodopirellula baltica SH 1] emb CAD78389.1 D-amino acid dehydrogenase, small chain [Pirellula sp.]				1.4.99.1
20061, 20062	24373267	23	2.00E-12	Shewanella oneidensis MR-1	transcriptional regulator [Shewanella oneidensis MR-1] gb AAN54754.1 transcriptional regulator [Shewanella oneidensis MR-1]				
20063, 20064	24637507	30	3.00E-19	Streptococcus thermophilus	Eps10P [Streptococcus thermophilus]				
20065, 20066	52081206	48	2.00E-43	Bacillus licheniformis ATCC 14580	cystathionine gamma-lyase YrhB [Bacillus licheniformis ATCC 14580] gb AAU24359.1 cystathionine gamma-lyase YrhB [Bacillus licheniformis ATCC 14580] ref YP_092416.1 YrhB [Bacillus licheniformis ATCC 14580] gb AAU41723.1 YrhB [Bacillus licheniformis DSM 13]				4.2.99.9
2007, 2008	57234396	41	7.00E-44	Dehalococcoides ethenogenes 195	ABC transporter, ATP-binding protein [Dehalococcoides ethenogenes 195] gb AAW39901.1 ABC transporter, ATP-binding protein [Dehalococcoides ethenogenes 195]				1.8.--
20071, 20072	48853602	54	2.00E-76	Cytophaga hutchinsonii	COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii]				
20073, 20074	53712266	50	3.00E-49	Bacteroides fragilis YCH46	putative S-adenosylmethionine-dependent methyltransferase [Bacteroides fragilis YCH46] db BAD47724.1 putative S-adenosylmethionine-dependent methyltransferase [Bacteroides fragilis YCH46]				2.1.1.-
20075, 20076	16331457	23	2.00E-10	Synechocystis sp. PCC 6803	hypothetical protein sl0405 [Synecocystis sp. PCC 6803] db BAA10255.1 sl0405 [Synecocystis sp. PCC 6803] pir S74337 hypothetical protein sl0405 - Synecocystis sp. (strain PCC 6803)				
20077, 20078	50929757	43	2.00E-33	Oryza sativa (japonica cultivar- group)	OSJNBa0088H09.2 [Oryza sativa (japonica cultivar-group)] emb CAE03444.1 OSJNBa0088H09.2 [Oryza sativa (japonica cultivar-group)]				6.2.1.3
20085, 20086	53796853	41	7.00E-38	Chloroflexus aurantiacus	COG0210: Superfamily I DNA and RNA helicases [Chloroflexus aurantiacus]				3.6.1.-
20087, 20088	29346486	44	8.00E-46	Bacteroides thetaitaomicron VPI-5482	two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO76183.1 two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-

20093, 20094	48855702	38	3.00E-16	Cytophaga hutchinsonii	COG3279: Response regulator of the LysR/AlgR family [Cytophaga hutchinsonii]		
				Legionella pneumophila subsp. pneumophila str. Philadelphia 1	glucose inhibited division protein B [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28937.1 glucose inhibited division protein B [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] probable 5-formyltetrahydrofolate cyclo-ligase [Clostridium perfringens str. 13] dbj BAB82030.1 probable 5-formyltetrahydrofolate cyclo-ligase [Clostridium perfringens str. 13]		6.3.3.2
20099, 20100	18311306	34	2.00E-19	Clostridium perfringens str. 13	RNA polymerase ECF-type sigma factor [Oceanobacillus ihayensis HTE831] dbj BAC14616.1 RNA polymerase ECF-type sigma factor [Oceanobacillus ihayensis HTE831]		
20105, 20106	23100115	32	5.00E-14	Oceanobacillus ihayensis HTE831	COG5343: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]		
20107, 20108	48855790	33	3.00E-15	Cytophaga hutchinsonii	hypothetical protein [Staphylococcus aureus]		
20109, 20110	28465878	37	5.00E-07	Staphylococcus aureus	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii]		2.7.3.-
2011, 2012	48854665	44	4.00E-61	Cytophaga hutchinsonii	hypothetical protein DP1860 [Desulfotalea psychrophila Lsv54] emb CAG36589.1 hypothetical protein [Desulfotalea psychrophila Lsv54] response regulator receiver:histidine kinase [Rhodopseudomonas palustris CGA009] emb CAE30230.1 response regulator receiver:histidine kinase [Rhodopseudomonas palustris CGA009]		1.3.-
20117, 20118	51245712	36	2.00E-18	Desulfotalea psychrophila Lsv54	hypothetical protein SPOA0125 [Silicibacter pomeroyi DSS-3] gb AAV97262.1 hypothetical protein SPOA0125 [Silicibacter pomeroyi DSS-3]		2.7.3.-
20121, 20122	39937848	48	2.00E-19	Rhodopseudomona s palustris CGA009	COG2202: FOG: PAS/PAC domain [Anabaena variabilis ATCC 29413]		
20127, 20128	56708912	28	5.00E-13	Silicibacter pomeroyi DSS-3	COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405]		2.7.3.-
2013, 2014	53763805	36	5.00E-38	Anabaena variabilis ATCC 29413	hypothetical protein BF1151 [Bacteroides fragilis YCH46] dbj BAD47901.1 conserved hypothetical protein [Bacteroides fragilis YCH46] glycerol-3-phosphate dehydrogenase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO77230.1 glycerol-3-phosphate dehydrogenase [Bacteroides thetaitaomicron VPI-5482]		1.1.1.94
20131, 20132	48859543	35	7.00E-32	Clostridium thermocellum ATCC 27405			
20135, 20136	53712443	33	1.00E-36	Bacteroides fragilis YCH46			
20137, 20138	29347533	39	7.00E-18	Bacteroides thetaitaomicron VPI-5482			

20139, 20140	23502026	78	2.00E-68	Brucella suis 1330	citrate synthase [Brucella suis 1330] gb AAN30068.1 citrate synthase [Brucella suis 1330]	Salmonella typhimurium LT2, section 37 of 220 of the complete genome	89	4.00E-25	4.1.3.7
20147, 20148	36955665	86	2.00E-63	Polaribacter filamentus	kynureninase [Polaribacter filamentus]	Polaribacter filamentus			
20149, 20150	48854546	40	4.00E-16	Cytophaga hutchinsonii	COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii]	kynureninase gene, complete cds	83	1.00E-61	3.7.1.3
20151, 20152	33862008	30	9.00E-17	Prochlorococcus marinus subsp. pastoris str. CCMP1986	ATP synthase, delta (OSCP) subunit [Prochlorococcus marinus subsp. pastoris str. CCMP1986]				3.6.3.14
20153, 20154	28348769	57	9.00E-39	Bacteroides thetaiotaomicron VPI-5482	phosphoribosylglycinamide formyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78466.1 phosphoribosylglycinamide formyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.1.2.2
20155, 20156	32474967	41	1.00E-40	Rhodopirellula baltica SH 1	hypothetical protein RB7682 [Rhodopirellula baltica SH 1] emb CAD75508.1 hypothetical protein [Pirellula sp.]				
20157, 20158	21674971	51	2.00E-30	Chlorobium tepidum TLS	DNA-directed RNA polymerase, alpha subunit [Chlorobium tepidum TLS] gb AAM73378.1 DNA-directed RNA polymerase, alpha subunit [Chlorobium tepidum TLS] sp Q8KAJ8 RPOA_CHLTE DNA-directed RNA polymerase alpha chain (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit)				2.7.7.6
20163, 20164	14602144	27	1.00E-09	Aeropyrum permix K1	hypothetical protein APE2556 [Aeropyrum permix K1] dbj BAA81573.1 1007aa long hypothetical protein [Aeropyrum permix K1] pir E72489 hypothetical protein APE2556 - Aeropyrum permix (strain K1)				1.2.1.2
20165, 20166	23014654	43	7.00E-15	Magnetospirillum magnetotacticum MS-1	hypothetical protein Magn03009102 [Magnetospirillum magnetotacticum MS-1]				
20167, 20168	21672847	34	6.00E-43	Chlorobium tepidum TLS	Oxa1/60 kDa IMP family protein [Chlorobium tepidum TLS] gb AAM71254.1 Oxa1/60 kDa IMP family protein [Chlorobium tepidum TLS] sp Q8KGG2 OXA1_CHLTE inner membrane protein oxaA				
20169, 20170	27366639	39	2.00E-22	Vibrio vulnificus CMCP6	Deoxycytidylate deaminase [Vibrio vulnificus CMCP6] gb AAO07156.1 Deoxycytidylate deaminase [Vibrio vulnificus CMCP6]				

2017, 2018	53715477	58	5.00E-99	Bacteroides fragilis YCH46	DNA-directed RNA polymerase beta chain [Bacteroides fragilis YCH46] dbj BAD50935.1 DNA-directed RNA polymerase beta chain [Bacteroides fragilis YCH46]	Bacteroides thetotaomicron VPI-5482, section 12 of 21 of the complete genome	87	2.00E-22	2.7.7.6
20173, 20174	20559952	37	1.00E-06	Pseudomonas aeruginosa	ORF_12; similar to Glycosyl transferases group 1 [Pseudomonas aeruginosa] gb AAM27564.1 ORF_12; similar to Glycosyl transferases group 1 [Pseudomonas aeruginosa]				
20175, 20176	20559952	42	1.00E-29	Pseudomonas aeruginosa	ORF_12; similar to Glycosyl transferases group 1 [Pseudomonas aeruginosa] gb AAM27564.1 ORF_12; similar to Glycosyl transferases group 1 [Pseudomonas aeruginosa]				
20179, 20180	53712067	28	7.00E-18	Bacteroides fragilis YCH46	AAA-metalloprotease FtsH with ATPase domain [Bacteroides fragilis YCH46] dbj BAD47525.1 AAA-metalloprotease FtsH with ATPase domain [Bacteroides fragilis YCH46]				3.4.24.-
20181, 20182	42524039	36	3.00E-13	Bdellovibrio bacteriovorus HD100	transcriptional regulator, LysR family [Bdellovibrio bacteriovorus HD100] emb CAE8041.1 transcriptional regulator, LysR family [Bdellovibrio bacteriovorus HD100]				
20183, 20184	48853811	46	1.00E-52	Cytophaga hutchinsonii	COG0587: DNA polymerase III, alpha subunit [Cytophaga hutchinsonii]				2.7.7.7
20185, 20186	48731833	73	1.00E-120	Pseudomonas fluorescens PFO-1	COG0034: Glutamine phosphoribosylpyrophosphate amidotransferase [Pseudomonas fluorescens PFO-1]	Pseudomonas syringae pv. tomato str. DC3000 section 14 of 21 of the complete genome	80	5.00E-11	2.4.2.14
20187, 20188	48856687	30	1.00E-25	Cytophaga hutchinsonii	COG2834: Outer membrane lipoprotein-sorting protein [Cytophaga hutchinsonii]				
20189, 20190	30249328	37	3.00E-11	Nitrosomonas europaea ATCC 19718	hypothetical protein NE1349 [Nitrosomonas europaea ATCC 19718] emb CAD85260.1 conserved hypothetical protein [Nitrosomonas europaea ATCC 19718]				
20191, 20192	45656787	49	7.00E-49	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_710808.1 Putative glycosyl transferase [Leptospira interrogans serovar Lai str. 56601] gb AAN47826.1 Putative glycosyl transferase [Leptospira interrogans serovar lai str. 56601] gb AAS71510.1 glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				
20193, 20194	48853832	56	5.00E-49	Cytophaga hutchinsonii	COG0484: DnaJ-class molecular chaperone with C-terminal Zn finger domain [Cytophaga hutchinsonii]				

20195, 20196	52079641	43	1.00E-21	14580	Bacillus licheniformis ATCC 14580	oligopeptide ABC transporter (binding protein) [Bacillus licheniformis ATCC 14580] gb AAU22794.1 oligopeptide ABC transporter (binding protein) [Bacillus licheniformis ATCC 14580] ref YP_090833.1 OppA [Bacillus licheniformis ATCC 14580] gb AAU40140.1 OppA [Bacillus licheniformis DSM 13]			
20197, 20198	28899115	53	4.00E-79	RIMD 2210633	Vibrio parahaemolyticus	putative ATP-dependent DNA helicase RecQ [Vibrio parahaemolyticus RIMD 2210633] dbj BAC0604.1 putative ATP-dependent DNA helicase RecQ [Vibrio parahaemolyticus]			3.6.1.-
20199, 20200	48763874	64	1.00E-26	Rhodospirillum rubrum	Rhodospirillum rubrum	COG0762: Predicted integral membrane protein [Rhodospirillum rubrum]			
20201, 20202	34332873	28	6.00E-16	12472	Chromobacterium violaceum ATCC 12472	conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_902918.1 hypothetical protein CV3248 [Chromobacterium violaceum ATCC 12472]			2.7.3.-
20205, 20206	15614300	42	8.00E-35	C-125	Bacillus halodurans C-125	homoserine dehydrogenase [Bacillus halodurans C-125] dbj BAB05456.1 homoserine dehydrogenase [Bacillus halodurans C-125] pir A83867 homoserine dehydrogenase BH1737 [Imported] - Bacillus halodurans (strain C-125)			1.1.1.3
20207, 20208	57158331	34	1.00E-34	Thermococcus kodakaraensis	Thermococcus kodakaraensis	tungsten-containing oxidoreductase [Thermococcus kodakaraensis] ref YP_182485.1 tungsten-containing oxidoreductase [Thermococcus kodakaraensis]			1.2.7.-
20209, 20210	48860188	39	3.00E-17	ATCC 27405	Clostridium thermocellum ATCC 27405	COG1539: Dihydropyrimidin aldolase [Clostridium thermocellum ATCC 27405]			4.1.2.25
2021, 2022	29350162	26	8.00E-17	VPI-5482	Bacteroides thetaiotaomicron VPI-5482	putative cytosine-specific methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79859.1 putative cytosine-specific methyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.1.1.73
20211, 20212	ABP7815 0	51	7.00E-32			Desc:N. gonorrhoeae amino acid sequence SEQ ID 2830. Org:Neisseria gonorrhoeae			
20215, 20216	21228805	29	1.00E-07	Methanosarcina mazei Go1	Methanosarcina mazei Go1	type I restriction-modification system specificity subunit [Methanosarcina mazei Go1] gb AAM32399.1 type I restriction-modification system specificity subunit [Methanosarcina mazei Go1]			3.1.21.3
20217, 20218	48856451	50	8.00E-72	Cytophaga hutchinsonii	Cytophaga hutchinsonii	COG0040: ATP phosphoribosyltransferase [Cytophaga hutchinsonii]			2.4.2.17
20223, 20224	53712340	62	3.00E-60	YCH46	Bacteroides fragilis YCH46	hypothetical protein BF1048 [Bacteroides fragilis YCH46] dbj BAD47798.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
20225, 20226	48856445	46	2.00E-43	Cytophaga hutchinsonii	Cytophaga hutchinsonii	hypothetical protein Chut02000167 [Cytophaga hutchinsonii]			

2023,	42521765	58	3.00E-63	Bdellovibrio bacteriovorus HD100	Acetylornithine/succinyl-diaminopimelate aminotransferase [Bdellovibrio bacteriovorus HD100] emb CAE77799.1]				2.6.1.11
20231,	48856539	30	4.00E-14	Cytophaga hutchinsonii	COG0791: Cell wall-associated hydrolases (invasion-associated proteins) [Cytophaga hutchinsonii]				
20233,	29348479	47	3.00E-60	Bacteroides thetataotomicron VPI-5482	Smf protein DNA processing chain A [Bacteroides thetataotomicron VPI- 5482] gb AAO78176.1] Smf protein DNA processing chain A [Bacteroides thetataotomicron VPI-5482]				
20235,	48854415	61	3.00E-77	Cytophaga hutchinsonii	COG3279: Response regulator of the LytR/AlgR family [Cytophaga hutchinsonii]				2.7.3.-
20237,	16077744	39	4.00E-21	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU06760 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12496.1] yeeA [Bacillus subtilis subsp. subtilis str. 168] pir E69792 conserved hypothetical protein yeeA - Bacillus subtilis				
20239,	48853949	60	1.00E-43	Cytophaga hutchinsonii	COG0187: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit [Cytophaga hutchinsonii]				5.99.1.3
20241,	48854339	75	1.00E-53	Cytophaga hutchinsonii	COG0178: Exonuclease ATPase subunit [Cytophaga hutchinsonii]	Desc: Genomic sequence of Lactococcus lactis IL1403.	81	2.00E-11	
20243,	48861416	77	3.00E-43	Microbulbifer degradans 2-40	COG0177: Predicted EndoIII-related endonuclease [Microbulbifer degradans 2-40]				4.2.99.1 8
20244,	53711581	61	9.00E-31	Bacteroides fragilis YCH46	ribonuclease HII [Bacteroides fragilis YCH46] dbj BAD47039.1] ribonuclease HII [Bacteroides fragilis YCH46]				3.1.26.4
20249,	46132462	74	1.00E-104	Ralstonia eutropha JMP134	COG0714: MoxR-like ATPases [Ralstonia eutropha JMP134]	Pseudomonas aeruginosa PAO1, section 259 of 529 of the complete genome	80	5.00E-32	
2025,	53763802	33	4.00E-25	Anabaena variabilis ATCC 29413	COG2319: FOG: WD40 repeat [Anabaena variabilis ATCC 29413]				2.7.1.37
20251,	31790565	61	3.00E-73	marine bacterium P99-3	phytoene desaturase [marine bacterium P99-3]				
20252,	AAV7501	44	4.00E-29		Desc: Neisseria meningitidis ORF 525 protein sequence SEQ ID NO:1498.				
20253,	29346875	28	2.00E-18	Bacteroides thetataotomicron VPI-5482	putative ABC transporter permease [Bacteroides thetataotomicron VPI-5482] gb AAO76572.1] putative ABC transporter permease [Bacteroides thetataotomicron VPI-5482]				

20257, 20258	37912867	42	1.00E-20	uncultured marine proteobacterium ANT8C10	predicted acetyltransferase [uncultured marine proteobacterium ANT8C10]				
20259, 20260	2411488	68	9.00E-94	Klebsiella pneumoniae	HsdR [Klebsiella pneumoniae] pir[T30329 hsdR protein - Klebsiella pneumoniae]	S. enterica hsdM, hsdS & hsdR genes 83	6.00E-10	3.1.21.3	
20263, 20264	53689679	35	4.00E-43	Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293	COG1540: Uncharacterized proteins, homologs of lactam utilization protein B [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]				
20265, 20266	39997172	35	5.00E-11	Geobacter sulfurreducens PCA	PPIC-type PPIASE domain protein [Geobacter sulfurreducens PCA]				
2027, 2028	48854724	37	2.00E-25	Cytophaga hutchinsonii	gb AAR35450.1 PPIC-type PPIASE domain protein [Geobacter sulfurreducens PCA]			5.2.1.8	
20277, 20278	16125143	31	1.00E-11	Caulobacter crescentus CB15	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-	
20279, 20280	56677851	30	3.00E-21	Silicibacter pomeroiyi DSS-3	hypothetical protein CO0890 [Caulobacter crescentus CB15]				
20283, 20284	48855019	47	2.00E-31	Cytophaga hutchinsonii	gb AAK22875.1 hypothetical protein [Caulobacter crescentus CB15] pir [G87359 hypothetical protein CO0890 [imported] - Caulobacter crescentus site-specific recombinase, resolvase family [Silicibacter pomeroiyi DSS-3] ref YP_166469.1 site-specific recombinase, resolvase family [Silicibacter pomeroiyi DSS-3]			2.4.1.18 2	
2029, 2030	45659045	56	1.00E-54	Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130	COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii]				
20291, 20292	48854156	41	9.00E-46	Cytophaga hutchinsonii	Inorganic pyrophosphatase [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130] ref NP_714220.1 Soluble inorganic pyrophosphatase [Leptospira interrogans serovar Lai str. 56601] gb AAN51238.1 Soluble inorganic pyrophosphatase [Leptospira interrogans serovar lai str. 56601] sp Q8E221 IPYR_LEPIN Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (Pase) gb AAS71768.1 inorganic pyrophosphatase [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130]			3.6.1.1	
20293, 20294	53712087	36	7.00E-42	Bacteroides fragilis YCH46	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] putative transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD47545.1 putative transcriptional regulator [Bacteroides fragilis YCH46]			2.7.3.-	

20295, 20296	34397292	50	6.00E-53	Porphyromonas gingivalis W83	translation elongation factor P [Porphyromonas gingivalis W83] ref NP_905456.1 translation elongation factor P [Porphyromonas gingivalis W83] sp Q7MV32 EFP2 PORGI Elongation factor P 2 (EF-P 2)	Union yellows phytoplasma OY-M DNA, complete genome	91	4.00E-10	
20299, 20300	15894950	57	6.00E-86	Clostridium acetobutylicum ATCC 824	Large subunit of NADH-dependent glutamate synthase [Clostridium acetobutylicum ATCC 824] gb AAK79639.1 Large subunit of NADH- dependent glutamate synthase [Clostridium acetobutylicum ATCC 824] pir D97106 large chain of NADH-dependent glutamate synthase CAC1673 [Imported] - Clostridium acetobutylicum	Clostridium saccharobutylicum glutamate synthase operon, complete sequence	83	2.00E-10	1.4.1.13
20305, 20306	31195963	63	4.00E-70	Anopheles gambiae	ENSANGP00000000454 [Anopheles gambiae]				4.2.1.22
20307, 20308	53759487	25	1.00E-15	Methylobacillus flagellatus KT	COG1587: Uroporphyrinogen-III synthase [Methylobacillus flagellatus KT]				4.2.1.75
2031, 2032	45160119	54	1.00E-45	Tetrahymena thermophila	mitogen activated protein kinase 4 [Tetrahymena thermophila]				2.7.1.-
20311, 20312	53714594	30	2.00E-22	Bacteroides fragilis YCH46	LacI family transcriptional regulator [Bacteroides fragilis YCH46] db BAD50052.1 LacI family transcriptional regulator [Bacteroides fragilis YCH46]				
20315, 20316	48856573	61	3.00E-31	Cytophaga hutchinsonii	COG2207: AraC-type DNA-binding domain-containing proteins [Cytophaga hutchinsonii]				2.1.1.63
20317, 20318	28876472	31	8.00E-16	Streptococcus pyogenes phage 315.6	putative DNA primase/helicase [Streptococcus pyogenes phage 315.6] ref NP_801685.1 putative DNA primase (phage associated) [Streptococcus pyogenes SSI-1] ref YP_059353.1 virulence-associated protein E [Streptococcus pyogenes MGAS10394] ref NP_665246.1 putative DNA primase/helicase - phage associated [Streptococcus pyogenes MGAS315] gb AA786170.1 virulence-associated protein E [Streptococcus pyogenes MGAS10394] gb AAM80049.1 putative DNA primase/helicase - phage associated [Streptococcus pyogenes phage 315.6] db BAC63518.1 putative DNA primase (phage associated) [Streptococcus pyogenes SSI-1]				
20321, 20322	56460815	57	2.00E-24	Idiomarina loihlensis L2TR	Anti-anti-sigma regulatory factor [Idiomarina loihlensis L2TR] gb AAV82547.1 Anti-anti-sigma regulatory factor [Idiomarina loihlensis L2TR]	Idiomarina loihlensis L2TR, complete genome	88	9.00E-07	
20327, 20328	48853783	56	5.00E-37	Cytophaga hutchinsonii	COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii]				2.7.7.7
20329, 20330	54031199	49	2.00E-51	Polaromonas sp. JS666	COG0318: Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II [Polaromonas sp. JS666]				6.2.1.3
20331, 20332	31194819	59	6.00E-78	Anopheles gambiae	ENSANGP000000002020 [Anopheles gambiae]				

20333, 20334	34398069	29	2.00E-10	Porphyrionas gingivalis W83	NADH:ubiquinone oxidoreductase, C subunit [Porphyrionas gingivalis W83] ref NP_096230.1 NADH:ubiquinone oxidoreductase, C subunit [Porphyrionas gingivalis W83]				
20335, 20336	21673146	54	3.00E-35	Chlorobium tepidum TLS	dTDP-4-dehydrohamnose reductase [Chlorobium tepidum TLS] gb AAM71553.1 dTDP-4-dehydrohamnose reductase [Chlorobium tepidum TLS]				1.1.1.13 3
20337, 20338	49482438	46	6.00E-21	Staphylococcus aureus subsp. aureus MRSA252	hypothetical protein SAR0197 [Staphylococcus aureus subsp. aureus MRSA252] emb CAG39224.1 hypothetical protein [Staphylococcus aureus subsp. aureus MRSA252]				
20339, 20340	37812000	37	1.00E-18	Aeromonas hydrophila	hypothetical protein [Aeromonas hydrophila]				
20341, 20342	53714775	34	6.00E-33	Bacteroides fragilis YCH46	transcription regulator [Bacteroides fragilis YCH46] db BAD50233.1 transcription regulator [Bacteroides fragilis YCH46]				
20343, 20344	23126871	36	7.00E-22	Nostoc punctiforme PCC 73102	COG0514: Superfamily II DNA helicase [Nostoc punctiforme PCC 73102]				3.6.1.-
20347, 20348	45916344	50	1.00E-48	Mesorhizobium sp. BNC1	COG2220: Predicted Zn-dependent hydrolases of the beta-lactamase fold [Mesorhizobium sp. BNC1]				
2035, 2036	29347576	46	1.00E-41	Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77273.1 two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-
20351, 20352	57159654	30	3.00E-08	Thermococcus kodakaraensis	predicted ATP-dependent endonuclease, OLD family [Thermococcus kodakaraensis] ref YP_183808.1 predicted ATP-dependent endonuclease, OLD family [Thermococcus kodakaraensis]				
20355, 20356	53797086	36	5.00E-44	Chloroflexus aurantiacus	COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus]				
20359, 20360	45512718	41	3.00E-15	Synechococcus elongatus PCC 7942	COG0463: Glycosyltransferases involved in cell wall biogenesis [Synechococcus elongatus PCC 7942]				
20363, 20364	48854281	26	3.00E-16	Cytophaga hutchinsonii	COG3182: Uncharacterized iron-regulated membrane protein [Cytophaga hutchinsonii]				1.8.1.2
20367, 20368	30249527	50	3.00E-27	Nitrosomonas europaea ATCC 19718	putative transposase [Nitrosomonas europaea ATCC 19718] emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718]				
20369, 20370	30249527	50	3.00E-27	Nitrosomonas europaea ATCC 19718	putative transposase [Nitrosomonas europaea ATCC 19718] emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718]				

20373, 20374 20375, 20376	37678997 2879819	72 47	9.00E-42 3.00E-45	Vibrio vulnificus YJ016 Pseudoalteromonas haloplanktis	type I site-specific restriction-modification system, R (restriction) subunit [Vibrio vulnificus YJ016] dbj BAC93577.1 type I site-specific restriction- modification system, R (restriction) subunit [Vibrio vulnificus YJ016] hypothetical protein [Pseudoalteromonas haloplanktis]	Mycoplasma mobile 163K complete genome	85 4.00E-09	3.1.21.3
20377, 20378	30268405	99	2.00E-95	Acinetobacter lwoffii	putative cation efflux system protein [Acinetobacter lwoffii]	Acinetobacter lwoffii plasmid pKLH202 including an aberrant mercury resistance transposon and insertion sequences IS1006.1, IS1006.D1 and IS1009	99 0	2.1.1.52
20379, 20380 20381, 20382 20383, 20384 20385, 20386 20389, 20390 20391, 20392 20393, 20394	53717736 48853602 48855539 48855760 48853597 48856222 53734766	40 45 67 65 55 25 39	3.00E-09 3.00E-43 4.00E-71 2.00E-67 4.00E-32 8.00E-07 7.00E-35	Burkholderia pseudomallei K96243 Cytophaga hutchinsonii Cytophaga hutchinsonii Cytophaga hutchinsonii Crocospaera watsonii WH 8501	spermidine n(1)-acetyltransferase [Burkholderia pseudomallei K96243] pseudomallei K96243 COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii] COG0142: Geranylgeranyl pyrophosphate synthase [Cytophaga hutchinsonii] COG1363: Cellulase M and related proteins [Cytophaga hutchinsonii] COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii] COG0438: Glycosyltransferase [Cytophaga hutchinsonii] COG0857: BioD-like N-terminal domain of phosphotransacetylase [Crocospaera watsonii WH 8501] acetate kinase [Thermotoga maritima MSB8] gb AAD35363.1 acetate kinase [Thermotoga maritima MSB8] sp Q9WYB1 ACKA_THEME Acetate kinase (Acetokinase) pir H72397 acetate kinase - Thermotoga maritima (strain MSB8)			
20395, 20396	15643044	50	4.00E-53	Thermotoga maritima MSB8	folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 folypolyglutamate synthase [Bacteroides fragilis YCH46]			2.7.2.1
20399, 20400	53714264	59	1.00E-66	Bacteroides fragilis YCH46				6.3.2.17

20401,	48854489	34	8.00E-14	Cytophaga hutchinsonii	hypothetical protein Chut02002688 [Cytophaga hutchinsonii]				
20402				Nitrosomonas europaea ATCC 19718	putative transposase [Nitrosomonas europaea ATCC 19718]				
20403,	30249527	47	2.00E-25		embICAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718]				
20404									
20405,	53714651	46	3.00E-58	Bacteroides fragilis YCH46	two-component system response regulator [Bacteroides fragilis YCH46]				3.1.1.61
20406					dbj BAD50109.1 two-component system response regulator [Bacteroides fragilis YCH46]				
20407,				Thiobacillus denitrificans ATCC 25259	COG2189: Adenine specific DNA methylase Mod [Thiobacillus denitrificans ATCC 25259]				2.1.1.72
20408	52006160	38	2.00E-52		COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Exiguobacterium sp. 255-15]				
20409,	46114055	37	7.00E-19	Exiguobacterium sp. 255-15	Desc:Putative P. abyssal orotidine-5'-phosphate decarboxylase.				
2041,	AAB9655	2	1.00E-19		Org:Pyrococcus abyssi				4.1.1.23
2042									
20411,	47226257	26	4.00E-14	Tetraodon nigroviridis	unnamed protein product [Tetraodon nigroviridis]				
20412									
20417,				Ralstonia metallidurans CH34	hypothetical protein Reut02000359 [Ralstonia metallidurans CH34]				
20418	48771615	25	5.00E-09						
20419,	9837393	50	3.00E-42	Flavobacterium johnsoniae	GldD [Flavobacterium johnsoniae]				
20420									
20421,						Clostridium tetani E88, section 5 of 10 of the complete genome	93	6.00E-07	3.6.1.-
20422	48854355	66	8.00E-44	Cytophaga hutchinsonii	COG1200: RecG-like helicase [Cytophaga hutchinsonii]				
20425,									
20426	48854339	62	6.00E-92	Cytophaga hutchinsonii	COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii]				
						Desc:Listeria innocua DNA sequence #684. Org:Listeria innocua			
20427,									
20428	48854339	75	2.00E-64	Cytophaga hutchinsonii	COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii]			82	7.00E-18
20429,									
20430	48856125	44	9.00E-37	Cytophaga hutchinsonii	COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii]				
2043,					hypothetical protein SSO2382 [Sulfolobus solfataricus P2] gb AAK42530.1				
2044	15899135	33	2.00E-09	Sulfolobus solfataricus P2	Conserved hypothetical protein [Sulfolobus solfataricus P2] pir C90409				
20431,					conserved hypothetical protein [imported] - Sulfolobus solfataricus				
20432	50590629	46	1.00E-43	Streptococcus suis 89/1591	COG4922: Uncharacterized protein conserved in bacteria [Streptococcus suis 89/1591]				

20433,	20434,	52008442	39	2.00E-10	Thiobacillus denitrificans ATCC 25259	COG4301: Uncharacterized conserved protein [Thiobacillus denitrificans ATCC 25259]			
20437,	20438,	48854312	31	1.00E-21	Cytophaga hutchinsonii	COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii]			
20441,	20442	12024595	65	2.00E-64	Flavobacterium johnsoniae	GldE [Flavobacterium johnsoniae]			
20443,	20444	12024595	65	2.00E-56	Flavobacterium johnsoniae	GldE [Flavobacterium johnsoniae]	Desc:Listeria innocua DNA sequence #684. Org:Listeria innocua	90	1.00E-06
20445,	20446	21673014	55	1.00E-26	Chlorobium tepidum TLS	phosphoserine phosphatase [Chlorobium tepidum TLS] gb AAM71421.1 phosphoserine phosphatase [Chlorobium tepidum TLS]			3.1.3.3
20447,	20448	21673014	55	1.00E-26	Chlorobium tepidum TLS	phosphoserine phosphatase [Chlorobium tepidum TLS] gb AAM71421.1 phosphoserine phosphatase [Chlorobium tepidum TLS]			3.1.3.3
20449,	20450	AAG3969	3	58		Desc:Arabidopsis thaliana protein fragment SEQ ID NO: 49152. Org:Arabidopsis thaliana			1.6.4.-
20451,	20452	29345783	63	1.00E-39	Bacteroides thetaiotaomicron VPI-5482	mannose-6-phosphate isomerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75480.1 mannose-6-phosphate isomerase [Bacteroides thetaiotaomicron VPI-5482]			5.3.1.8
20453,	20454	53713904	55	2.00E-56	Bacteroides fragilis YCH46	exonuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 exonuclease ABC subunit A [Bacteroides fragilis YCH46]			
20455,	20456	48856624	33	6.00E-07	Cytophaga hutchinsonii	COG5520: O-Glycosyl hydrolase [Cytophaga hutchinsonii]			
20457,	20458	21242451	30	5.00E-26	Xanthomonas axonopodis pv. citri str. 306	Mg-protoporphylin IX monomethyl ester oxidative cyclase [Xanthomonas axonopodis pv. citri str. 306] gb AAM36569.1 Mg-protoporphylin IX monomethyl ester oxidative cyclase [Xanthomonas axonopodis pv. citri str. 306]			1.97.1.4
20459,	20460	53714371	23	2.00E-11	Bacteroides fragilis YCH46	putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] dbj BAD49829.1 putative ATPase involved in DNA repair [Bacteroides fragilis YCH46]			
20461,	20462	48855075	45	7.00E-25	Cytophaga hutchinsonii	COG0302: GTP cyclohydrolase I [Cytophaga hutchinsonii]			3.5.4.16
20463,	20464	48854735	42	9.00E-35	Cytophaga hutchinsonii	COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Cytophaga hutchinsonii]			1.1.1.18
20465,	20466	48854735	42	9.00E-35	Cytophaga hutchinsonii	COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Cytophaga hutchinsonii]			4
									4

20467, 20468	53713193	25	1.00E-10	Bacteroides fragilis YCH46	hypothetical protein BF1903 [Bacteroides fragilis YCH46] dbj BAD48651.1 conserved hypothetical protein [Bacteroides fragilis YCH46]					
20469, 20470	29347576	43	2.00E-47	Bacteroides thetaitotaomicron VPI-5482	two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77273.1 two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-	
20471, 20472	29349611	46	6.00E-61	Bacteroides thetaitotaomicron VPI-5482	tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79308.1 tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A018 MIAA_BACTN tRNA delta(2)-isopentenylpyrophosphate transferase (IPP transferase) (isopentenyl-diphosphate:tRNA isopentenyltransferase) (IPTase) (IPTT)				2.5.1.8	
20475, 20476	12082815	45	8.00E-50	Streptomyces venezuelae	cystathionine beta-synthase [Streptomyces venezuelae]					4.2.1.22
20481, 20482	48860637	54	7.00E-41	Microbulbifer degradans 2-40	COG1638: TRAP-type C4-dicarboxylate transport system, periplasmic component [Microbulbifer degradans 2-40]					
20483, 20484	52007804	39	3.00E-38	Thiobacillus denitrificans ATCC 25259	hypothetical protein TdenA01000099 [Thiobacillus denitrificans ATCC 25259]					
20489, 20490	48782075	28	3.00E-15	Burkholderia fungorum LB400	COG0463: Glycosyltransferases involved in cell wall biogenesis [Burkholderia fungorum LB400]					2.-.-.-
20491, 20492	48853898	48	2.00E-50	Cytophaga hutchinsonii	COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii]					2.1.1.-
20493, 20494	48853898	48	2.00E-49	Cytophaga hutchinsonii	COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii]					2.1.1.-
20495, 20496	ABB4747	37	8.00E-33		Desc:Listeria monocytogenes protein #181. Org:Listeria monocytogenes					1.8.-.-
20497, 20498	53687332	27	9.00E-07	Nostoc punctiforme PCC 73102	COG0457: FOG: TPR repeat [Nostoc punctiforme PCC 73102]					
20499, 20500	48862689	50	3.00E-37	Microbulbifer degradans 2-40	hypothetical protein Mdeg02001782 [Microbulbifer degradans 2-40]					
205, 206	15894850	67	2.00E-84	Clostridium acetobutylicum ATCC 824	Fructose-1,6-bisphosphatase (Yyde B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] gb AAK79539.1 Fructose-1,6-bisphosphatase (Yyde B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] pir JH97093 fructose-bisphosphatase (EC 3.1.3.11) [similarity] - Clostridium acetobutylicum	Desc:Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1485. Org:Staphylococcus epidermidis	85	5.00E-13	3.1.3.11	

20503, 20504	51246763	40	1.00E-48	Desulfotalea psychrophila LSV54	hypothetical protein DP2911 [Desulfotalea psychrophila LSV54] emb[CAG37640.1] conserved hypothetical protein [Desulfotalea psychrophila LSV54]			
20505, 20506	51246763	37	1.00E-35	Desulfotalea psychrophila LSV54	hypothetical protein DP2911 [Desulfotalea psychrophila LSV54] emb[CAG37640.1] conserved hypothetical protein [Desulfotalea psychrophila LSV54]			
20507, 20508	34762717	26	2.00E-09	Fusobacterium nucleatum subsp. vincentii ATCC 49256	TETRA TRICOPEPTIDE REPEAT FAMILY PROTEIN [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24695.1 TETRA TRICOPEPTIDE REPEAT FAMILY PROTEIN [Fusobacterium nucleatum subsp. vincentii ATCC 49256]			
20509, 20510	6498214	42	7.00E-21	Agrobacterium tumefaciens	tiol41 [Agrobacterium tumefaciens] ref NP_053281.1 Hypothetical gene [Agrobacterium tumefaciens]			
2051, 2052	21673647	59	2.00E-35	Chlorobium tepidum TLS	peptide chain release factor 3 [Chlorobium tepidum TLS] gb AAM72054.1 peptide chain release factor 3 [Chlorobium tepidum TLS]			
20511, 20512	48854805	36	3.00E-13	Cytophaga hutchinsonii	hypothetical protein Chui02002487 [Cytophaga hutchinsonii]			
20513, 20514	29349663	56	8.00E-48	Bacteroides thetaiotaomicron VPI-5482	DNA replication and repair protein RecF, ABC family ATPase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79360.1 DNA replication and repair protein RecF, ABC family ATPase [Bacteroides thetaiotaomicron VPI-5482] sp Q89ZW6 REC_F_BACTN DNA replication and repair protein recF			
20515, 20516	48854136	23	4.00E-11	Cytophaga hutchinsonii	COG1566: Multidrug resistance efflux pump [Cytophaga hutchinsonii]			
20517, 20518	48854136	25	7.00E-11	Cytophaga hutchinsonii	COG1566: Multidrug resistance efflux pump [Cytophaga hutchinsonii]			
20521, 20522	53715653	26	1.00E-08	Bacteroides fragilis YCH46	hypothetical protein BF4373 [Bacteroides fragilis YCH46] dbj BAD51111.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
20525, 20526	52853848	64	3.00E-29	Psychrobacter sp. 273-4	COG0818: Diacylglycerol kinase [Psychrobacter sp. 273-4]			2.7.1.10 7
20527, 20528	48854088	31	2.00E-10	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]			
20529, 20530	48854088	32	1.00E-12	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]			
2053, 2054	50083323	25	2.00E-14	Acinetobacter sp. ADP1	putative amidohydrolase (isochorismatase) [Acinetobacter sp. ADP1] emb CAG67011.1 putative amidohydrolase (isochorismatase)			3.3.2.1
20531, 20532	53712055	43	1.00E-46	Bacteroides fragilis YCH46	[Acinetobacter sp. ADP1] putative peptidase [Bacteroides fragilis YCH46] dbj BAD47513.1 putative peptidase [Bacteroides fragilis YCH46]			3.5.1.-

20533, 20534	37519796	26	7.00E-07	Gloebacter violaceus PCC 7421	hypothetical protein glr0227 [Gloebacter violaceus PCC 7421] dbj BAC88168.1 glr0227 [Gloebacter violaceus PCC 7421]				
20535, 20536	51245433	32	5.00E-19	Desulfotalea psychrophila LSv54	hypothetical protein DP1581 [Desulfotalea psychrophila LSv54] emb CAG36310.1 unknown protein [Desulfotalea psychrophila LSv54]				
20537, 20538	33595943	41	1.00E-40	Bordetella parapertussis 12822	hypothetical protein BPP1276 [Bordetella parapertussis 12822] emb CAE36577.1 conserved hypothetical protein [Bordetella parapertussis]				
20539, 20540	33595943	41	1.00E-40	Bordetella parapertussis 12822	hypothetical protein BPP1276 [Bordetella parapertussis 12822] emb CAE36577.1 conserved hypothetical protein [Bordetella parapertussis]				
20543, 20544	48854899	55	2.00E-51	Cytophaga hutchinsonii	COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii]				2.1.1.-
20545, 20546	26989001	28	3.00E-16	Pseudomonas putida KT2440	hypothetical protein PP2277 [Pseudomonas putida KT2440] gb AAAN67890.1 hypothetical protein [Pseudomonas putida KT2440] Methylated DNA-protein cysteine methyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK81195.1 Methylated DNA-protein cysteine methyltransferase [Clostridium acetobutylicum ATCC 824] pir H97300 methylated DNA-protein cysteine methyltransferase [imported] - Clostridium acetobutylicum				2.1.1.63
20553, 20554	48854014	54	8.00E-52	Cytophaga hutchinsonii	COG1104: Cysteine sulfinate desulfinate/cysteine desulfurase and related enzymes [Cytophaga hutchinsonii]				4.4.1.-
20555, 20556	48853459	42	2.00E-13	Cytophaga hutchinsonii	COG0247: Fe-S oxidoreductase [Cytophaga hutchinsonii]				
20557, 20558	29345486	53	3.00E-45	Bacteroides thetaiotaomicron VPI-5482	transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75183.1 transposase [Bacteroides thetaiotaomicron VPI-5482]				
20559, 20560	48855592	25	1.00E-09	Cytophaga hutchinsonii	COG1305: Transglutaminase-like enzymes, putative cysteine proteases [Cytophaga hutchinsonii]				
20561, 20562	15608970	54	2.00E-10	Mycobacterium tuberculosis H37Rv	Possible haloalkane dehalogenase [Mycobacterium tuberculosis H37Rv] ref NP_855516.1 Possible haloalkane dehalogenase [Mycobacterium bovis AF2122/97] ref NP_336339.1 haloalkane dehalogenase [Mycobacterium tuberculosis CDC1551] gb AAK46153.1 haloalkane dehalogenase [Mycobacterium tuberculosis CDC1551] sp P64303 DHA2_MYCTU Haloalkane dehalogenase 2 pir B70722 hypothetical protein Rv1833c - Mycobacterium tuberculosis (strain H37Rv) emb CAB01469.1 Possible haloalkane dehalogenase [Mycobacterium tuberculosis H37Rv] emb CAD94567.1 Possible haloalkane dehalogenase [Mycobacterium bovis AF2122/97] sp P64304 DHA2_MYCBO Haloalkane dehalogenase 2				

20563,	48854215	43	5.00E-50	Cytophaga hutchinsonii	COG1646: Predicted phosphate-binding enzymes, TIM-barrel fold [Cytophaga hutchinsonii]				
20564					flavoprotein NADH-dependent oxidoreductase [Azoarcus sp. EbN1] emb CAI08136.1 Flavoprotein NADH-dependent oxidoreductase [Azoarcus sp. EbN1]				1.---
20565,	56477448	51	4.00E-75	Azoarcus sp. EbN1	adenylate cyclase-related protein [Shewanella oneidensis MR-1] gb AA054394.1 adenylate cyclase-related protein [Shewanella oneidensis MR-1]				4.6.1.1
20567,	24372907	29	9.00E-14	Shewanella oneidensis MR-1	COG2141: Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases [Rubrobacter xylanophilus DSM 9941]				1.5.99.9
20568	53766201	42	1.00E-49	Rubrobacter xylanophilus DSM 9941	pyruvate carboxylase [Geobacillus stearothermophilus]				6.4.1.1
20573,	1695686	45	2.00E-27	Geobacillus stearothermophilus	pyruvate carboxylase [Geobacillus stearothermophilus]				6.4.1.1
20575,				Geobacillus stearothermophilus	pyruvate carboxylase [Geobacillus stearothermophilus]				6.4.1.1
20576	1695686	42	8.00E-40	Geobacillus stearothermophilus	COG1533: DNA repair photolyase [Cytophaga hutchinsonii]				
20577,				Cytophaga hutchinsonii	COG1533: DNA repair photolyase [Cytophaga hutchinsonii]				
20578	48856872	52	9.00E-70	Cytophaga hutchinsonii	COG1533: DNA repair photolyase [Cytophaga hutchinsonii]				
20579,				Cytophaga hutchinsonii	putative DNA-binding protein [Erwinia carotovora subsp. atroseptica SCR1043] emb CAG75811.1 putative DNA-binding protein [Erwinia carotovora subsp. atroseptica SCR1043]				
20580	48856872	54	1.00E-66	Erwinia carotovora subsp. atroseptica SCR1043	COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii]				
20585,				Erwinia carotovora subsp. atroseptica SCR1043	COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii]				
20586	50121835	48	1.00E-34	Cytophaga hutchinsonii	COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii]				
20589,	48855375	41	7.00E-17	Cytophaga hutchinsonii	type I restriction enzyme R protein [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58658.1 type I restriction enzyme R protein [Vibrio parahaemolyticus]			81	5.00E-54 3.1.21.3
20590				Cytophaga hutchinsonii	hypothetical protein nfa45100 [Nocardia farcinica IFM 10152] dbj BAD59361.1 hypothetical protein [Nocardia farcinica IFM 10152]				
20591,				Cytophaga hutchinsonii	hypothetical protein nfa45100 [Nocardia farcinica IFM 10152] dbj BAD59361.1 hypothetical protein [Nocardia farcinica IFM 10152]				
20592	48855375	41	2.00E-16	Cytophaga hutchinsonii	Transcriptional regulatory protein degU gb AAC41439.1 transcriptional activator protein pir J9835 transcription activator - Bacillus brevis				3.1.1.61
20595,				Vibrio parahaemolyticus RIMD 2210633					
20596	28897169	83	1.00E-120	Vibrio parahaemolyticus RIMD 2210633					
20601,				Nocardia farcinica IFM 10152					
20602	54026483	41	2.00E-48	Nocardia farcinica IFM 10152					
20603,				Nocardia farcinica IFM 10152					
20604	54026483	41	6.00E-49	Nocardia farcinica IFM 10152					
20605,									
20606	1706361	35	3.00E-20						

20607,	27365565	36	7.00E-21	Vibrio vulnificus CMCP6	Transcriptional regulator [Vibrio vulnificus CMCP6] ref NP_934898.1				3.1.1.61
20608					Transcriptional regulator [Vibrio vulnificus YJ016] gb AAO10620.1				
20619,					Transcriptional regulator [Vibrio vulnificus CMCP6] gb AAK31574.1				
20620	53711964	31	3.00E-09	Bacteroides fragilis YCH46	regulator [Vibrio vulnificus YJ016]				
20621,					aminopeptidase N [Bacteroides fragilis YCH46] dbj BAD47422.1				
20622	48855430	25	8.00E-14	Cytophaga hutchinsonii	aminopeptidase N [Bacteroides fragilis YCH46]				
20623,					hypothetical protein Chut02001765 [Cytophaga hutchinsonii]				
20624	48855430	25	1.00E-15	Cytophaga hutchinsonii	hypothetical protein Chut02001765 [Cytophaga hutchinsonii]				
20625,					hypothetical maturase [Photobacterium profundum SS9] emb CAG22679.1	Photobacterium profundum SS9			
20626	54302486	69	1.00E-102	Photobacterium profundum SS9	hypothetical maturase [Photobacterium profundum]	chromosome 2; segment 3/7	84	1.00E-14	2.7.7.49
20627,					COG2258: Uncharacterized protein conserved in bacteria [Nostoc punctiforme PCC 73102]				
20628	23124249	38	2.00E-39	Nostoc punctiforme PCC 73102	dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46]				
20629,					dbj BAD50186.1 dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46]				2.4.1.83
20630	53714728	67	4.00E-57	Bacteroides fragilis YCH46	response regulator [Porphyromonas gingivalis W83] ref NP_905164.1				
2063,					response regulator [Porphyromonas gingivalis W83]				
2064	34396999	57	2.00E-53	Porphyromonas gingivalis W83	response regulator [Porphyromonas gingivalis W83]				
20639,					COG1475: Predicted transcriptional regulators [Cytophaga hutchinsonii]				
20640	48854401	49	3.00E-40	Cytophaga hutchinsonii	inorganic pyrophosphatase [Methanosarcina acetivorans C2A]				
					gb AAO06052.1 inorganic pyrophosphatase [Methanosarcina acetivorans str. C2A] sp Q8TMI3 PVR_METAC inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (PPase)				3.6.1.1
20641,					probable two-component response regulator [Chromobacterium violaceum ATCC 12472] ref NP_903174.1 probable two-component response regulator [Chromobacterium violaceum ATCC 12472]				
20642	20091497	60	2.00E-49	Methanosarcina acetivorans C2A	COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii]				2.7.3.-
20645,					riboflavin biosynthesis protein ribD [Bacteroides thetaiotaomicron VPI-5482]				
20646	34104808	42	2.00E-30	Chromobacterium violaceum ATCC 12472	gb AAO78833.1 riboflavin biosynthesis protein ribD [Bacteroides thetaiotaomicron VPI-5482]				
20649,					hypothetical protein MMA0240 [Neisseria meningitidis Z2491]				
20650	48853602	51	2.00E-69	Cytophaga hutchinsonii	emb CAB83548.1 hypothetical protein MMA0240 [Neisseria meningitidis Z2491] pir D82018 hypothetical protein MMA0240 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)				
20651,									
20652	29349136	44	1.00E-11	Bacteroides thetaiotaomicron VPI-5482					
20653,									
20654	15793258	54	1.00E-38	Neisseria meningitidis Z2491					3.4.13.9

20657, 20658, 20659, 20660	46580426 48854181	72 30	1.00E-104 4.00E-17	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough Cytophaga hutchinsonii	hypothetical protein DVU2019 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AA596494.1 conserved hypothetical protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] COG0323: DNA mismatch repair enzyme (predicted ATPase) [Cytophaga hutchinsonii]				3.4.21.5 3
20663, 20664	53715149	42	2.00E-32	Bacteroides fragilis YCH46	two-component system sensor histidine kinase [Bacteroides fragilis YCH46] dbj BAD50607.1 two-component system sensor histidine kinase [Bacteroides fragilis YCH46] sp Q08408 PRX_BACFR Sensor protein rprX				2.7.3.-
20667, 20668 20669, 20670 2067, 2068	2500093 48855137 48855683	75 64 56	6.00E-69 4.00E-27 4.00E-39	Cytophaga hutchinsonii Cytophaga hutchinsonii	RecA protein (Recombinase A) gb AAC44506.1 RecA COG0131: Imidazoleglycerol-phosphate dehydratase [Cytophaga hutchinsonii] COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii]	Streptococcus suis partial recA gene for homologous recombination factor, allele 9	91	2.00E-15	3.1.- 3.1.3.15
20671, 20672	29346789	62	1.00E-56	Bacteroides thetaiotaomicron VPI-5482	phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide (ProFAR) isomerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76486.1 phosphoribosylformimino-5-aminimidazole carboxamide ribonucleotide (ProFAR) isomerase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A7Z5 HIS4_BACTN 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase (Phosphoribosylformimino-5-aminimidazole carboxamide ribotide isomerase)				5.3.1.16
20673, 20674, 20675, 20676	56708297 48856350	29 31	1.00E-11 1.00E-15	Francisella tularensis subsp. tularensis Schu 4 Cytophaga hutchinsonii	glycosyl transferases group 1 family protein [Francisella tularensis subsp. tularensis Schu 4] emb CAG45868.1 glycosyl transferases group 1 family protein [Francisella tularensis subsp. tularensis] hypothetical protein Chut02000065 [Cytophaga hutchinsonii]				2.-.-.-
20681, 20682	46198910	64	1.00E-52	Thermus thermophilus HB27	phenylacetyl-CoA ligase [Thermus thermophilus HB27] gb AAS80950.1 phenylacetyl-CoA ligase [Thermus thermophilus HB27]				6.2.1.30
20685, 20686	48858283	57	1.00E-40	Clostridium thermocellum ATCC 27405	COG2304: Uncharacterized protein containing a von Willebrand factor type A (vWA) domain [Clostridium thermocellum ATCC 27405]				

20687,	53715279	43	1.00E-48	Bacteroides fragilis YCH46	putative methyltransferase [Bacteroides fragilis YCH46] dbj BAD50737.1 putative methyltransferase [Bacteroides fragilis YCH46]				2.4.99.-
20688,	53795507	59	2.00E-34	Chloroflexus aurantiacus	COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Chloroflexus aurantiacus]				1.6.6.9
20691,	50084651	38	2.00E-14	Acinetobacter sp. ADP1	hypothetical protein ACIAD1480 [Acinetobacter sp. ADP1] emb CAG368339.1 hypothetical protein [Acinetobacter sp. ADP1]				
20692				Bacteroides thetaiotaomicron VPI-5482	putative Tricorm-like protease [Bacteroides thetaiotaomicron VPI-5482] gb AAO76515.1 putative Tricorm-like protease [Bacteroides thetaiotaomicron VPI-5482]				
20693,	29346818	28	7.00E-19						
20694				Idiomarina loihiensis L2TR	Prolyl 4-hydroxylase alpha subunit homolog, 2OG-Fe(II) oxygenase family [Idiomarina loihiensis L2TR] gb AAV81086.1 Prolyl 4-hydroxylase alpha subunit homolog, 2OG-Fe(II) oxygenase family [Idiomarina loihiensis L2TR]				
20697,	56459354	38	8.00E-29	Cytophaga hutchinsonii	COG0644: Dehydrogenases (flavoproteins) [Cytophaga hutchinsonii]				
20698,	48854244	35	2.00E-42						
20700				Clostridium acetobutylicum ATCC 824	Fructose-1,6-bisphosphatase (YDE B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] gb AAK79539.1 Fructose-1,6-bisphosphatase (YDE B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] pir H97093 fructose-bisphosphatase (EC 3.1.3.11) [similarity] - Clostridium acetobutylicum	Desc:Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1485. Org:Staphylococcus epidermidis	88	4.00E-11	3.1.3.11
207,	15894850	69	9.00E-94						
20701,	29610797	40	1.00E-19	Streptomyces avermitilis MA-4680	putative type III polyketide synthase [Streptomyces avermitilis MA-4680] ref NP_828307.1 putative type III polyketide synthase [Streptomyces avermitilis MA-4680] dbj BAB69299.1 PhlD homolog (polyketide synthase) [Streptomyces avermitilis]				2.3.1.74
20702									
20705,	23099733	42	8.00E-14	Oceanobacillus ihayensis HTE831	hypothetical protein OB2278 [Oceanobacillus ihayensis HTE831] dbj BAC14234.1 hypothetical conserved protein [Oceanobacillus ihayensis HTE831]				
20706									
20709,	45655699	35	2.00E-33	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	hypothetical protein LIC20117 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_714691.1 conserved hyperthermophilic protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51706.1 conserved hyperthermophilic protein [Leptospira interrogans serovar lai str. 56601] gb AAS72145.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				
20710									
2071,	48856332	52	2.00E-26	Cytophaga hutchinsonii	hypothetical protein Chut02000044 [Cytophaga hutchinsonii]				
2072									

20713, 20714	16263990	37	1.00E-52	Sinorhizobium meliloti 1021	hypothetical protein Smb20252 [Sinorhizobium meliloti 1021] pir B95872 hypothetical protein [Imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymb emb CAC48642.1 HYPOTHETICAL PROTEIN [Sinorhizobium meliloti 1021]				1.12.99. 1
20715, 20716	49478996	40	1.00E-20	Bacillus thuringiensis serovar konkukian str. 97-27	beta-1,3-N-acetylglucosaminyltransferase [Bacillus thuringiensis serovar konkukian str. 97-27] gb AA161198.1 beta-1,3-N- acetylglucosaminyltransferase [Bacillus thuringiensis serovar konkukian str. 97-27]				2.-.-.-
20717, 20718	48787592	29	1.00E-21	Burkholderia fungorum LB400	COG3593: Predicted ATP-dependent endonuclease of the OLD family [Burkholderia fungorum LB400]				
20721, 20722	48863242	36	2.00E-08	Microbulbifer degradans 2-40	hypothetical protein Mdeg02001316 [Microbulbifer degradans 2-40]				
20723, 20724	29349346	46	1.00E-47	Bacteroides thetaiotaomicron VPI-5482	ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gb AAO79043.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]				3.6.1.-
20725, 20726	53715187	40	6.00E-31	Bacteroides fragilis YCH46	methionyl-tRNA formyltransferase [Bacteroides fragilis YCH46] dbj BAD50645.1 methionyl-tRNA formyltransferase [Bacteroides fragilis YCH46]				2.1.2.9
20727, 20728	21230408	64	9.00E-31	Xanthomonas campestris pv. campestris str. ATCC 33913	2-amino-3-ketobutyrate CoA ligase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM40249.1 2-amino-3-ketobutyrate CoA ligase [Xanthomonas campestris pv. campestris str. ATCC 33913]				2.3.1.29
2073, 2074	48847412	28	1.00E-06	Geobacter metallireducens GS-15	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]				
20731, 20732	48855267	39	2.00E-13	Cytophaga hutchinsonii	COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Cytophaga hutchinsonii]				
20733, 20734	29350148	31	2.00E-07	Bacteroides thetaiotaomicron VPI-5482	transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_812706.1 transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_811980.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] ref NP_810669.1 transposase, invertase [Bacteroides thetaiotaomicron VPI- 5482] ref NP_810516.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] ref NP_809398.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO79845.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78900.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78174.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76863.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76710.1 transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75592.1 transposase [Bacteroides thetaiotaomicron VPI-5482]				

20735,	48855460	26	6.00E-09	Cytophaga hutchinsonii	hypothetical protein Chut02001797 [Cytophaga hutchinsonii]				
20736									
20737,				Bacteroides fragilis YCH46	tRNA/rRNA methyltransferase [Bacteroides fragilis YCH46] dbj BAD49725.1				2.1.1.34
20738	53714267	40	1.00E-08		tRNA/rRNA methyltransferase [Bacteroides fragilis YCH46]				
20739,				Bacteroides thetaiotaomicron VPI-5482	ATP-dependent DNA helicase [Bacteroides thetaiotaomicron VPI-5482]				
20740	29346067	45	8.00E-30		gb AAO75764.1 ATP-dependent DNA helicase [Bacteroides thetaiotaomicron VPI-5482]				3.6.1.-
20741,	AAG2841	2	1.00E-06		Desc:Arabidopsis thaliana protein fragment SEQ ID NO: 33619.				
20742	2	25	1.00E-06		Org:Arabidopsis thaliana				
20743,				Psychrobacter sp.					
20744	52853852	33	5.00E-34	273-4	COG0442: Polyl-rRNA synthetase [Psychrobacter sp. 273-4]				
20745,				Bacteroides fragilis YCH46	hypothetical protein BF1758 [Bacteroides fragilis YCH46] dbj BAD48505.1				
20746	53713047	82	2.00E-54		conserved hypothetical protein [Bacteroides fragilis YCH46]				
20751,				Cytophaga hutchinsonii					
20752	48855690	47	2.00E-39		COG0352: Thiamine monophosphate synthase [Cytophaga hutchinsonii]				2.5.1.3
20753,				Escherichia coli CFT073	Hypothetical protein ydhS [Escherichia coli CFT073] gb AAN80520.1				
20754	26247915	34	7.00E-21		Hypothetical protein ydhS [Escherichia coli CFT073]				
20755,				Tannerella forsythensis					
20756	28274157	32	3.00E-17		HexA [Tannerella forsythensis]				
20759,	AAW2308	5	2.00E-50		Desc:Microscilla furvescens esterase 53sc2. Org:Microscilla furvescens				3.1.1.47
20760	5	50	2.00E-50		COG1463: ABC-type transport system involved in resistance to organic solvents, periplasmic component [Cytophaga hutchinsonii]				
20763,				Cytophaga hutchinsonii					
20764	48853578	32	1.00E-26						
20765,						Escherichia coli locus of enterocyte effacement, right hand side	93	1.00E-09	
20766									
20767,				Bacteroides thetaiotaomicron VPI-5482	D-alanine--D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482]				
20768	29349121	41	4.00E-55		gb AAO78818.1 D-alanine--D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A1F3 DDL_BACTN D-alanine--D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase)				6.3.2.4
20769,				Cytophaga hutchinsonii					
20770	48853465	53	9.00E-24		COG0653: Preprotein translocase subunit SecA (ATPase, RNA helicase) [Cytophaga hutchinsonii]				
2077,				Bacteroides fragilis YCH46	ATP-dependent Clp protease ATP-binding subunit [Bacteroides fragilis YCH46] dbj BAD50819.1 ATP-dependent Clp protease ATP-binding subunit [Bacteroides fragilis YCH46]				3.4.24.-
2078	53715361	65	1.00E-112						

20771, 20772	29348669	56	5.00E-65	Bacteroides thetaiotaomicron VPI-5482	DNA polymerase I [Bacteroides thetaiotaomicron VPI-5482] gb AA078366.1 DNA polymerase I [Bacteroides thetaiotaomicron VPI-5482]				2.7.7.7
20773, 20774	53715279	48	3.00E-53	Bacteroides fragilis YCH46	putative methyltransferase [Bacteroides fragilis YCH46] dbj BAD50737.1 putative methyltransferase [Bacteroides fragilis YCH46]	Desc:Empedobacter r brevis aminopeptidase related coding sequence SEQ ID NO: 15. Org:Empedobacter r brevis	92	8.00E-09	2.1.1.-
20777, 20778	48853807	50	2.00E-64	Cytophaga hutchinsonii	COG0793: Periplasmic protease [Cytophaga hutchinsonii]				3.4.21.-
20779, 20780	24637483	33	7.00E-17	Streptococcus thermophilus	Eps9K [Streptococcus thermophilus]				
20781, 20782	33861469	45	5.00E-60	Prochlorococcus marinus subsp. pastoris str. CCMP1986	Pyruvate kinase [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19371.1 Pyrivate kinase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]	Bacillus sphaericus putative acetyl-CoA carboxylase alpha subunit (accA) gene, partial cds; 6- phosphofructokinase (pfk) gene, complete cds; and putative pyruvate kinase (pykA) gene, partial cds	91	7.00E-10	2.7.1.40
20787, 20788	48855782	30	3.00E-08	Cytophaga hutchinsonii	hypothetical protein Chut02000991 [Cytophaga hutchinsonii]				
20789, 20790	50983054	64	7.00E-41	Dictyostellum discoideum	glucose-6-phosphate isomerase [Dictyostellum discoideum]	Vibrio cholerae O1 blovar eltor str. N16961 chromosome I, section 33 of 251 of the complete chromosome	88	7.00E-11	5.3.1.9
2079, 2080	54022239	25	8.00E-07	Nocardia farcinica IFM 10152	hypothetical protein nfa2750 [Nocardia farcinica IFM 10152] dbj BAD55117.1 hypothetical protein [Nocardia farcinica IFM 10152]				
20791, 20792	45523117	41	5.00E-43	Crocospaera watsonii WH 8501	COG4301: Uncharacterized conserved protein [Crocospaera watsonii WH 8501]				

20793,	20092474	28	4.00E-08	Methanosarcina acetivorans C2A	N-acetyltransferase [Methanosarcina acetivorans C2A] gb AAM07029.1 N-acetyltransferase [Methanosarcina acetivorans str. C2A]			
20794	52853377	78	7.00E-94	Psychrobacter sp. 273-4	COG0845: Membrane-fusion protein [Psychrobacter sp. 273-4]			
20795,				Bradyrhizobium japonicum USDA 110	hypothetical protein brl7549 [Bradyrhizobium japonicum USDA 110] dbj BAC52814.1 brl7549 [Bradyrhizobium japonicum USDA 110]			
20796	27382660	29	1.00E-12	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0909 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76016.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
20797,	29346319	55	9.00E-66	Salmonella enterica	Sty SBLI [Salmonella enterica]			3.1.21.3
20798	1679868	69	3.00E-97	Bacteroides uniformis	Tn10-like transposase [Bacteroides uniformis]			
20799,	37962667	46	6.00E-45	Gloeobacter violaceus PCC 7421	hypothetical protein gll0560 [Gloeobacter violaceus PCC 7421] dbj BAC88501.1 gll0560 [Gloeobacter violaceus PCC 7421]			
20800	37520129	33	4.00E-11	Geobacter metallireducens GS-15	COG1463: ABC-type transport system involved in resistance to organic solvents, periplasmic component [Geobacter metallireducens GS-15]			
20801,	48844754	30	9.00E-29	Cytophaga hutchinsonii	COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii]			
20802	48853637	26	1.00E-08	Bacteroides fragilis YCH46	hypothetical protein BF1415 [Bacteroides fragilis YCH46] dbj BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
20803,	53712708	60	1.00E-63	Microbulbifer degradans 2-40	COG4067: Uncharacterized protein conserved in archaea [Microbulbifer degradans 2-40]			
20804	48863156	33	8.00E-13	Haemophilus influenzae R2866	COG2865: Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlafen [Haemophilus influenzae R2866]			
20805,	42632161	59	3.00E-63	Desulfotalea psychrophila LSV54	hypothetical protein DP2911 [Desulfotalea psychrophila LSV54] emb CA37640.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]			
20806	51246763	40	2.00E-32	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			2.7.3.-
20807,	45657883	42	5.00E-37	Microbulbifer degradans 2-40	COG0642: Signal transduction histidine kinase [Microbulbifer degradans 2-40]			2.7.3.-
20808	48864300	45	6.00E-59					

20829, 20830	39995426	40	2.00E-16	Geobacter sulfurreducens PCA	hypothetical protein GSU0317 [Geobacter sulfurreducens PCA] gb AAR33650.1 conserved hypothetical protein [Geobacter sulfurreducens PCA]				
2083, 2084	53715372	48	1.00E-68	Bacteroides fragilis YCH46	putative GTP-binding protein [Bacteroides fragilis YCH46] dbj BAD50830.1 putative GTP-binding protein [Bacteroides fragilis YCH46]				
20831, 20832	34330256	41	4.00E-33	Chromobacterium violaceum ATCC 12472	conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_899878.1 hypothetical protein CV0208 [Chromobacterium violaceum ATCC 12472]				2.7.3.-
20833, 20834	27228587	36	3.00E-15	Pseudomonas resinovorans	helicase [Pseudomonas resinovorans] dbj BAC41615.1 helicase				
20835, 20836	48853912	55	2.00E-68	Cytophaga hutchinsonii	COG1166: Arginine decarboxylase (spermidine biosynthesis) [Cytophaga hutchinsonii]				4.1.1.19
20837, 20838	48854312	30	2.00E-13	Cytophaga hutchinsonii	COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii]				
20839, 20840	48855972	49	8.00E-22	Cytophaga hutchinsonii	hypothetical protein Chut02001199 [Cytophaga hutchinsonii]				
20841, 20842	44004501	46	3.00E-35	Bacillus cereus ATCC 10987	acetyltransferase, GNAT family protein [Bacillus cereus ATCC 10987] gb AA545012.1 acetyltransferase, GNAT family protein [Bacillus cereus ATCC 10987]				2.3.1.-
20843, 20844	48856970	57	2.00E-82	Cytophaga hutchinsonii	COG1077: Actin-like ATPase involved in cell morphogenesis [Cytophaga hutchinsonii]				
20845, 20846	48856970	67	1.00E-29	Cytophaga hutchinsonii	COG1077: Actin-like ATPase involved in cell morphogenesis [Cytophaga hutchinsonii]				
20847, 20848	52853377	78	1.00E-117	Psychrobacter sp. 273-4	COG0845: Membrane-fusion protein [Psychrobacter sp. 273-4]				
20849, 20850	14579394	72	2.00E-84	Yersinia enterocolitica	unknown [Yersinia enterocolitica] ref NP_863558.1 unknown [Yersinia enterocolitica]				
20853, 20854	52550522	31	9.00E-13	uncultured archaeon GZfos9D8	Bpml endonuclease-methyltransferase fusion protein type IIIG [uncultured archaeon GZfos9D8]				
20855, 20856	53758942	42	4.00E-11	Methylococcus capsulatus str. Bath	conserved domain protein [Methylococcus capsulatus str. Bath] ref YP_113621.1 hypothetical protein MCA1152 [Methylococcus capsulatus str. Bath]				
20857, 20858	53712850	36	3.00E-09	Bacteroides fragilis YCH46	siderophore (sulfactin) biosynthesis regulatory protein [Bacteroides fragilis YCH46] dbj BAD48308.1 siderophore (sulfactin) biosynthesis regulatory protein [Bacteroides fragilis YCH46]				
20859, 20860	32470723	43	3.00E-43	Rhodopirellula baltica SH 1	probable acylaminoacyl-peptidase [Rhodopirellula baltica SH 1] emb CAD71387.1 probable acylaminoacyl-peptidase [Pirellula sp.]				
20861, 20862	48855767	57	4.00E-37	Cytophaga hutchinsonii	COG0123: Deacetylases, including yeast histone deacetylase and acetoin utilization protein [Cytophaga hutchinsonii]				

20865,	53735944	36	3.00E-26	Crocospaera watsonii WH 8501	COG0463: Glycosyltransferases involved in cell wall biogenesis [Crocospaera watsonii WH 8501]			2.7.3.1
20866	53735944	36	3.00E-26	Chloroflexus aurantiacus	COG0665: Glycine/D-amino acid oxidases (deaminating) [Chloroflexus aurantiacus]			
2087,	53795653	28	9.00E-09	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT1527 [Bacteroides thetaiotaomicron VPI-5482]			
20873,	29346937	29	2.00E-08	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	hypothetical protein lpg1073 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			
20874	52841307	37	4.00E-09	Bacteroides fragilis YCH46	peptidyl-tRNA hydrolase [Bacteroides fragilis YCH46]			
20875,	53712488	62	2.00E-41	Flavobacterium johnsoniae	peptidyl-tRNA hydrolase [Bacteroides fragilis YCH46]			3.1.1.29
20876	5360168	38	3.00E-44	Microbulbifer degradans 2-40	GidB [Flavobacterium johnsoniae]			
20879,	48862596	51	3.00E-64	Bacteroides thetaiotaomicron VPI-5482	COG3022: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40]			
20880	29349616	43	5.00E-37	Bacteroides fragilis YCH46	phosphohydrolase [Bacteroides thetaiotaomicron VPI-5482]			
20881,	53712874	42	7.00E-30	Bacteroides fragilis YCH46	phosphohydrolase [Bacteroides thetaiotaomicron VPI-5482]			
20882	46114055	50	3.00E-11	Exiguobacterium sp. 255-15	ABC transporter ATP-binding protein [Bacteroides fragilis YCH46]			
20883,	48854337	25	6.00E-09	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Exiguobacterium sp. 255-15]			
20884	48856773	25	1.00E-09	Cytophaga hutchinsonii	COG1280: Putative threonine efflux protein [Cytophaga hutchinsonii]			
20885,	53715439	74	4.00E-67	Bacteroides fragilis YCH46	COG4529: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
20886	29349252	58	2.00E-72	Bacteroides thetaiotaomicron VPI-5482	DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46]			2.7.7.6
20887,	45508610	30	2.00E-09	Anabaena variabilis ATCC 29413	dbj BAD50897.1 DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46]			
20888	53712874	42	7.00E-30	Bacteroides fragilis YCH46	ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]			3.6.1.-
20889,	46114055	50	3.00E-11	Exiguobacterium sp. 255-15	dbj AAO78949.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]			
20890	48854337	25	6.00E-09	Cytophaga hutchinsonii	COG2202: FOG: PAS/PAC domain [Anabaena variabilis ATCC 29413]			2.7.3.-
20891,	48856773	25	1.00E-09	Cytophaga hutchinsonii				
20892	53715439	74	4.00E-67	Bacteroides fragilis YCH46				
20893,	29349252	58	2.00E-72	Bacteroides thetaiotaomicron VPI-5482				
20894	45508610	30	2.00E-09	Anabaena variabilis ATCC 29413				
20895,	53712874	42	7.00E-30	Bacteroides fragilis YCH46				
20896	46114055	50	3.00E-11	Exiguobacterium sp. 255-15				
20897,	48854337	25	6.00E-09	Cytophaga hutchinsonii				
20898	48856773	25	1.00E-09	Cytophaga hutchinsonii				

209,210	53684756	57	1.00E-61	Desulfitobacterium hafnense DCB-2	COG0587: DNA polymerase III, alpha subunit [Desulfitobacterium hafnense DCB-2]			2.7.7.7
20901,20902	28900685	50	2.00E-16	Vibrio parahaemolyticus RIMD 2210633	putative AraC-family transcriptional regulatory protein [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62173.1 putative AraC-family transcriptional regulatory protein [Vibrio parahaemolyticus]			
20903,20904	48787592	32	1.00E-28	Burkholderia fungorum LB400	COG3593: Predicted ATP-dependent endonuclease of the OLD family [Burkholderia fungorum LB400]			
20905,20906	48854967	51	1.00E-23	Cytophaga hutchinsonii	COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii]			
20907,20908	48855702	36	3.00E-26	Cytophaga hutchinsonii	COG3279: Response regulator of the LytR/AlgR family [Cytophaga hutchinsonii]			
20909,20910	23126057	32	6.00E-12	Nostoc punctiforme PCC 73102	COG0457: FOG: TPR repeat [Nostoc punctiforme PCC 73102]			
2091,2092	55819298	36	2.00E-16	Mimivirus	unknown [Mimivirus] gb AAV50692.1 unknown [Mimivirus]			
20911,20912	17936631	45	7.00E-59	Agrobacterium tumefaciens str. C58	acyl-CoA thioesterase II [Agrobacterium tumefaciens str. C58] gb AAL43737.1 acyl-CoA thioesterase II [Agrobacterium tumefaciens str. C58] pir AC2915 acyl-CoA thioesterase II [imported] - Agrobacterium tumefaciens (strain C58, Dupont)		3.1.2.-	
20913,20914	48729722	36	7.00E-21	Pseudomonas fluorescens PFO-1	COG2194: Predicted membrane-associated, metal-dependent hydrolase [Pseudomonas fluorescens PFO-1]			
20917,20918	53731382	73	5.00E-62	Methanococcoides burtonii DSM 6242	COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Methanococcoides burtonii DSM 6242]			3.1.21.3
20919,20920	48854426	65	9.00E-62	Cytophaga hutchinsonii	COG0692: Uracil DNA glycosylase [Cytophaga hutchinsonii]			3.2.2.-
20921,20922	48854014	50	2.00E-56	Cytophaga hutchinsonii	COG1104: Cysteine sulfinate desulfinate/cysteine desulfurase and related enzymes [Cytophaga hutchinsonii]			4.4.1.-
20923,20924	24371964	40	1.00E-37	Shewanella oneidensis MR-1	hypothetical protein SO0366 [Shewanella oneidensis MR-1] gb AAN53451.1			
20927,20928	29346947	42	1.00E-52	Bacteroides thetaiotaomicron VPI-5482	putative NADH dehydrogenase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76644.1 putative NADH dehydrogenase [Bacteroides thetaiotaomicron VPI-5482]			1.6.99.3
20929,20930	51244305	44	2.00E-31	Desulfotalea psychrophila LSv54	hypothetical protein DP0453 [Desulfotalea psychrophila LSv54] emb CAG35182.1 conserved hypothetical protein [Desulfotalea psychrophila LSv54]			
2093,2094	14600644	25	1.00E-06	Aeropyrum pernix K1	hypothetical protein APE0340 [Aeropyrum pernix K1] dbj BAA79295.1 749aa long hypothetical protein [Aeropyrum pernix K1] pir C72725 hypothetical protein APE0340 - Aeropyrum pernix (strain K1)			

20931, 20932	48853570	35	1.00E-13	Cytophaga hutchinsonii	COG0161: Adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Cytophaga hutchinsonii]			2.6.1.62
20933, 20934	4164093	29	2.00E-24	Bacteroides fragilis	BfmC [Bacteroides fragilis]			
20935, 20936	27367976	42	1.00E-41	Vibrio vulnificus CMCP6	Spermidine synthase [Vibrio vulnificus CMCP6] gb AAO08493.1 Spermidine synthase [Vibrio vulnificus CMCP6] sp Q8D3Q3 SPEE_VIBVU Spermidine synthase (Putrescine aminopropyltransferase) (SPDSY)			2.5.1.16
20937, 20938	48856983	32	2.00E-12	Cytophaga hutchinsonii	COG0782: Transcription elongation factor [Cytophaga hutchinsonii]			
20939, 20940	53711795	43	2.00E-36	Bacteroides fragilis YCH46	putative outer membrane protein [Bacteroides fragilis YCH46] dbj BAD47253.1 putative outer membrane protein [Bacteroides fragilis YCH46]			
20945, 20946	48856079	61	3.00E-87	Cytophaga hutchinsonii	COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii]			1.8.-.-
20951, 20952	53711856	38	2.00E-23	Bacteroides fragilis YCH46	5'-nucleotidase precursor [Bacteroides fragilis YCH46] dbj BAD47314.1 5'-nucleotidase precursor [Bacteroides fragilis YCH46]			3.1.3.5
20953, 20954	29347250	68	4.00E-70	Bacteroides thetaiotaomicron VPI-5482	histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76947.1 histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A6N7 SYH_BACTN Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HisRS)			6.1.1.21
20955, 20956	53712142	37	1.00E-59	Bacteroides fragilis YCH46	putative N-acyl-D-glucosamine 2-epimerase [Bacteroides fragilis YCH46] dbj BAD47600.1 putative N-acyl-D-glucosamine 2-epimerase [Bacteroides fragilis YCH46]			2.7.7.22
20957, 20958	53759663	48	7.00E-63	Methylobacillus flagellatus KT	COG1236: Predicted exonuclease of the beta-lactamase fold involved in RNA processing [Methylobacillus flagellatus KT]			
20961, 20962	51245718	43	1.00E-27	Desulfotalea psychrophila LSV54	related to low molecular weight heat shock protein (Hsp17) [Desulfotalea psychrophila LSV54] emb CAG36595.1 related to low molecular weight heat shock protein (Hsp17) [Desulfotalea psychrophila LSV54]			
20963, 20964	34396493	38	1.00E-35	Porphyromonas gingivalis W83	ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83] ref NP_904660.1 ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83]			3.6.1.-
20965, 20966	53715375	39	2.00E-17	Bacteroides fragilis YCH46	hypothetical protein BF4091 [Bacteroides fragilis YCH46] dbj BAD50833.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
20967, 20968	29349228	39	1.00E-15	Bacteroides thetaiotaomicron VPI-5482	putative DNA polymerase III, delta subunit [Bacteroides thetaiotaomicron VPI-5482] gb AAO78925.1 putative DNA polymerase III, delta subunit [Bacteroides thetaiotaomicron VPI-5482]			

20969, 20970	53712115	35	2.00E-41	acyl-carrier-protein fragilis YCH46]	3-oxoacyl-[acyl-carrier-protein] synthase [Bacteroides fragilis YCH46]				2.3.1.41
2097, 2098	48853620	32	2.00E-19	Cytophaga hutchinsonii]	COG4252: Predicted transmembrane sensor domain [Cytophaga hutchinsonii]				
20971, 20972	48862684	43	4.00E-41	Microbulbifer degradans 2-40]	COG3228: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40]				
20973, 20974	53718224	50	1.00E-49	Burkholderia pseudomallei K96243]	hypothetical protein BPSL0582 [Burkholderia pseudomallei K96243]				
20977, 20978	34763977	39	2.00E-22	Fusobacterium nucleatum subsp. vincentii ATCC 49256]	Magnesium and cobalt transport protein corA [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA23536.1 Magnesium and cobalt transport protein corA [Fusobacterium nucleatum subsp. vincentii ATCC 49256]				
20979, 20980	42526734	66	8.00E-70	Treponema denticola ATCC 35405]	zinc ABC transporter, ATP-binding protein [Treponema denticola ATCC 35405] gb AAS11743.1 zinc ABC transporter, ATP-binding protein [Treponema denticola ATCC 35405]	Oceanobacillus ihayensis HTE831 genomic DNA, section 2/13	89	1.00E-07	1.8.-.-
20983, 20984	34396491	54	8.00E-27	Porphyromonas gingivalis W83]	GTP-binding protein [Porphyromonas gingivalis W83] ref NP_904658.1 GTP-binding protein [Porphyromonas gingivalis W83]				
20985, 20986	52143029	42	4.00E-22	Bacillus cereus ZK]	hypothetical protein BCZK2210 [Bacillus cereus ZK] gb AAU18048.1 conserved hypothetical protein [Bacillus cereus ZK]				
20987, 20988	53712846	55	2.00E-21	Bacteroides fragilis YCH46]	AG-specific adenine glycosylase [Bacteroides fragilis YCH46] dbj BAD48304.1 AG-specific adenine glycosylase [Bacteroides fragilis YCH46]				3.2.2.-
20989, 20990	56476791	37	3.00E-24	Azoarcus sp. Ebn1]	adenine specific DNA methylase MOD [Azoarcus sp. Ebn1] emb CAI07479.1 Adenine specific DNA methylase MOD [Azoarcus sp. Ebn1]				
2099, 2100	45358866	43	6.00E-34	Methanococcus maripaludis S2]	Sensory transduction histidine kinase [Methanococcus maripaludis S2] emb CAF30859.1 Sensory transduction histidine kinase [Methanococcus maripaludis S2]				2.7.3.-
20991, 20992	31195967	82	7.00E-43	Anopheles gambiae]	ENSANGP00000016322 [Anopheles gambiae]				1.6.4.5
20993, 20994	23479053	27	5.00E-09	Plasmodium yoelii yoelii]	mature-parasite-infected erythrocyte surface antigen [Plasmodium yoelii yoelii]				
20995, 20996	53711509	37	3.00E-30	Bacteroides fragilis YCH46]	ribonuclease III [Bacteroides fragilis YCH46] dbj BAD46967.1 ribonuclease III [Bacteroides fragilis YCH46]				3.1.26.3
20997, 20998	23103544	31	4.00E-21	Azotobacter vinelandii]	COG1251: NAD(P)H-nitrite reductase [Azotobacter vinelandii]				1.6.6.4

20999, 21000	29345821	52	1.00E-64	Bacteroides thetaiotaomicron VPI-5482	CysQ, sulfite synthesis pathway protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO75518.1 CysQ, sulfite synthesis pathway protein [Bacteroides thetaiotaomicron VPI-5482]			3.1.3.25
21, 22	48854298	67	6.00E-95	Cytophaga hutchinsonii	COG4867: Uncharacterized protein with a von Willebrand factor type A (VWA) domain [Cytophaga hutchinsonii]			
21001,				Cytophaga				
21002	48854958	61	4.00E-66	hutchinsonii	COG1432: Uncharacterized conserved protein [Cytophaga hutchinsonii]			
21003,				Rhodopirellula	hypothetical protein RB7682 [Rhodopirellula baltica SH 1] emb CAD75508.1			
21004	32474967	46	3.00E-53	baltica SH 1	hypothetical protein [Pirellula sp.]			
21005,				Cytophaga				
21006	48856607	31	1.00E-22	hutchinsonii	COG1321: Mn-dependent transcriptional regulator [Cytophaga hutchinsonii]			
21008,				Cytophaga				
21010	48856112	31	2.00E-32	hutchinsonii	COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
2101,				Exiguobacterium				
2102	45533048	40	2.00E-16	sp. 255-15	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Exiguobacterium sp. 255-15]			2.7.3.-
21013,				Aquifex aeolicus				
21014	15605827	26	1.00E-17	VF5	hypothetical protein aq_294 [Aquifex aeolicus VF5] gb AAC06602.1 putative protein [Aquifex aeolicus VF5] pir H70326 hypothetical protein aq_294 - Aquifex aeolicus			
21017,				Bacteroides fragilis				
21018	53712185	46	2.00E-29	YCH46	alanine racemase [Bacteroides fragilis YCH46]			5.1.1.1
21019,				Rubrobacter				
21020	46106876	46	7.00E-24	xylanophilus DSM 9941	COG4585: Signal transduction histidine kinase [Rubrobacter xylanophilus DSM 9941]			2.7.3.-
21021,				Bacteroides				
21022	29348881	49	5.00E-55	thetaiotaomicron VPI-5482	putative hydrogenase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78578.1 putative hydrogenase [Bacteroides thetaiotaomicron VPI-5482]			1.-.-.-
21023,				Polaromonas sp.				
21024	54032941	43	4.00E-26	JS666	COG0225: Peptide methionine sulfoxide reductase [Polaromonas sp. JS666]			1.8.4.6
21025,				Chlorobium				
21026	21674157	35	5.00E-16	tepidum TLS	hypothetical protein [Chlorobium tepidum TLS]			
				Desulfovibrio				
21027,				vulgaris subsp.	hypothetical protein DVU2025 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96500.1 conserved hypothetical protein			
21028	46580432	42	6.00E-50	Hildenborough	[Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			
21029,				Bacteroides fragilis				
21030	53714701	59	4.00E-58	YCH46	histidyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD50159.1 histidyl-tRNA synthetase [Bacteroides fragilis YCH46]			6.1.1.21
2103,				Exiguobacterium				
2104	45533048	38	1.00E-16	sp. 255-15	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Exiguobacterium sp. 255-15]			2.7.3.-

21031, 21032, 21035, 21036, 21037, 21038	53713593 68 4838064 34 36955846 64	1.00E-44 1.00E-13 1.00E-60	Bacteroides fragilis YCH46 Methanosarcina barkeri str. fusaro Polaribacter filamentus	ATP-dependent protease [Bacteroides fragilis YCH46] dbj BAD49051.1 ATP dependent protease [Bacteroides fragilis YCH46] COG3920: Signal transduction histidine kinase [Methanosarcina barkeri str. fusaro]	Pasteurella multocida subsp. multocida str. Pm70 section 201 of 204 of the complete genome	91 1.00E-063	3.4.21.5 3
21039, 21040	29347646 42	5.00E-18	Bacteroides thetaiotaomicron VPI-5482	nicotinate-nucleotide adenyltransferase [Polaribacter filamentus] hypothetical protein BT2236 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77343.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A5K3 YM36_BACTN Hypothetical UPF0102 protein BT2236			2.7.3.- 2.7.7.18
21041, 21042	50123026 57	5.00E-12	Erwinia carotovora subsp. atroseptica SCRI1043	phosphoenolpyruvate carboxykinase [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG77003.1 phosphoenolpyruvate carboxykinase [Erwinia carotovora subsp. atroseptica SCRI1043] putative DNA mismatch repair protein [Bacteroides fragilis YCH46] dbj BAD50625.1 putative DNA mismatch repair protein [Bacteroides fragilis YCH46]			4.1.1.49
21045, 21046	53715167 46	9.00E-16	Bacteroides fragilis YCH46	DNA mismatch repair protein mutS [Bacteroides fragilis YCH46] dbj BAD51320.1 DNA mismatch repair protein mutS [Bacteroides fragilis YCH46]			
21047, 21048	53715862 65	3.00E-63	Bacteroides fragilis YCH46	asparagine synthetase (asnB) [Methanocaldococcus jannaschii DSM 2661] gb AAB99058.1 asparagine synthetase (asnB) [Methanocaldococcus jannaschii DSM 2661]			6.3.5.4
21055, 21056	15669245 48	6.00E-48	Methanocaldococ- cus jannaschii DSM 2661	leucyl-tRNA synthetase [Porphyromonas gingivalis W83] ref NP_905058.1 leucyl-tRNA synthetase [Porphyromonas gingivalis W83] sp Q7MW49 SYL_PORGI Leucyl-tRNA synthetase (Leucine-tRNA ligase) (LeuRS)			6.1.1.4
21057, 21058	34396892 56	6.00E-49	Porphyromonas gingivalis W83	oxidoreductase [Bdellovibrio bacteriovorus HD100] emb CAE79695.1 oxidoreductase [Bdellovibrio bacteriovorus HD100]			1.1.1.-
21059, 21060	42523322 26	7.00E-11	Bdellovibrio bacteriovorus HD100	hypothetical protein VPA1269 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62612.1 hypothetical protein [Vibrio parahaemolyticus]			
21063, 21064	28901124 54	2.00E-71	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VPA1269 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62612.1 hypothetical protein [Vibrio parahaemolyticus]			
21065, 21066	28901124 63	8.00E-84	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VPA1269 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62612.1 hypothetical protein [Vibrio parahaemolyticus]			

21069, 21070	48855120	56	6.00E-23	Cytophaga hutchinsonii	COG0495: Leucyl-tRNA synthetase [Cytophaga hutchinsonii]			6.1.1.4
2107, 2108	1334389	69	2.00E-45	Emericella nidulans	unnamed protein product [Emericella nidulans] pir D22735 hypothetical nox3 protein - Emericella nidulans mitochondrion	83	9.00E-57	
21071, 21072	48854784	62	5.00E-50	Cytophaga hutchinsonii	COG0044: Dihydroorotase and related cyclic amidohydrolases [Cytophaga hutchinsonii]			3.5.2.3
21073, 21074	15793258	57	1.00E-38	Neisseria meningitidis Z2491	hypothetical protein NMA0240 [Neisseria meningitidis Z2491] emb CAB83548.1 hypothetical protein NMA0240 [Neisseria meningitidis Z2491] pir D82018 hypothetical protein NMA0240 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)			3.4.13.9
21075, 21076	29349136	44	1.00E-11	Bacteroides thetaiotaomicron VPI-5482	riboflavin biosynthesis protein ribD [Bacteroides thetaiotaomicron VPI-5482] gb AAO78833.1 riboflavin biosynthesis protein ribD [Bacteroides thetaiotaomicron VPI-5482]			
21079, 21080	53715167	43	2.00E-17	Bacteroides fragilis YCH46	putative DNA mismatch repair protein [Bacteroides fragilis YCH46] dbj BAD50625.1 putative DNA mismatch repair protein [Bacteroides fragilis YCH46]			
21081, 21082	48856925	24	2.00E-12	Cytophaga hutchinsonii	COG1309: Transcriptional regulator [Cytophaga hutchinsonii]			
21085, 21086	48853462	24	3.00E-08	Cytophaga hutchinsonii	COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii]			
21089, 21090	27366595	33	6.00E-22	Vibrio vulnificus CMCP6	Response regulator [Vibrio vulnificus CMCP6] ref NP_936705.1 probable response regulator [Vibrio vulnificus YJ016] gb AAO07112.1 Response regulator [Vibrio vulnificus CMCP6] dbj BAC96675.1 probable response regulator [Vibrio vulnificus YJ016]			2.7.3.-
21093, 21094	48864200	26	5.00E-32	Microbulbifer degradans 2-40	COG0784: FOG; CheY-like receiver [Microbulbifer degradans 2-40]			
21095, 21096	8101030	42	2.00E-66	Prevotella sp. RS2	MdsD protein [Prevotella sp. RS2]			3.4.21.-

21097, 21098	24372547	29	1.00E-08	Shewanella oneidensis MR-1	hypothetical spermidine synthase [Shewanella oneidensis MR-1] gb AA54034.1 conserved hypothetical protein [Shewanella oneidensis MR-1]			2.5.1.16
211, 212	48733660	52	2.00E-59	Pseudomonas fluorescens PfO-1	COG1638: TRAP-type C4-dicarboxylate transport system, periplasmic component [Pseudomonas fluorescens PfO-1]			
21109, 21110	15899493	23	2.00E-09	Sulfolobus solfataricus P2	hypothetical protein SSO2778 [Sulfolobus solfataricus P2] gb AAK42888.1 Conserved hypothetical protein [Sulfolobus solfataricus P2] pir A90454 conserved hypothetical protein [imported] - Sulfolobus solfataricus			
21113, 21114	53714728	61	9.00E-65	Bacteroides fragilis YCH46	dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] gb BAD50186.1 dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46]			2.4.1.83
21117, 21118	42526734	70	2.00E-52	Treponema denticola ATCC 35405	zinc ABC transporter, ATP-binding protein [Treponema denticola ATCC 35405] gb AAS11743.1 zinc ABC transporter, ATP-binding protein [Treponema denticola ATCC 35405]			1.8.--
21119, 21120	28210167	57	3.00E-35	Clostridium tetani E88	hypothetical protein CTC00414 [Clostridium tetani E88] gb AAO35048.1 conserved protein [Clostridium tetani E88]			
21123, 21124	16329878	36	2.00E-30	Synechocystis sp. PCC 6803	hypothetical protein slr1135 [Synechocystis sp. PCC 6803] dbj BAA17286.1 slr1135 [Synechocystis sp. PCC 6803] pir S77439 hypothetical protein slr1135 - Synechocystis sp. (strain PCC 6803)			
21127, 21128	30249527	48	4.00E-27	Nitrosomonas europaea ATCC 19718	putative transposase [Nitrosomonas europaea ATCC 19718] emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718]			
21129, 21130	34397295	53	7.00E-45	Porphyromonas gingivalis W83	phosphoserine aminotransferase [Porphyromonas gingivalis W83] ref NP_905459.1 phosphoserine aminotransferase [Porphyromonas gingivalis W83]			2.6.1.52
21131, 21132	16263258	34	3.00E-09	Sinorhizobium meliloti 1021	Putative methyltransferase [Sinorhizobium meliloti 1021] gb AAK65463.1 Putative methyltransferase [Sinorhizobium meliloti 1021] pir E95362 probable methyltransferase [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymA			
21137, 21138	48854435	42	5.00E-44	Cytophaga hutchinsonii	COG1331: Highly conserved protein containing a thioredoxin domain [Cytophaga hutchinsonii]			
21141, 21142	45657883	54	5.00E-35	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			2.7.3.-

21143,	34397331	62	4.00E-37	Porphyromonas gingivalis W83	crossover junction endodeoxyribonuclease RuvC [Porphyromonas gingivalis W83] refNP_905495.1 crossover junction endodeoxyribonuclease RuvC [Porphyromonas gingivalis W83] spIQ7MUZ6[RUV_C_PORGI Crossover junction endodeoxyribonuclease ruvC (Holliday junction nuclease ruvC) (Holliday junction resolvase ruvC)]				3.1.22.4
21144,	48854305	50	3.00E-17	Cytophaga hutchinsonii	COG0026: Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase) [Cytophaga hutchinsonii]				4.1.1.21
21147,	48870478	31	2.00E-19	Pedococcus pentosaceus ATCC 25745	COG0237: Dephospho-CoA kinase [Pedococcus pentosaceus ATCC 25745]				2.7.1.24
21149,	48856710	59	2.00E-26	Cytophaga hutchinsonii	COG0714: MoxR-like ATPases [Cytophaga hutchinsonii]				
2115,	48854087	48	3.00E-52	Cytophaga hutchinsonii	COG3386: Gluconolactonase [Cytophaga hutchinsonii]				3.1.1.17
21151,	54302486	73	2.00E-88	Photobacterium profundum SS9	hypothetical maturase [Photobacterium profundum SS9] emb CAG22679.1	Photobacterium profundum SS9 chromosome 2; segment 3/7	82	3.00E-14	2.7.7.49
21153,	37222112	66	4.00E-73	uncultured bacterium	Uvs063 [uncultured bacterium]				
21157,	53712499	39	3.00E-36	Bacteroides fragilis YCH46	putative transcriptional regulator [Bacteroides fragilis YCH46]				
21161,	48853518	35	2.00E-46	Cytophaga hutchinsonii	COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii]				
21163,	48854368	70	6.00E-79	Cytophaga hutchinsonii	COG1137: ABC-type (unclassified) transport system, ATPase component [Cytophaga hutchinsonii]				1.8.-
21165,	53712201	59	4.00E-60	Bacteroides fragilis YCH46	phosphohydrolase [Bacteroides fragilis YCH46] dbj BAD47659.1 phosphohydrolase [Bacteroides fragilis YCH46]				
21167,	53712176	32	4.00E-13	Bacteroides fragilis YCH46	putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD47634.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46]				
21169,	48855703	39	1.00E-28	Cytophaga hutchinsonii	COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii]				2.7.3.-
2117,	15838090	29	1.00E-10	Xylella fastidiosa 9a5c	hypothetical protein XF1489 [Xylella fastidiosa 9a5c] gb AAF84298.1				
21171,	57168375	47	9.00E-21	Campylobacter coli RM2228	hypothetical protein XF1489 [Xylella fastidiosa 9a5c] p rf E82675				
21172					hypothetical protein XF1489 [imported] - Xylella fastidiosa (strain 9a5c) molybdenum cofactor biosynthesis protein C [Campylobacter coli RM2228] gb EAL56857.1 molybdenum cofactor biosynthesis protein C [Campylobacter coli RM2228]				

21173,	28829330	38	2.00E-26	Dictyostellum discoidium	hypothetical protein [Dictyostellum discoidium]				5.2.1.8
21174,	28829330	41	7.00E-19	Dictyostellum discoidium	hypothetical protein [Dictyostellum discoidium]				
21175,	28829330	41	7.00E-19	Dictyostellum discoidium	hypothetical protein [Dictyostellum discoidium]				
21176,	28829330	41	7.00E-19	Dictyostellum discoidium	hypothetical protein [Dictyostellum discoidium]				
21177,	24373446	29	3.00E-09	Shewanella oneidensis MR-1	HlyD family-related protein [Shewanella oneidensis MR-1] gb AAO54933.1				
21178,	24373446	29	3.00E-09	Shewanella oneidensis MR-1	HlyD family-related protein [Shewanella oneidensis MR-1]				
21181,				Vibrio vulnificus	Putative transcriptional regulator [Vibrio vulnificus CMCP6] gb AAO11505.1				
21182,	27366450	64	4.00E-30	CMCP6	Putative transcriptional regulator [Vibrio vulnificus CMCP6]				
21183,				Cytophaga hutchinsonii	COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii]				4.1.3.-
21184,	48856398	51	3.00E-65	Cytophaga hutchinsonii	COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii]				4.1.3.-
21185,	48856398	55	1.00E-50	Cytophaga hutchinsonii	COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii]				
21186,	48856398	55	1.00E-50	Cytophaga hutchinsonii	COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii]				
21187,	48854194	45	3.00E-38	Cytophaga hutchinsonii	COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii]				
21188,	48854194	45	3.00E-38	Cytophaga hutchinsonii	COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii]				
21189,	48854194	46	6.00E-48	Cytophaga hutchinsonii	COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii]				
21190,	48854194	46	6.00E-48	Cytophaga hutchinsonii	COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii]				
21191,				Porphyromonas gingivalis W83	membrane protein, putative [Porphyromonas gingivalis W83]				
21192,	34396654	32	3.00E-28	Porphyromonas gingivalis W83	ref NP_904821.1 membrane protein, putative [Porphyromonas gingivalis W83] sp P60036 OXAA_PORGI inner membrane protein oxaA				
21193,				Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase/response regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482]				
21194,	29348306	40	5.00E-22	Bacteroides thetaiotaomicron VPI-5482	regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482]				
21195,				Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase/response regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482]				
21196,	29348306	40	6.00E-22	Bacteroides thetaiotaomicron VPI-5482	regulator, hybrid ('one-component system') [Bacteroides thetaiotaomicron VPI-5482]				
21197,				Bacteroides thetaiotaomicron VPI-5482	conserved hypothetical protein, putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO75921.1 conserved				
21198,	29346224	30	2.00E-21	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein, putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482]				
21199,	29346224	30	2.00E-21	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein, putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482]				
21200,	48856980	43	3.00E-27	Cytophaga hutchinsonii	COG1522: Transcriptional regulators [Cytophaga hutchinsonii]				
21201,	48856980	43	3.00E-27	Cytophaga hutchinsonii	COG1522: Transcriptional regulators [Cytophaga hutchinsonii]				
21202,	48856980	43	3.00E-27	Cytophaga hutchinsonii	COG1522: Transcriptional regulators [Cytophaga hutchinsonii]				
21207,				Bacteroides fragilis YCH46	putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1 putative				
21208,	53713469	46	2.00E-51	Bacteroides fragilis YCH46	helicase [Bacteroides fragilis YCH46]				
					Acinetobacter sp. ADP1 complete genome	91	6.00E-07		

21209, 21210	53717167	27	4.00E-23	Burkholderia mallei ATCC 23344	sensory box histidine kinase/response regulator [Burkholderia mallei ATCC 23344] gb AAU46707.1 sensory box histidine kinase/response regulator [Burkholderia mallei ATCC 23344]			2.7.-
2121, 2122	ABU0070 6	34	3.00E-31		Desc:S. pneumoniae type 4 strain protein from coding region #273. Org:Streptococcus pneumoniae type 4 strain.			5.1.3.14
21215, 21216	53712889	32	1.00E-26	Bacteroides fragilis YCH46	putative ABC transporter permease [Bacteroides fragilis YCH46] dbj BAD48347.1 putative ABC transporter permease [Bacteroides fragilis YCH46]			
21217, 21218	6498243	39	7.00E-32	Agrobacterium tumefaciens	tiort70 [Agrobacterium tumefaciens] ref NP_053310.1 Hypothetical gene [Agrobacterium tumefaciens]			
21219, 21220	26988659	34	4.00E-37	Pseudomonas putida KT2440	hypothetical protein PP1931 [Pseudomonas putida KT2440] gb AAN67548.1 conserved hypothetical protein [Pseudomonas putida KT2440]			
21223, 21224	48853912	50	2.00E-49	Cytophaga hutchinsonii	COG1166: Arginine decarboxylase (spermidine biosynthesis) [Cytophaga hutchinsonii]			
21225, 21226	48853912	51	2.00E-48	Cytophaga hutchinsonii	COG1166: Arginine decarboxylase (spermidine biosynthesis) [Cytophaga hutchinsonii]			
21227, 21228	9658004	59	3.00E-45	Vibrio cholerae O1 biovar eltor str. N16961	MutT/nudix family protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_232982.1 MutT/nudix family protein [Vibrio cholerae O1 biovar eltor str. N16961] pir G82439 MutT/nudix family protein VCA0592 [Imported] - Vibrio cholerae (strain N16961 serogroup O1)			
21229, 21230	31195231	55	2.00E-80	Anopheles gambiae	ENSANGP00000001058 [Anopheles gambiae] gb EAA02216.1 ENSANGP000000001058 [Anopheles gambiae str. PEST] ref XP_561308.1 ENSANGP000000001058 [Anopheles gambiae str. PEST]			1.1.1.34
2123, 2124	48854732	25	4.00E-15	Cytophaga hutchinsonii	COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii]			
21231, 21232	48855521	29	2.00E-17	Cytophaga hutchinsonii	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii]			
21233, 21234	53713656	53	4.00E-78	Bacteroides fragilis YCH46	two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD49114.1 two-component system response regulator [Bacteroides fragilis YCH46]	Desulfotalea psychrophila Lsv54 chromosome	93 4.00E-08	
21237, 21238	48854416	27	2.00E-13	Cytophaga hutchinsonii	COG3275: Putative regulator of cell autolysis [Cytophaga hutchinsonii]			2.7.3.-
21239, 21240	48854415	38	1.00E-35	Cytophaga hutchinsonii	COG3279: Response regulator of the LysR/Agr family [Cytophaga hutchinsonii]			
21241, 21242	48855448	29	4.00E-26	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]			

21243, 21244	37528315	48	9.00E-76	TT01	Photorhabdus luminescens subsp. laumondii	Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_931390.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930919.1 Transposase, IS4 Family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930911.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930800.1 Transposase, IS4 Family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930791.1 Transposase, IS4 Family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_928662.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_928429.1 Transposase, IS4 Family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_927713.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_927691.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16866.1 Transposase, IS4 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16580.1 Transposase, IS4 fa				
21245, 21246	24373937	51	9.00E-49	Shewanella oneidensis MR-1	Shewanella oneidensis MR-1	CDP-diacylglycerol--serine O-phosphatidyltransferase [Shewanella oneidensis MR-1] phosphatidyltransferase [Shewanella oneidensis MR-1]				2.7.8.8
21247, 21248	24373937	50	6.00E-54	Shewanella oneidensis MR-1	Shewanella oneidensis MR-1	CDP-diacylglycerol--serine O-phosphatidyltransferase [Shewanella oneidensis MR-1] CDP-diacylglycerol--serine O-phosphatidyltransferase [Shewanella oneidensis MR-1]				2.7.8.8
2125, 2126	29349895	43	1.00E-44	Bacteroides thetaiotaomicron VPI-5482	Bacteroides thetaiotaomicron VPI-5482	putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79592.1 putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicron VPI-5482]				3.2.1.-
21253, 21254	53764144	43	3.00E-65	Anabaena variabilis ATCC 29413	Anabaena variabilis ATCC 29413	COG1770: Protease II [Anabaena variabilis ATCC 29413]				3.4.21.8
21255, 21256	31195963	66	1.00E-56	Anopheles gambiae	Anopheles gambiae	ENSANGP00000000454 [Anopheles gambiae]				4.2.1.22
21257, 21258	31195963	65	2.00E-50	Anopheles gambiae	Anopheles gambiae	ENSANGP00000000454 [Anopheles gambiae]				4.2.1.22
21259, 21260	53686269	48	8.00E-60	Desulfitobacterium hafnense DCB-2	Desulfitobacterium hafnense DCB-2	COG0535: Predicted Fe-S oxidoreductases [Desulfitobacterium hafnense DCB-2]				
21261, 21262	53714074	49	1.00E-47	Bacteroides fragilis YCH46	Bacteroides fragilis YCH46	hypothetical protein BF2782 [Bacteroides fragilis YCH46] dbj BAD49532.1 hypothetical protein [Bacteroides fragilis YCH46]				
21263, 21264	29348700	29	1.00E-21	Bacteroides thetaiotaomicron VPI-5482	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3291 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78397.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				

21265,	46156085	27	1.00E-10	Haemophilus sommus 2336	COG3298: Predicted 3'-5' exonuclease related to the exonuclease domain of PoB [Haemophilus somnus 2336]			
21266				Bacteroides thetaiotaomicron VPI-5482	putative transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482]			
21267,	29346046	30	3.00E-29	Bacteroides thetaiotaomicron VPI-5482	gb AAO75743.1 putative transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482]			
21268				Bacteroides thetaiotaomicron VPI-5482	TonB [Bacteroides thetaiotaomicron VPI-5482] gb AAO79003.1 TonB [Bacteroides thetaiotaomicron VPI-5482]			
21269,	29349306	33	3.00E-12	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70144.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			2.7.3.-
2127,	45657421	42	2.00E-13	Bacteroides fragilis YCH46	hypothetical protein BF0893 [Bacteroides fragilis YCH46] dbj BAD47644.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
21273,	53712186	42	4.00E-13	Porphyromonas gingivalis W83	peptide chain release factor 3 [Porphyromonas gingivalis W83] ref NP_904540.1 peptide chain release factor 3 [Porphyromonas gingivalis W83]			3.6.1.48
21274				Cytophaga hutchinsonii	COG1432: Uncharacterized conserved protein [Cytophaga hutchinsonii]			
21275,	34396372	67	3.00E-87	Parachlamydia sp. UWE25	putative rRNA methylase [Parachlamydia sp. UWE25] emb CAF24516.1 putative rRNA methylase [Parachlamydia sp. UWE25]			2.1.1.-
21276	48447426	28	5.00E-08	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT1139 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76246.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
21277,	29346549	42	4.00E-25	Idiomarina lohiensis L2TR	Probable aminopeptidase [Idiomarina lohiensis L2TR] gb AAV81546.1 Probable aminopeptidase [Idiomarina lohiensis L2TR]			
21278	56459814	26	1.00E-12	Xanthomonas axonopodis pv. citri str. 306	hypothetical protein XAC0026 [Xanthomonas axonopodis pv. citri str. 306] gb AAM34918.1 conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306]			3.4.17.2 1
21279,	21240800	28	5.00E-24	Chloroflexus aurantiacus	COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus]			
21280	53797086	36	8.00E-47	Rhodopirellula baltica SH 1	cryptic haloacid dehalogenase 1 [Rhodopirellula baltica SH 1] emb CAD73861.1 cryptic haloacid dehalogenase 1 [Pirellula sp.]			3.8.1.3
21281,	32473181	34	5.00E-30	Pseudomonas aeruginosa PAO1	hypothetical protein PA4882 [Pseudomonas aeruginosa PAO1] pir D83036 hypothetical protein PA4882 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_253569.1 hypothetical protein PA4882 [Pseudomonas aeruginosa PAO1]			1.6.6.1
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21305, 21306	36955884	78	1.00E-51	Polaribacter filamentus	NAD kinase [Polaribacter filamentus] ATP-dependent helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76161.1 ATP-dependent helicase [Bacteroides thetaiotaomicron VPI-5482]	Polaribacter filamentus NAD kinase gene, complete cds	84	7.00E-42	2.7.1.23
21309, 21310	29346464	25	2.00E-13	Bacteroides thetaitaomicron VPI-5482	adenylate cyclase-related protein [Shewanella oneidensis MR-1] gb AAN54394.1 adenylate cyclase-related protein [Shewanella oneidensis MR-1]				3.6.1.-
21311, 21312	24372907	31	1.00E-12	Shewanella oneidensis MR-1					4.6.1.1
21313, 21314	46105876	36	3.00E-48	Rubrobacter xylanophilus DSM 9941	COG0520: Selenocysteine lyase [Rubrobacter xylanophilus DSM 9941]				4.4.1.-
21317, 21318	22255857	60	1.00E-100	Micromonospora echinospora	CalR4 [Micromonospora echinospora] fusion protein of probable Na-dependent permease domain and histidine kinase domain of putative two-component sensor [Azoarcus sp. Ebn1] emb CAI06216.1 Fusion protein of probable Na-dependent permease domain and histidine kinase domain of putative two-component sensor [Azoarcus sp. Ebn1]	Oryza sativa (japonica cultivar- group), predicted mRNA	88	5.00E-173	3.4.21.5
21323, 21324	56475528	38	1.00E-19	Azoarcus sp. Ebn1	putative anti-sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO76072.1 putative anti-sigma factor [Bacteroides thetaiotaomicron VPI-5482]				
21329, 21330	29346375	31	4.00E-18	Bacteroides thetaitaomicron VPI-5482	unknown [Branchiostoma floridae]				2.4.2.-
2133, 2134	20302775	44	1.00E-36	Branchiostoma floridae	Desc: Lactococcus lactis protein ymgC. Org: Lactococcus lactis IL1403 COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Cytophaga hutchinsonii]				
21331, 21332	ABB5457	52	9.00E-20	Cytophaga hutchinsonii	COG0796: Glutamate racemase [Pseudomonas syringae pv. syringae B728a]				1.8.-
21333, 21334	48856353	72	2.00E-78	Pseudomonas syringae pv. syringae B728a	COG0710: Acetyltransferase (isoleucine patch superfamily) [Methanosarcina barkeri str. fusaro]				5.1.1.3
21335, 21336	46188261	44	7.00E-52	Methanosarcina barkeri str. fusaro	COG1012: NAD-dependent aldehyde dehydrogenases [Cytophaga hutchinsonii]				2.3.1.18
21337, 21338	48838984	70	6.00E-59	Cytophaga hutchinsonii	COG1012: NAD-dependent aldehyde dehydrogenases [Cytophaga hutchinsonii]				
21339, 21340	48855746	54	8.00E-43	Cytophaga hutchinsonii	COG1012: NAD-dependent aldehyde dehydrogenases [Cytophaga hutchinsonii]				1.2.1.9
21341, 21342	48855746	59	4.00E-56	Cytophaga hutchinsonii					

21347,	53715241	33	5.00E-14	Bacteroides fragilis YCH46	hypothetical protein BF3957 [Bacteroides fragilis YCH46] dbj BAD50699.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
21348,	53762545	40	6.00E-35	Ralstonia eutropha JMP134	COG0500: SAM-dependent methyltransferases [Ralstonia eutropha JMP134]			
2135,	48854339	55	6.00E-85	Cytophaga hutchinsonii	COG0178: Exonuclease ATPase subunit [Cytophaga hutchinsonii]			
2136				Bacteroides thetaiotaomicron VPI-5482	outer membrane efflux protein [Bacteroides thetaiotaomicron VPI-5482]			
21351,	29345970	31	7.00E-22	Bacteroides fragilis YCH46	putative endonuclease [Bacteroides fragilis YCH46]			
21352	53712972	56	7.00E-27	Campylobacter jejuni	putative integral membrane protein [Campylobacter jejuni]			
21353,	8572750	29	9.00E-09	Porphyrromonas gingivalis W83	conserved hypothetical protein [Porphyrromonas gingivalis W83]			
21354	34396430	34	1.00E-34	Porphyrromonas gingivalis W83	ref NP_904597.1 hypothetical protein PG0276 [Porphyrromonas gingivalis W83]			
21359,	34397012	66	9.00E-74	Porphyrromonas gingivalis W83	ABC transporter, ATP-binding protein [Porphyrromonas gingivalis W83]			
21360				Bacteroides fragilis YCH46	ref NP_905177.1 ABC transporter, ATP-binding protein [Porphyrromonas gingivalis W83]			1.8.-.-
21365,	53714385	31	2.00E-15	Nostoc sp. PCC 7120	putative glycosylhydrolase [Bacteroides fragilis YCH46] dbj BAD49843.1 putative glycosylhydrolase [Bacteroides fragilis YCH46]			3.2.1.17
21366	17228761	23	5.00E-16	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein air1266 [Nostoc sp. PCC 7120] pir AG1964 hypothetical protein air1266 [imported] - Nostoc sp. (strain PCC 7120)			
21371,	29347543	34	2.00E-29	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482]			
21372				Bacteroides thetaiotaomicron VPI-5482	gb AAO77240.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
21373,	29347543	36	2.00E-36	Cytophaga hutchinsonii	hypothetical protein BT2133 [Bacteroides thetaiotaomicron VPI-5482]			
21374	48854733	63	1.00E-68	Geobacillus kaustophilus HTA426	hypothetical protein GK2088 [Geobacillus kaustophilus HTA426]			3.5.4.16
21375,				Geobacillus kaustophilus HTA426	dbj BAD76373.1 hypothetical conserved protein [Geobacillus kaustophilus HTA426]			3.1.2.6
21376	56420623	31	6.00E-20	Cytophaga hutchinsonii	COG0491: Zn-dependent hydrolases, including glyoxylases [Cytophaga hutchinsonii]			3.1.2.6
21377,	48855054	32	5.00E-36	Cytophaga hutchinsonii				
21378								
21379,								
21380								
21381,								
21382								

2139,	20808385	28	6.00E-23	Thermoanaerobacter tengcongensis MB4	Diaminopimelate decarboxylase [Thermoanaerobacter tengcongensis MB4]				4.1.1.20
2140	ABP3882								
21395,	2	55	1.00E-36		Desc:Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3667. Org:Staphylococcus epidermidis				2.1.1.61
21396									
21397,	AAU3889	42	3.00E-52		Desc:C. pneumoniae CT287 homologue CPn0438. Org:Chlamydia pneumoniae				2.1.1.61
21398	5								
21399,	AAU3889	44	1.00E-49		Desc:C. pneumoniae CT287 homologue CPn0438. Org:Chlamydia pneumoniae				2.1.1.61
21400	5								
21403,				Vibrio					
21404	28901123	46	4.00E-38	parahaemolyticus RIMD 2210633	hypothetical protein VPA1268 [Vibrio parahaemolyticus RIMD 2210633] dbj[BAC62611.1] hypothetical protein [Vibrio parahaemolyticus]				
21405,	AAU3443	29	5.00E-12		Desc:Porphyromonas gingivalis protein PG95. Org:Porphyromonas gingivalis				
21406	4								
21409,				Bacillus cereus	Cell cycle protein MesJ [Bacillus cereus ATCC 14579] gb AAP07166.1] Cell cycle protein MesJ [Bacillus cereus ATCC 14579]				
21410	30018334	33	2.00E-27	ATCC 14579					
21411,				Silicibacter	glutamine amidotransferase, class-I [Silicibacter pomeroyi ref YP_166322.1] glutamine amidotransferase, class-I [Silicibacter pomeroyi DSS-3]				6.3.5.2
21412	56677705	47	5.00E-49	pomeroyi DSS-3					
21413,				Photobacterium	hypothetical protein PBPRA1799 [Photobacterium profundum SS9] emb CAG20204.1] hypothetical protein [Photobacterium profundum]			92	1.00E-11
21414	54309886	46	3.00E-58	profundum SS9					
				Legionella					
				pneumophila					
21415,				subsp.	hypothetical protein lpg1991 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28060.1] hypothetical protein lpg1991 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]				
21416	52842208	22	9.00E-08	Philadelphia 1					
					peptide ABC transporter, peptide-binding protein, putative [Campylobacter lari RM2100] gb EAL54465.1] peptide ABC transporter, peptide-binding protein, putative [Campylobacter lari RM2100]				
21417,				Campylobacter lari					
21418	57241353	35	2.00E-14	RM2100					
21421,				Haemophilus					
21422	46133173	27	4.00E-13	Influenzae R2866	COG1216: Predicted glycosyltransferases [Haemophilus influenzae R2866]				
21423,				Crocospaera	COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Crocospaera watsonii WH 8501]				
21424	53735011	37	5.00E-33	watsonii WH 8501					
				Bacteroides					
21425,				thetataomicron	topoisomerase IV subunit A [Bacteroides thetataomicron VPI-5482] gb AAO78685.1] topoisomerase IV subunit A [Bacteroides thetataomicron VPI-5482]				
21426	29348988	40	3.00E-56	VPI-5482					
21429,				Bacteroides	putative DNA repair protein [Bacteroides thetataomicron VPI-5482] gb AAO75185.1] putative DNA repair protein [Bacteroides thetataomicron VPI-5482]				
21430	29345488	49	1.00E-26	VPI-5482					

2143, 2144	48853949	73	1.00E-126	Cytophaga hutchinsonii	COG0187: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit [Cytophaga hutchinsonii]			5.99.1.-
21437, 21438	29346728	23	1.00E-12	Bacteroides thetataoimicron VPI-5482	signaling protein without kinase domain [Bacteroides thetataoimicron VPI- 5482] gb AAO76425.1 signaling protein without kinase domain [Bacteroides thetataoimicron VPI-5482]			2.7.3.-
21439, 21440	462651	64	1.00E-56	Fusobacterium nucleatum	Modification methylase FnuDI (Cytosine-specific methyltransferase FnuDI) (M.FnuDI) gb AAC05695.1 FnuDI DNA modification methyltransferase [Fusobacterium nucleatum]	Fusobacterium nucleatum adenylosuccinate synthetase (purA), FnuDI restriction endonuclease (fnuDIR), and FnuDI DNA modification methyltransferase (fnuDIM) genes, complete cds	83	5.00E-07 2.1.1.73
21441, 21442	53712295	50	5.00E-38	Bacteroides fragilis YCH46	pantoate-beta-alanine ligase [Bacteroides fragilis YCH46] db BAD47753.1			6.3.2.1
21443, 21444	4163101	37	2.00E-20	Erwinia chrysanthemi	pantoate-beta-alanine ligase [Bacteroides fragilis YCH46] transcriptional activator [Erwinia chrysanthemi]			
21445, 21446	20807153	35	3.00E-40	Thermoanaerobact er tengcongensis MB4	predicted glycosyltransferases [Thermoanaerobacter tengcongensis MB4] gb AAM23928.1 predicted glycosyltransferases [Thermoanaerobacter tengcongensis MB4]			2.4.-.-
21447, 21448	48855909	39	4.00E-22	Cytophaga hutchinsonii	COG0326: Molecular chaperone, HSP90 family [Cytophaga hutchinsonii] Beta-lactamase class C family protein [Idiomarina loihiensis L2TR] gb AAV80889.1 Beta-lactamase class C family protein [Idiomarina loihiensis L2TR]			3.5.2.6
21451, 21452	56459157	41	3.00E-33	Idiomarina loihiensis L2TR	COG0155: Sulfite reductase, beta subunit (hemoprotein) [Cytophaga hutchinsonii]			
21453, 21454	48854475	42	7.00E-45	Cytophaga hutchinsonii	hypothetical protein RB12778 [Rhodopirellula ballica SH 1] emb CAD7775.1 conserved hypothetical protein [Pirellula sp.]			
21455, 21456	17229700	24	9.00E-14	Nostoc sp. PCC 7120	transcriptional regulator [Nostoc sp. PCC 7120] db BAB73907.1 transcriptional regulator [Nostoc sp. PCC 7120] pir AB2082 transcription regulator air2208 [imported] - Nostoc sp. (strain PCC 7120)			
21457, 21458	53712258	54	5.00E-38	Bacteroides fragilis YCH46	peptidyl-dipeptidase [Bacteroides fragilis YCH46] db BAD47716.1 peptidyl- dipeptidase [Bacteroides fragilis YCH46]			3.4.15.5

21459, 21460	29348812	61	4.00E-74	Bacteroides thetataomicron VPI-5482	putative nitrogen utilization substance protein [Bacteroides thetataomicron VPI-5482] gb AAO78509.1 putative nitrogen utilization substance protein [Bacteroides thetataomicron VPI-5482]				
21461, 21462	53715107	32	1.00E-33	Bacteroides fragilis YCH46	putative N-acetylmuramoyl-L-alanine amidase AmiA [Bacteroides fragilis YCH46] dbj BAD50565.1 putative N-acetylmuramoyl-L-alanine amidase AmiA [Bacteroides fragilis YCH46]				3.5.1.28
21463, 21464	45510657	68	8.00E-83	Anabaena variabilis ATCC 29413	COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Anabaena variabilis ATCC 29413]				3.1.21.3
21465, 21466	52426179	30	2.00E-11	Mannheimia succiniciproducens MBEL55E	hypothetical protein MS2124 [Mannheimia succiniciproducens MBEL55E] gb AAU38731.1 unknown [Mannheimia succiniciproducens MBEL55E]				3.2.1.41
21469, 21470	45657883	41	3.00E-24	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				2.7.3.-
21475, 21476	48853532	37	4.00E-24	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]				
21481, 21482	29347959	42	2.00E-55	Bacteroides thetataomicron VPI-5482	putative carboxypeptidase [Bacteroides thetataomicron VPI-5482] gb AAO77656.1 putative carboxypeptidase [Bacteroides thetataomicron VPI-5482]				3.4.17.1 3
21487, 21488	48863883	26	2.00E-18	Microbulbifer degradans 2-40	COG3250: Beta-galactosidase/beta-glucuronidase [Microbulbifer degradans 2-40]				
21491, 21492	53711667	58	8.00E-30	Bacteroides fragilis YCH46	hypothetical protein BF0376 [Bacteroides fragilis YCH46] dbj BAD47125.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
21493, 21494	54308987	55	7.00E-24	Photobacterium profundum SS9	hypothetical protein PBPR1800 [Photobacterium profundum SS9] emb CAG20205.1 hypothetical protein [Photobacterium profundum]				
21495, 21496	29346626	26	1.00E-10	Bacteroides thetataomicron VPI-5482	putative two-component system sensor protein, without kinase domain [Bacteroides thetataomicron VPI-5482] gb AAO76323.1 putative two- component system sensor protein, without kinase domain [Bacteroides thetataomicron VPI-5482]				
21499, 21500	45658436	30	1.00E-13	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711250.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar Lai str. 56601] gb AAN48268.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar lai str. 56601] gb AAS71159.1 alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				3.4.11.5

21505, 21506	51246488	55	1.00E-32	Desulfotalea psychrophila LSV54	hypothetical protein DP2838 [Desulfotalea psychrophila LSV54] emb CAG37365.1 hypothetical protein [Desulfotalea psychrophila LSV54]				
21507, 21508	53713193	33	5.00E-15	Bacteroides fragilis YCH46	hypothetical protein BF1903 [Bacteroides fragilis YCH46] dbj BAD48651.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
21509, 21510	46906236	34	2.00E-20	Listeria monocytogenes str. 4b F2365	diphosphomevalonate decarboxylase [Listeria monocytogenes str. 4b F2365] gb AA02802.1 diphosphomevalonate decarboxylase [Listeria monocytogenes str. 4b F2365]				4.1.1.33
2151, 2152	15612940	44	8.00E-25	Bacillus halodurans C-125	hypothetical protein BH0377 [Bacillus halodurans C-125] dbj BAB04096.1 BH0377 [Bacillus halodurans C-125] pir A83697 hypothetical protein BH0377 [imported] - Bacillus halodurans (strain C-125)				
21511, 21512	27379522	44	5.00E-15	Bradyrhizobium japonicum USDA 110	hypothetical protein bir4411 [Bradyrhizobium japonicum USDA 110] dbj BAC49676.1 bir4411 [Bradyrhizobium japonicum USDA 110]				
21513, 21514	48856112	33	5.00E-24	Cytophaga hutchinsonii	COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
21519, 21520	53715398	53	2.00E-57	Bacteroides fragilis YCH46	two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD50856.1 two-component system response regulator [Bacteroides fragilis YCH46]				
21521, 21522	32476021	59	1.00E-62	Rhodopirellula baltica SH 1	X-Pro dipeptidyl-peptidase [Rhodopirellula baltica SH 1] emb CAD76400.1 X Pro dipeptidyl-peptidase [Pirellula sp.] sp P59825 PEPX_RHOBA Putative Xaa-Pro dipeptidyl-peptidase (X-Pro dipeptidyl-peptidase) (X-prolyl-dipeptidyl aminopeptidase) (X-PDAP)				3.4.14.1 1
21523, 21524	42525031	36	2.00E-32	Bdellovibrio bacteriovorus HD100	type I restriction-modification system, S subunit [Bdellovibrio bacteriovorus HD100] emb CAE81065.1 type I restriction-modification system, S subunit [Bdellovibrio bacteriovorus HD100]				3.1.21.3
21525, 21526	48855000	52	1.00E-49	Cytophaga hutchinsonii	COG2509: Uncharacterized FAD-dependent dehydrogenases [Cytophaga hutchinsonii]				
21529, 21530	48858932	35	1.00E-24	Glostridium thermocellum ATCC 27405	COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405]				2.7.3.-
2153, 2154	17230943	35	5.00E-32	Nostoc sp. PCC 7120	ATP-dependent DNA helicase [Nostoc sp. PCC 7120] pir AD2237 ATP- dependent DNA helicase [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75150.1 ATP-dependent DNA helicase [Nostoc sp. PCC 7120]				
21535, 21536	48854182	42	6.00E-20	Cytophaga hutchinsonii	COG1472: Beta-glucosidase-related glycosidases [Cytophaga hutchinsonii]				
21541, 21542	48854793	43	1.00E-54	Cytophaga hutchinsonii	COG1109: Phosphomannomutase [Cytophaga hutchinsonii]				5.4.2.8

21543, 21544	31194451	67	1.00E-78	Anopheles gambiae	ENSANGP0000015516 [Anopheles gambiae] lysine-sensitive aspartokinase III [Haemophilus ducreyi 35000HP] ref NP_873799.1 lysine-sensitive aspartokinase III [Haemophilus ducreyi 35000HP]			3.4.21.-
21545, 21546	33148669	34	1.00E-24	Haemophilus ducreyi 35000HP				2.7.2.4
21547, 21548	54302486	73	6.00E-99	Photobacterium profundum SS9	hypothetical maturase [Photobacterium profundum SS9] emb CAG22679.1 hypothetical maturase [Photobacterium profundum]	Photobacterium profundum SS9 chromosome 2; segment 3/7		
2155, 2156	42523179	51	4.00E-68	Bdellovibrio bacteriovorus HD100	putative formyltransferase [Bdellovibrio bacteriovorus HD100] emb CAE79552.1 putative formyltransferase [Bdellovibrio bacteriovorus HD100]		84	7.00E-19 2.7.7.49
21551, 21552	15613179	42	5.00E-19	Bacillus halodurans C-125	hypothetical protein BH0616 [Bacillus halodurans C-125] dbj BAB04335.1 BH0616 [Bacillus halodurans C-125] pir H83726 hypothetical protein BH0616 [imported] - Bacillus halodurans (strain C-125)			2.1.2.9
21553, 21554	48854781	31	2.00E-10	Cytophaga hutchinsonii	hypothetical protein Chut02002457 [Cytophaga hutchinsonii]			
21557, 21558	24214122	41	7.00E-32	Leptospira interrogans serovar Lai str. 56601	Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AA048621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601]			
21563, 21564	19704846	31	5.00E-08	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Phosphatidylinositol-4-phosphate 5-kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93640.1 hypothetical exported 24-amino acid repeat protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			2.7.1.88
21567, 21568	46141620	59	3.00E-28	Psychrobacter sp. 273-4	COG3335: Transposase and inactivated derivatives [Psychrobacter sp. 273- 4]			
21569, 21570	53715439	64	2.00E-57	Bacteroides fragilis YCH46	DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46] dbj BAD50897.1 DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46]			2.7.7.6
2157, 2158	53714076	28	4.00E-15	Bacteroides fragilis YCH46	putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD49534.1 putative glycosyltransferase [Bacteroides fragilis YCH46]			
21571, 21572	37525750	59	9.00E-52	Photorhabdus luminescens subsp. laumondii TTO1	hypothetical protein plu1816 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE14109.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1]			
21573, 21574	22094882	49	3.00E-10	Flavobacterium johnsoniae	GldH [Flavobacterium johnsoniae]			

21577,	48859857	30	2.00E-26	Clostridium thermoceillum ATCC 27405	COG0653: Preprotein translocase subunit SecA (ATPase, RNA helicase) [Clostridium thermoceillum ATCC 27405]				
21578	ABB9930				Desc:Amino acid sequence of DNA-methyltransferase M.Eaci. Org: Eubacterium acidaminophilum				2.1.1.72
21579,	9	34	2.00E-33						
21580				Rhodospirillum	hypothetical protein RB4512 [Rhodospirillum batlica SH 1] emb[CAD73832.1]				
21583,	32473152	39	5.00E-29	batlica SH 1	conserved hypothetical protein [Prelilla sp.]				
21584				Cytophaga	COG1060: Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes [Cytophaga hutchinsonii]				
21585,	48855692	71	2.00E-88	hutchinsonii					
21586									
21587,				Bacteroides fragilis	hypothetical protein BF4373 [Bacteroides fragilis YCH46] dbj[BAD51111.1]				
21588	53715653	33	3.00E-14	YCH46	conserved hypothetical protein [Bacteroides fragilis YCH46]				
21589,				Bacteroides	LacI family transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482]				
21590,	29349021	44	8.00E-24	thetaiotaomicron VPI-5482	gbjAAO78718.1] LacI family transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482]				
2159,				Bacteroides	NADH dehydrogenase I, chain I [Bacteroides thetaiotaomicron VPI-5482]				1.6.5.3
2160	29349471	47	1.00E-36	thetaiotaomicron VPI-5482	gbjAAO79188.1] NADH dehydrogenase I, chain I [Bacteroides thetaiotaomicron VPI-5482]				
21591,					hypothetical protein BSU31500 [Bacillus subtilis subsp. subtilis str. 168]				
21592	16080202	45	3.00E-29	Bacillus subtilis subsp. subtilis str. 168	embjCAB07916.1] unknown [Bacillus subtilis] emb[CAB15139.1] yuxK [Bacillus subtilis subsp. subtilis str. 168] pir[B55220 hypothetical protein yuxK - Bacillus subtilis] gbjAAA64944.1] unknown sp[P40761] YUXK_BACSU				
21593,				Cytophaga	Hypothetical protein yuxK (ORF2)				
21594	48854071	45	1.00E-26	hutchinsonii	COG2207: AraC-type DNA-binding domain-containing proteins [Cytophaga hutchinsonii]				
21599,				Geobacter					
21600	39995668	26	7.00E-22	sulfurreducens PCA	hypothetical protein GSU0561 [Geobacter sulfurreducens PCA]				
21601,					gbjAAR33892.1] conserved domain protein [Geobacter sulfurreducens PCA]				
21602	48854901	44	7.00E-28	Cytophaga hutchinsonii	COG3696: Putative silver efflux pump [Cytophaga hutchinsonii]				
21603,				Cytophaga					
21604	48856151	52	1.00E-29	hutchinsonii	hypothetical protein Chut02001392 [Cytophaga hutchinsonii]				
21605,				Shewanella					
21606	24371725	38	2.00E-17	oneidensis MR-1	hypothetical protein SO0125 [Shewanella oneidensis MR-1] gbjAAN53212.1]				
21607,					conserved hypothetical protein [Shewanella oneidensis MR-1]				
21608	41690520	83	7.00E-85	Psychrobacter sp. 273-4	COG2050: Uncharacterized protein, possibly involved in aromatic compounds catabolism [Psychrobacter sp. 273-4]				
2161,				Nostoc punctiforme					
2162	23124542	32	2.00E-17	PCC 73102	COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102]				2.7.3.-

21613,	29347486	38	3.00E-29	Bacteroides thetaiotaomicron VPI-5482	acetohydroxyacid synthase small subunit [Bacteroides thetaiotaomicron VPI-5482] gb AAO77183.1 acetohydroxyacid synthase small subunit				4.1.3.18
21614				Bacteroides thetaiotaomicron VPI-5482	putative dTDP-4-dehydrothiamine reductase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76837.1 putative dTDP-4-dehydrothiamine reductase				1.1.1.13
21615,	29347140	46	2.00E-31	Bacteroides thetaiotaomicron VPI-5482	UDP-glucose/GDP-mannose dehydrogenase family protein [Chlorobium tepidum TLS] gb AAM71474.1 UDP-glucose/GDP-mannose dehydrogenase family protein [Chlorobium tepidum TLS]				1.1.1.-
21617,	21673067	48	2.00E-27	Chlorobium tepidum TLS	COG2038: NaMN:DMB phosphoribosyltransferase [Microbulbifer degradans 2-40]				2.4.2.21
21618	48861664	62	3.00E-31	Microbulbifer degradans 2-40	hypothetical protein STH2171 [Symbiobacterium thermophilum IAM 14863] dbj BAD41156.1 conserved hypothetical protein [Symbiobacterium thermophilum IAM 14863]				
21619,	51893309	37	2.00E-14	Symbiobacterium thermophilum IAM 14863	COG0686: Alanine dehydrogenase [Cytophaga hutchinsonii]				1.4.1.1
21620	48856852	45	2.00E-24	Cytophaga hutchinsonii	pyruvate phosphate dikinase [Porphyromonas gingivalis W83] ref NP_905238.1 pyruvate phosphate dikinase [Porphyromonas gingivalis W83]				
21623,	34397073	75	2.00E-71	Porphyromonas gingivalis W83	hypothetical protein RB6958 [Rhodopirella baltica SH 1] emb CAD75097.1 conserved hypothetical protein [Pirella sp.]			87	2.00E-15/2.7.9.1
21624	32474556	33	2.00E-21	Rhodopirella baltica SH 1	hypothetical protein Chut0202457 [Cytophaga hutchinsonii]				
21631,	48854781	32	7.00E-15	Cytophaga hutchinsonii	COG1404: Subtilisin-like serine proteases [Cytophaga hutchinsonii]				
21632	48853939	32	2.00E-07	Cytophaga hutchinsonii	tpg/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] ref YP_027843.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne] ref NP_844138.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAP25624.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAT30812.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] gb AAT53894.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne]				
21637,	47526988	29	2.00E-10	Bacillus anthracis str. 'Ames Ancestor'	COG0013: Alanyl-tRNA synthetase [Cytophaga hutchinsonii]				
21638				Cytophaga hutchinsonii	putative peptidase [Bacteroides fragilis YCH46] dbj BAD47513.1 putative peptidase [Bacteroides fragilis YCH46]			86	4.00E-17/6.1.1.7
21641,	48854966	71	1.00E-100	Bacteroides fragilis YCH46					3.5.1.-
21642	53712055	48	8.00E-38						
21643,									
21644									

21645,	46202712	36	2.00E-17	Magnetospirillum magnetotacticum MS-1	COG4623: Predicted soluble lytic transglycosylase fused to an ABC-type amino acid-binding protein [Magnetospirillum magnetotacticum MS-1]			3.2.1.-
21646								
21647,	53714082	41	4.00E-12	Bacteroides fragilis YCH46	putative excisionase [Bacteroides fragilis YCH46] dbj BAD49540.1 putative excisionase [Bacteroides fragilis YCH46]			
21648								
2165,								
2165,	32474556	33	2.00E-21	Rhodopirellula batlica SH 1	hypothetical protein RB6958 [Rhodopirellula batlica SH 1] emb CAD75097.1 conserved hypothetical protein [Pirellula sp.]			
21651,								
21652	14531032	47	2.00E-48	Flavobacterium johnsoniae	Fjo14 [Flavobacterium johnsoniae]			
21653,								
21654	29346131	37	1.00E-48	Bacteroides thetaiotaomicron VPI-5482	DNA repair and recombination protein, putative helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75828.1 DNA repair and recombination protein, putative helicase [Bacteroides thetaiotaomicron VPI-5482]			
21655,								
21656	37962667	46	3.00E-34	Bacteroides uniformis	Tn10-like transposase [Bacteroides uniformis]			
21659,								
21660	15793683	40	9.00E-20	Neisseria meningitidis Z2491	hypothetical protein NMA0704 [Neisseria meningitidis Z2491] emb CAB83991.1 hypothetical protein NMA0704 [Neisseria meningitidis Z2491] pir E81913 hypothetical protein NMA0704 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)			4.6.1.10
21661,								
21662	53714846	47	8.00E-50	Bacteroides fragilis YCH46	putative cation efflux system transmembrane protein [Bacteroides fragilis YCH46] dbj BAD50304.1 putative cation efflux system transmembrane protein [Bacteroides fragilis YCH46]			
21663,								
21664	33864121	37	1.00E-20	Prochlorococcus marinus str. MIT 9313	LybB protein homolog [Prochlorococcus marinus str. MIT 9313] emb CAE22029.1 LybB protein homolog [Prochlorococcus marinus str. MIT 9313] sp Q7V477 ISPH_PROMM 4-hydroxy-3-methylbut-2-enyl diphosphate reductase			
21665,								
21666	48856755	59	2.00E-61	Cytophaga hutchinsonii	COG0139: Phosphoribosyl-AMP cyclohydrolase [Cytophaga hutchinsonii]			3.5.4.19
21667,								
21668	51244305	43	9.00E-41	Desulfotalea psychrophila LSV54	hypothetical protein DP0453 [Desulfotalea psychrophila LSV54] emb CAG35182.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]			
21671,								
21672	48863666	32	4.00E-07	Microbulifer degradans 2-40	COG3428: Predicted membrane protein [Microbulifer degradans 2-40]			
21673,								
21674	52632010	30	2.00E-15	uncultured archaeon GZfos12E1	conserved hypothetical protein [uncultured archaeon GZfos12E1]			
21675,								
21676	53714587	69	3.00E-28	Bacteroides fragilis YCH46	50S ribosomal protein L31 type B [Bacteroides fragilis YCH46] dbj BAD500045.1 50S ribosomal protein L31 type B [Bacteroides fragilis YCH46]			
21677,								
21678	56964929	50	9.00E-11	Bacillus clausii KSM-K16	glycosyltransferase [Bacillus clausii KSM-K16] dbj BAD65699.1 glycosyltransferase [Bacillus clausii KSM-K16]			

21679, 21680	48855461	39	1.00E-40	Cytophaga hutchinsonii	COG5000: Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation [Cytophaga hutchinsonii]		2.7.3.-
21683, 21684	53712087	40	3.00E-20	Bacteroides fragilis YCH46	putative transcriptional regulator [Bacteroides fragilis dbj BAD47545.1 putative transcriptional regulator [Bacteroides fragilis YCH46]		
21689, 21690	48856079	62	9.00E-67	Cytophaga hutchinsonii	COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii]		1.8.-.-
21693, 21694	29348486	54	4.00E-33	Bacteroides thetataoamicon	ribonuclease R [Bacteroides thetaiotaomicron VPI-5482] gb AAO78183.1 ribonuclease R [Bacteroides thetaiotaomicron VPI-5482]		3.1.-.-
21695, 21696	53712881	40	1.00E-45	Bacteroides fragilis YCH46	hypothetical protein BF1590 [Bacteroides fragilis YCH46] dbj BAD48339.1 conserved hypothetical protein [Bacteroides fragilis YCH46]		2.-.-.-
21697, 21698	53713905	26	7.00E-12	Bacteroides fragilis YCH46	LysM-repeat proteins and domains [Bacteroides fragilis YCH46] dbj BAD49363.1 LysM-repeat proteins and domains [Bacteroides fragilis YCH46]		
21699, 21700	46580228	30	2.00E-10	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	protein-export membrane protein SecF [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96295.1 protein-export membrane protein SecF [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]		
21701, 21702	29347584	35	4.00E-20	Bacteroides thetataoamicon VPI-5482	ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI- 5482] gb AAO77281.1 ABC transporter ATP-binding protein [Bacteroides thetataoamicon VPI-5482]		
21703, 21704	52841257	49	7.00E-48	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	ribose-phosphate pyrophosphokinase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27109.1 ribose-phosphate pyrophosphokinase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAM00625.1 unknown [Legionella pneumophila]		2.7.6.1
21705, 21706	53712038	32	3.00E-26	Bacteroides fragilis YCH46	hypothetical protein BF0745 [Bacteroides fragilis YCH46] dbj BAD47496.1 conserved hypothetical protein [Bacteroides fragilis YCH46]		
21707, 21708	14531035	47	1.00E-47	Flavobacterium johnsoniae	gliding motility protein GldG [Flavobacterium johnsoniae] probable: Putative GlnAc transferase [Azoarcus sp. EbN1] emb CAI06955.1 probable: Putative GlnAc transferase [Azoarcus sp. EbN1]		
21709, 21710	56476267	38	9.00E-10	Azoarcus sp. EbN1	putative peptidase [Bacteroides fragilis YCH46] dbj BAD47513.1 putative peptidase [Bacteroides fragilis YCH46]		
2171, 2172	53712055	43	1.00E-52	Bacteroides fragilis YCH46	related to isochorismate synthase (MenF) [Desulfotalea psychrophila LSw54] emb CAG34983.1 related to isochorismate synthase (MenF) [Desulfotalea psychrophila LSw54]		3.5.1.-
21711, 21712	51244106	36	9.00E-15	Desulfotalea psychrophila LSw54			5.4.99.6

21713, 21714	48854285	35	3.00E-39	Cytophaga hutchinsonii	COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
21715, 21716	57229242	24	2.00E-11	Cryptococcus neoformans var. neoformans JEC21	conserved hypothetical protein [Cryptococcus neoformans var. neoformans JEC21]				2.3.1.51
21717, 21718	29346221	43	4.00E-42	Bacteroides thetaiotaomicron VPI-5482	putative tRNA/rRNA methyltransferase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO75918.1 putative tRNA/rRNA methyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.1.1.-
21719, 21720	24374852	54	7.00E-41	Shewanella oneidensis MR-1	antioxidant, AhpC/TSA family [Shewanella oneidensis MR-1] gb AAN56339.1 antioxidant, AhpC/TSA family [Shewanella oneidensis MR- 1]				1.11.1.-
21725, 21726	32470723	51	4.00E-84	Rhodopirellula baltica SH 1	probable acylaminoacyl-peptidase [Rhodopirellula baltica SH 1] emb CAD71387.1 probable acylaminoacyl-peptidase [Pirellula sp.]				3.4.19.1
21727, 21728	29345713	42	9.00E-44	Bacteroides thetaiotaomicron VPI-5482	putative patatin-like phospholipase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75410.1 putative patatin-like phospholipase [Bacteroides thetaiotaomicron VPI-5482]				3.4.21.-
21729, 21730	42519768	43	1.00E-31	Lactobacillus johnsonii NCC 533	chromosome partitioning protein ParB [Lactobacillus johnsonii NCC 533] gb AAS09664.1 chromosome partitioning protein ParB [Lactobacillus johnsonii NCC 533]				
2173, 2174	48856045	24	1.00E-08	Cytophaga hutchinsonii	hypothetical protein Chut02001277 [Cytophaga hutchinsonii]				
21737, 21738	39997374	32	1.00E-21	Geobacter sulfurreducens PCA	hypothetical protein GSU2276 [Geobacter sulfurreducens PCA] gb AAR35652.1 conserved hypothetical protein [Geobacter sulfurreducens PCA]				
21739, 21740	55246965	65	6.00E-36	Anopheles gambiae str. PEST	ENSANGP000000000220 [Anopheles gambiae str. PEST] ref XP_561052.1 ENSANGP000000000220 [Anopheles gambiae str. PEST]				
21741, 21742	48854452	58	6.00E-30	Cytophaga hutchinsonii	COG0034: Glutamine phosphoribosylpyrophosphate amidotransferase [Cytophaga hutchinsonii]				
21743, 21744	ABJ19039	40	9.00E-14		Desc:Pathogen specific antigen related staphylococcal protein SEQ ID No 288. Org:Staphylococcus sp				3.2.1.17
21745, 21746	53711478	44	1.00E-36	Bacteroides fragilis YCH46	hypothetical protein BF0187 [Bacteroides fragilis YCH46] db BAD46936.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
21749, 21750	16080777	41	4.00E-49	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU37240 [Bacillus subtilis subsp. subtilis str. 168] emb CAA90049.1 unknown, similar to E.coli cardiolipin synthase [Bacillus subtilis] emb CAB15752.1 ywiE [Bacillus subtilis subsp. subtilis str. 168] pir S60089 cardiolipin synthetase homolog ywiE - Bacillus subtilis spiP45860 CLS1_BACSU Probable cardiolipin synthetase 1 (Cardiolipin synthase 1) (CL synthase 1)				2.7.8.-

21757,	48855885	76	1.00E-115	Cytophaga hutchinsonii	COG0209: Ribonucleotide reductase, alpha subunit [Cytophaga hutchinsonii]			1.17.4.1
21758								
21759,	46316555	38	3.00E-07	Burkholderia cepacia R18194	COG1289: Predicted membrane protein [Burkholderia cepacia R18194]			
21760								
21765,	48855808	42	3.00E-12	Cytophaga hutchinsonii	COG0694: Thioredoxin-like proteins and domains [Cytophaga hutchinsonii]			
21766								
21769,	48853783	52	7.00E-42	Cytophaga hutchinsonii	COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii]			2.7.7.7
21770								
2177,				uncultured archaeon				
2178	52550493	45	1.00E-51	GZfos9D8	conserved hypothetical protein [uncultured archaeon GZfos9D8]			2.8.1.6
21771,								
21772	34397936	29	3.00E-14	Porphyromonas gingivalis W83	hypothetical protein PG2030 [Porphyromonas gingivalis W83] ref NP_906097.1 hypothetical protein PG2030 [Porphyromonas gingivalis W83]			
21773,				Symbiobacterium thermophilum IAM 14863	oligopeptide ABC transporter substrate-binding protein [Symbiobacterium thermophilum IAM 14863] dbj BAD39113.1 oligopeptide ABC transporter substrate-binding protein [Symbiobacterium thermophilum IAM 14863]			
21774	51891266	28	1.00E-18	Lactobacillus				
21775,	15212071	31	3.00E-16	helveticus	mevalonate diphosphate decarboxylase [Lactobacillus helveticus]			4.1.1.33
21776								
21779,				Bacteroides fragilis	endopeptidase Clp ATP-binding chain B [Bacteroides fragilis YCH46]			
21780	53712497	52	9.00E-29	YCH46	dbj BAD47955.1 endopeptidase Clp ATP-binding chain B [Bacteroides fragilis YCH46]			
21781,				Trichodesmium				
21782	48890583	30	9.00E-21	erythraeum IMS101	COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101]			
21787,								
21788	21233748	47	2.00E-10	Proteus vulgaris	transposase [Proteus vulgaris] dbj BAB93648.1 transposase [Proteus vulgaris]			
21789,				Bacillus cereus	DNA-binding response regulator [Bacillus cereus G9241] gb JAL16839.1			
21790	47564364	43	1.00E-30	G9241	DNA-binding response regulator [Bacillus cereus G9241]			
				uncultured archaeon				
2179,								
2180	52550493	47	2.00E-58	GZfos9D8	conserved hypothetical protein [uncultured archaeon GZfos9D8]			2.8.1.6
21793,				Desulfotribacterium				
21794	53685139	31	5.00E-13	hafnense DCB-2	hypothetical protein Desu02002249 [Desulfotribacterium hafnense DCB-2]			
21795,				Chromobacterium violaceum ATCC 12472	probable sensory transduction histidine kinase [Chromobacterium violaceum ATCC 12472] ref NP_902929.1 probable sensory transduction histidine kinase [Chromobacterium violaceum ATCC 12472]			2.7.-
21796	34104565	36	4.00E-23	12472				

21797, 21798	27366595	33	2.00E-21	Vibrio vulnificus CMCP6	Response regulator [Vibrio vulnificus CMCP6] ref NP_938705.1 probable response regulator [Vibrio vulnificus YJ016] gb AAO07112.1 Response regulator [Vibrio vulnificus CMCP6] dbj BAC96675.1 probable response regulator [Vibrio vulnificus YJ016]				2.7.3.-
21801, 21802	53715865	53	1.00E-69	Bacteroides fragilis YCH46	leucyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD51323.1 leucyl- tRNA synthetase [Bacteroides fragilis YCH46]				6.1.1.4
21803, 21804	46118176	37	8.00E-13	Crocospaera watsonii WH 8501	COG2207: AraC-type DNA-binding domain-containing proteins				
21805, 21806	27817220	38	2.00E-28	Nostoc sp. ATCC 53789	[Crocospaera watsonii WH 8501] penicillin-binding protein-like protein [Nostoc sp. ATCC 53789]				3.5.2.6
21809, 21810	29349306	35	8.00E-10	Bacteroides thetaiotaomicron VPI-5482	TonB [Bacteroides thetaiotaomicron VPI-5482] gb AAO79003.1 TonB [Bacteroides thetaiotaomicron VPI-5482]				
2181, 2182	18312445	46	4.00E-48	Pyrobaculum aerophilum str. IM2	hypothetical protein PAE1163 [Pyrobaculum aerophilum str. IM2] gb AAL63294.1 conserved hypothetical protein [Pyrobaculum aerophilum str. IM2]				
21811, 21812	52853435	89	1.00E-117	Psychrobacter sp. 273-4	COG2801: Transposase and inactivated derivatives [Psychrobacter sp. 273- 4] ref ZP_00146915.2 COG2801: Transposase and inactivated derivatives [Psychrobacter sp. 273-4]				
21815, 21816	25011383	33	4.00E-08	Streptococcus agalactiae NEM316	hypothetical protein gbs1341 [Streptococcus agalactiae NEM316] emb CAD47000.1 unknown [Streptococcus agalactiae NEM316]				
21817, 21818	AAY2914 6	34	1.00E-34		Desc:Amino acid sequence of a virulence factor encoded by ORF11738. Org:Pseudomonas aeruginosa				
21819, 21820	48853536	40	1.00E-47	Cytophaga hutchinsonii	COG1619: Uncharacterized proteins, homologs of microcin C7 resistance protein MccF [Cytophaga hutchinsonii]				3.4.17.1 3
21821, 21822	28897146	38	5.00E-45	Vibrio parahaemolyticus RIMD 2210633	putative hemolysin [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58635.1 putative hemolysin [Vibrio parahaemolyticus]				
21823, 21824	29345972	70	4.00E-47	Bacteroides thetaiotaomicron VPI-5482	putative ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO75669.1 putative ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482]				1.8.-.-
21825, 21826	48837702	58	3.00E-53	Methanosarcina barkeri str. fusaro	COG1001: Adenine deaminase [Methanosarcina barkeri str. fusaro]				3.5.4.2
21829, 21830	38637719	26	4.00E-10	Cupriavidus necator	hypothetical protein PHG054 [Cupriavidus necator] gb AAP85807.1 hypothetical protein PHG054 [Ralstonia eutropha]				
2183, 2184	15644379	38	1.00E-09	Thermotoga maritima MSB8	hypothetical protein TM1631 [Thermotoga maritima MSB8] gb AAD36698.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir G72229 conserved hypothetical protein - Thermotoga maritima (strain MSB8)				

21833, 21834	48855019	50	1.00E-26	Cytophaga hutchinsonii	COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii]			2.4.1.18 2
21835, 21836	48850961	69	1.00E-40	Novosphingobium aromaticivorans DSM 12444	COG0250: Transcription antiterminator [Novosphingobium aromaticivorans DSM 12444]			
21839, 21840	1710105	55	3.00E-65	Plasmid pWQ799	UDP-N-acetylglucosamine 2-epimerase (UDP-GlcNAc-2-epimerase) gb AAC98403.1 UDP-N-acetylglucosamine 2-epimerase [Plasmid pWQ799]			5.1.3.14
21841, 21842	51246488	36	5.00E-29	Desulfotalea psychrophila Lsv54	hypothetical protein DP2636 [Desulfotalea psychrophila Lsv54] emb CAG37365.1 hypothetical protein [Desulfotalea psychrophila Lsv54]			
21845, 21846	29349812	34	2.00E-35	Bacteroides thetaiotaomicron VPI-5482	putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] gb AAO79509.1 putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482]			
21849, 21850	48853433	45	6.00E-23	Cytophaga hutchinsonii	COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii]			
2185, 2186	15644379	38	1.00E-09	Thermotoga maritima MSB8	hypothetical protein TM1631 [Thermotoga maritima MSB8] gb AAD38698.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir G72229 conserved hypothetical protein - Thermotoga maritima (strain MSB8)			
21855, 21856	53714426	34	1.00E-06	Bacteroides fragilis YCH46	hypothetical protein BF3139 [Bacteroides fragilis YCH46] dbj BAD49884.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
21857, 21858	45657883	39	3.00E-20	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			2.7.3.-
21859, 21860	48854752	54	2.00E-74	Cytophaga hutchinsonii	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii]			2.7.3.-
21861, 21862	29349616	42	3.00E-28	Bacteroides thetaiotaomicron VPI-5482	phosphohydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79313.1 phosphohydrolase [Bacteroides thetaiotaomicron VPI-5482]			
21863, 21864	48855471	29	8.00E-15	Cytophaga hutchinsonii	COG1622: Heme/copper-type cytochrome/quinol oxidases, subunit 2 [Cytophaga hutchinsonii]			
21865, 21866	53711569	33	4.00E-19	Bacteroides fragilis YCH46	hypothetical protein BF0278 [Bacteroides fragilis YCH46] dbj BAD47027.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			

21867,	15616393	31	1.00E-09	Bacillus halodurans C-125	hypothetical protein BH3831 [Bacillus halodurans C-125] dbj BAB07550.1 BH3831 [Bacillus halodurans C-125] pir G84128 hypothetical protein BH3831 [imported] - Bacillus halodurans (strain C-125)				
21868	28209996	40	1.00E-21	Clostridium tetani E88	putative polysaccharide deacetylase [Clostridium tetani E88] gb AAO34877.1 putative polysaccharide deacetylase [Clostridium tetani E88]				
21875,	30023301	32	9.00E-13	Bacillus cereus ATCC 14579	Amylovoran biosynthesis AmsK [Bacillus cereus ATCC 14579] gb AAP12133.1 Amylovoran biosynthesis AmsK [Bacillus cereus ATCC 14579]				
21876	21674545	42	2.00E-20	Chlorobium tepidum TLS	DNA methylase, putative [Chlorobium tepidum TLS] gb AAM72952.1 DNA methylase, putative [Chlorobium tepidum TLS]				
21877,	29345821	47	3.00E-39	Bacteroides thetaiotaomicron VPI-5482	CysQ, sulfite synthesis pathway protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO75518.1 CysQ, sulfite synthesis pathway protein [Bacteroides thetaiotaomicron VPI-5482]				3.1.3.25
21878	48855702	39	9.00E-38	Cytophaga hutchinsonii	COG3279: Response regulator of the LytR/AlgR family [Cytophaga hutchinsonii]				2.7.-.-
21885,	28210229	51	1.00E-41	Clostridium tetani E88	putative mechanosensitive ion-channel [Clostridium tetani E88] gb AAO35110.1 putative mechanosensitive ion-channel [Clostridium tetani E88]				
21886	53712201	61	5.00E-61	Bacteroides fragilis YCH46	phosphohydrolase [Bacteroides fragilis YCH46] dbj BAD47659.1 phosphohydrolase [Bacteroides fragilis YCH46]				
21891,	34397829	35	1.00E-08	Porphyromonas gingivalis W83	hypothetical protein PG1908 [Porphyromonas gingivalis W83] ref NP_905991.1 hypothetical protein PG1908 [Porphyromonas gingivalis W83]				
21892	32474355	51	8.00E-37	Rhodopirellula baltica SH 1	purine nucleoside phosphorylase [Rhodopirellula baltica SH 1] emb CAD74895.1 purine nucleoside phosphorylase [Pirellula sp.]				2.4.2.1
21895,	53714831	46	4.00E-57	Bacteroides fragilis YCH46	putative N-acetylmuramoyl-L-alanine amidase [Bacteroides fragilis YCH46] dbj BAD50289.1 putative N-acetylmuramoyl-L-alanine amidase [Bacteroides fragilis YCH46]				3.5.1.28
21896	37521381	27	6.00E-13	Gloeobacter violaceus PCC 7421	hypothetical protein gl11812 [Gloeobacter violaceus PCC 7421] dbj BAC89753.1 gl11812 [Gloeobacter violaceus PCC 7421]				
21897,	52008037	43	4.00E-52	Thiobacillus denitrificans ATCC 25259	COG0189: Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase) [Thiobacillus denitrificans ATCC 25259]				
21898	46142535	43	7.00E-15	Methanococcus burtonii DSM 6242	COG0381: UDP-N-acetylglucosamine 2-epimerase [Methanococcus burtonii DSM 6242]				5.1.3.14

21907, 21908 21909, 21910	150457 29335922	50 31	1.00E-46 2.00E-21	Streptomyces aureofaciens Bacteroides thetaitaomicron	chloroperoxidase CPO-A2 [Streptomyces aureofaciens] pir S27614 bromide peroxidase (EC 1.11.1.-) BPO1 - Streptomyces aureofaciens sp P29715 BPA2_STRAU Non-haem bromoperoxidase BPO-A2 (Bromide peroxidase) (BPO2) mobilization protein C [Bacteroides thetaiotaomicron] ref NP_818961.1 mobilization protein C [Bacteroides thetaiotaomicron]				1.11.1.1 0
21911, 21912 21913, 21914	29348628 48854577	71 56	2.00E-92 4.00E-39	Bacteroides thetaitaomicron VPI-5482 Cytophaga hutchinsonii	S-adenosylmethionine synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78325.1 S-adenosylmethionine synthetase [Bacteroides thetaitaomicron VPI-5482] sp Q8A2T6 METK_BACTN S- adenosylmethionine synthetase (Methionine adenosyltransferase) (AdoMet synthetase) (MAT) COG0769: UDP-N-acetyluramyl tripeptide synthase [Cytophaga hutchinsonii]	Anopheles gambiae ENSANGP00000000 0138 (ENSANGG0000000 00136) mRNA, partial cds	81	1.00E-29	2.5.1.6
21915, 21916 21921, 21922	29348444 10956806	47 60	2.00E-59 2.00E-66	Bacteroides thetaitaomicron VPI-5482 Riemerella anatipestifer	carboxy-terminal processing protease precursor [Bacteroides thetaitaomicron VPI-5482] gb AAO78141.1 carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482] transposase [Riemerella anatipestifer] gb AAD33096.1 transposase [Riemerella anatipestifer]				3.4.21.-
21923, 21924 21925, 21926 21927, 21928 21929, 21930 2193, 2194	15615497 48855386 48766082 48853984 48864533	32 28 29 43 38	1.00E-10 1.00E-07 7.00E-15 4.00E-37 2.00E-10	Bacillus halodurans C-125 Cytophaga hutchinsonii Rhodospirillum rubrum Cytophaga hutchinsonii Microbulifer degradans 2-40	aryldialkylphosphatase [Bacillus halodurans C-125] db BAB06654.1 aryldialkylphosphatase [Bacillus halodurans C-125] pir G84016 aryldialkylphosphatase BH2935 [Imported] - Bacillus halodurans (strain C- 125) COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii] COG0520: Selenocysteine lyase [Rhodospirillum rubrum] COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii] COG3291: FOG: PKD repeat [Microbulifer degradans 2-40]				
21931, 21932 21935, 21936 21939, 21940	48854966 53714728 48862079	75 67 50	6.00E-93 3.00E-45 6.00E-47	Cytophaga hutchinsonii Bacteroides fragilis YCH46 Microbulifer degradans 2-40	COG0013: Alanyl-tRNA synthetase [Cytophaga hutchinsonii] dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] db BAD50186.1 dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] COG3738: Uncharacterized protein conserved in bacteria [Microbulifer degradans 2-40]	S.pombe chromosome I cosmid c23C11	88	2.00E-09	6.1.1.7 2.4.1.83

21941,	48856049	56	7.00E-59	Cytophaga hutchinsonii	hypothetical protein Chui02001282 [Cytophaga hutchinsonii]				
21942				Dechloromonas aromatica RCB	COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB]				2.7.3.-
21943,	41723898	31	1.00E-24		similar to formate hydrogen-lyase transcriptional activator for fdhF, hyc and hyp operons [Shigella flexneri 2a str. 301] gb AAN44037.1 similar to formate hydrogen-lyase transcriptional activator for fdhF, hyc and hyp operons [Shigella flexneri 2a str. 301]				
21945,	24113820	56	3.00E-63	Shigella flexneri 2a str. 301					
21946				Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS71873.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				2.7.3.-
21947,	45659150	32	3.00E-18	Candida glabrata	unnamed protein product [Candida glabrata] emb CAG61479.1 unnamed protein product [Candida glabrata CBS138]				6.4.1.1
21948	50292171	38	3.00E-14	Bacteroides fragilis YCH46	two-component system response regulator [Bacteroides fragilis YCH46] db BAD51034.1 two-component system response regulator [Bacteroides fragilis YCH46]				
21949,	53715576	37	9.00E-48	uncultured archaeon	capsular polysaccharide biosynthesis protein [uncultured archaeon GZfos18F2]				
21950	52548765	28	2.00E-18	Bacteroides fragilis YCH46	endopeptidase Clp ATP-binding chain B [Bacteroides fragilis YCH46] db BAD47955.1 endopeptidase Clp ATP-binding chain B [Bacteroides fragilis YCH46]				
21951,	53712497	46	8.00E-29	Pseudomonas syringae pv. tomato str. DC3000	ISP11, transposase OrfB [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794264.1 ISP11, transposase OrfB [Pseudomonas syringae pv. tomato str. DC3000]				
21952,	28854897	53	3.00E-28	Petunia integrifolia subsp. inflata	putative fructokinase 2; S2 self-incompatibility locus-linked 3.16 protein [Petunia integrifolia subsp. inflata]				2.7.1.4
21953,	33329200	32	2.00E-14	Streptococcus suis 89/1591	COG0366: Glycosidases [Streptococcus suis 89/1591]				2.4.1.5
21954,	50590978	33	2.00E-27	Pseudomonas syringae	replication protein - Pseudomonas syringae plasmid pPS10 emb CAA41700.1 replication protein [Pseudomonas syringae]				
21955,	95009	31	1.00E-20	Porphyromonas gingivalis W83	trigger factor, putative [Porphyromonas gingivalis W83] ref NP_905027.1 trigger factor, putative [Porphyromonas gingivalis W83]				
21956,	34398861	48	2.00E-27	Bdellovibrio bacteriovorus HD100	predicted exonuclease of the beta-lactamase family [Bdellovibrio bacteriovorus HD100] emb CAE79883.1 predicted exonuclease of the beta-lactamase family [Bdellovibrio bacteriovorus HD100]				
21957,	42523510	64	2.00E-42						

21969, 21970	16332154	53	2.00E-44	Synechocystis sp. PCC 6803	2-hydroxyaciddehydrogenase [Synechocystis sp. PCC 6803] dbj BAA18694.1 2-hydroxyaciddehydrogenase [Synechocystis sp. PCC 6803] pir S76782 D-2-hydroxy-acid dehydrogenase (EC 1.1.99.6) - Synechocystis sp. (strain PCC 6803)				1.1.1.28
2197, 2198	53715576	37	2.00E-40	Bacteroides fragilis YCH46	two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD51034.1 two-component system response regulator [Bacteroides fragilis YCH46]				
21971, 21972	25010929	38	5.00E-28	Streptococcus agalactiae NEM316	hypothetical protein gbs0874 [Streptococcus agalactiae NEM316] emb CAD46518.1 Unknown [Streptococcus agalactiae NEM316] sp Q8E5V5 GLGA_STRA3 Glycogen synthase (Starch [bacterial glycogen] synthase)				2.4.1.21
21973, 21974	53734963	27	1.00E-17	Crocospaera watsonii WH 8501	COG0500: SAM-dependent methyltransferases [Crocospaera watsonii WH 8501]				2.1.1.48
21977, 21978	29349340	57	1.00E-100	Bacteroides thetataoamicon VPI-5482	DNA primase [Bacteroides thetataoamicon VPI-5482] gb AAO79037.1 DNA primase [Bacteroides thetataoamicon VPI-5482]				2.7.7.-
21981, 21982	48854644	47	4.00E-42	Cytophaga hutchinsonii	COG2003: DNA repair proteins [Cytophaga hutchinsonii]				
21983, 21984	53713311	40	2.00E-21	Bacteroides fragilis YCH46	hypothetical protein BF2022 [Bacteroides fragilis YCH46] dbj BAD48769.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				3.4.13.9
21985, 21986	53715627	38	1.00E-24	Bacteroides fragilis YCH46	putative haloacid dehalogenase-like hydrolase [Bacteroides fragilis YCH46] dbj BAD51085.1 putative haloacid dehalogenase-like hydrolase [Bacteroides fragilis YCH46]				
21987, 21988	48854286	36	4.00E-12	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]				

21889, 21990	29144603	54	8.00E-53	Salmonella enterica subsp. enterica serovar Typhi Ty2	Vi polysaccharide biosynthesis protein, UDP-glucose/GDP-mannose dehydrogenase [Salmonella enterica subsp. enterica serovar Typhi ref NP_458740.1 Vi polysaccharide biosynthesis protein, UDP-glucose/GDP- mannose dehydrogenase [Salmonella enterica subsp. enterica serovar Typhi str. CT18] gb AAO71805.1 Vi polysaccharide biosynthesis protein, UDP- glucose/GDP-mannose dehydrogenase [Salmonella enterica subsp. enterica serovar Typhi Ty2] emb CAD06781.1 Vi polysaccharide biosynthesis protein, UDP-glucose/GDP-mannose dehydrogenase [Salmonella enterica subsp. enterica serovar Typhi] emb CAA47991.1 unnamed protein product [Salmonella typhi] pir AH1041 Vi polysaccharide biosynthesis protein, UDP- glucose/ GDP-mannose dehydrogenase (EC 1.1.1.-) [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18) pir B36892 Vi polysaccharide biosynthetic protein VlpA - Salmonella typhi sp Q04972 VIPA_SALT1 Vi polysaccharide biosynthesis protein vipA/viB dbj BAA03192.1 WcdA protein [Salmonella typhi]	1.1.1.-
2199, 2200	48892769	31	2.00E-08	Trichodesmium erythraeum IMS101	COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] two-component system response regulator [Bacteroides fragilis YCH46]	
21991, 21992	53715398	49	4.00E-58	Bacteroides fragilis YCH46	dbj BAD50856.1 two-component system response regulator [Bacteroides fragilis YCH46]	2.7.3.-
21993, 21994	13183744	47	7.00E-23	Pseudomonas aeruginosa	unknown [Pseudomonas aeruginosa]	2.7.7.38
21995, 21996	53714262	29	1.00E-15	Bacteroides fragilis YCH46	putative nucleotide-diphosphate sugar epimerase [Bacteroides fragilis YCH46] dbj BAD49720.1 putative nucleotide-diphosphate sugar epimerase [Bacteroides fragilis YCH46]	
21997, 21998	29348988	36	9.00E-48	Bacteroides thetaiotaomicron VPI-5482	topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482] gb AAO78685.1 topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482]	
21999, 22000	16119697	40	4.00E-25	Agrobacterium tumefaciens str. C58	hypothetical protein AGR_pAT_692 [Agrobacterium tumefaciens str. C58] gb AAK90844.1 AGR_pAT_692p [Agrobacterium tumefaciens str. C58] sp Q8UUK7 DP42_AGR15 DNA polymerase IV 2 (Pol IV 2)	2.7.7.7
22001, 22002	53713347	45	2.00E-42	Bacteroides fragilis YCH46	tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] dbj BAD48805.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]	
22005, 22006	24371966	40	3.00E-38	Shewanella oneidensis MR-1	helicase [Shewanella oneidensis MR-1] gb AAN63453.1 helicase [Shewanella oneidensis MR-1]	
22009, 22010	48782956	37	9.00E-32	Burkholderia fungorum LB400	COG1475: Predicted transcriptional regulators [Burkholderia fungorum LB400]	

22013,	45505171	41	4.00E-17	Homo sapiens	kyphoscoliosis peptidase [Homo sapiens]				
22014					hypothetical protein NMA1791 [Neisseria meningitidis Z2491]				
22019,				Neisseria	emb CAB85017.1 hypothetical protein [Neisseria meningitidis Z2491]				
22020	15794682	42	4.00E-66	meningitidis Z2491	pir E81804 hypothetical protein NMA1791 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)				
22021,				Oryza sativa	phosphodiesterase/alkaline phosphatase D-like protein [Oryza sativa]				
22022	50910003	37	9.00E-28	(japonica cultivar-group)	(japonica cultivar-group)] dbj BAD34083.1 phosphodiesterase/alkaline phosphatase D-like protein [Oryza sativa (japonica cultivar-group)]				
22023,				Wollinella					
22024	34556505	36	7.00E-28	succinogenes DSM 1740	WLAC PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09220.1				2.4.1.-
22025,				Chloroflexus	WLAC PROTEIN [Wollinella succinogenes]				
22026	53794823	41	5.00E-29	aurantiacus	COG1131: ABC-type multidrug transport system, ATPase component [Chloroflexus aurantiacus]				1.8.-.-
22027,				Cytophaga					
22028	48854853	36	2.00E-32	hutchinsonii	COG0345: Pyrroline-5-carboxylate reductase [Cytophaga hutchinsonii]				1.5.1.2
22029,				Chlorobium	UDP-glucose/GDP-mannose dehydrogenase family protein [Chlorobium]				
22030	21673067	44	1.00E-27	tepidum TLS	tepidum TLS] gb AAM71474.1 UDP-glucose/GDP-mannose dehydrogenase family protein [Chlorobium tepidum TLS]				1.1.1.-
22031,				Photobacterium	hypothetical protein PBPR1316 [Photobacterium profundum SS9]				
22032	54308509	48	7.00E-70	profundum SS9	emb CAG19727.1 hypothetical protein [Photobacterium profundum]				
22033,				Cytophaga					
22034	48855611	24	4.00E-08	hutchinsonii	COG3696: Putative silver efflux pump [Cytophaga hutchinsonii]				
22035,				Chromobacterium	conserved hypothetical protein [Chromobacterium violaceum ATCC 12472]				
22036	34101691	52	2.00E-51	violaceum ATCC 12472	ref NP_900051.1 hypothetical protein CV0381 [Chromobacterium violaceum ATCC 12472]				
22037,					phosphoenolpyruvate synthase [Aquifex aeolicus VF5] gb AAC07865.1				
22038	15607086	52	6.00E-78	Aquifex aeolicus VF5	phosphoenolpyruvate synthase [Aquifex aeolicus VF5] pir G70483 pyruvate, water dikinase (EC 2.7.9.2) - Aquifex aeolicus sp O67899 PPSA_AQUAE				2.7.9.2
22039,				Nostoc sp. PCC 7120	Phosphoenolpyruvate synthase (Pyruvate, water dikinase) (PEP synthase)				
22040	17230890	29	4.00E-09	7120	hypothetical protein ali3398 [Nostoc sp. PCC 7120] pir AG2230 hypothetical protein ali3398 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75097.1				
22041,				Cytophaga	ali3398 [Nostoc sp. PCC 7120]				
22042	48853745	33	1.00E-22	hutchinsonii	hypothetical protein Chut02003380 [Cytophaga hutchinsonii]				
22047,				Methanococcus	COG0668: Small-conductance mechanosensitive channel				
22048	53731688	35	6.00E-32	burtonii DSM 6242	[Methanococcus burtonii DSM 6242]				
22049,				Cytophaga	COG2120: Uncharacterized proteins, LmbE homologs [Cytophaga]				
22050	48853718	31	1.00E-35	hutchinsonii	hutchinsonii]				

2205, 2206	34762878	30	7.00E-07	Fusobacterium nucleatum subsp. vincentii ATCC 49256	Transcription antitermination protein nusG [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24529.1 Transcription antitermination protein nusG [Fusobacterium nucleatum subsp. vincentii ATCC 49256]				
22051, 22052	15607112	42	1.00E-25	Aquifex aeolicus VF5	shikimate kinase [Aquifex aeolicus VF5] gb AAC07875.1 shikimate kinase [Aquifex aeolicus VF5] pir A70487 shikimate kinase - Aquifex aeolicus sp O67925 AROK_AQUAE Shikimate kinase (SK)				2.7.1.71
22053, 22054	29348444	50	5.00E-72	Bacteroides thetaiotaomicron VPI-5482	carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO78141.1 carboxy-terminal processing protease precursor [Bacteroides thetaiotaomicron VPI-5482]				3.4.21.-
22057, 22058	48853721	38	1.00E-11	Cytophaga hutchinsonii	hypothetical protein Chut02003580 [Cytophaga hutchinsonii]				
22059, 22060	48856113	45	4.00E-23	Cytophaga hutchinsonii	COG0212: 5-formyltetrahydrofolate cyclo-ligase [Cytophaga hutchinsonii]				6.3.3.2
22061, 22062	29345572	47	3.00E-32	Bacteroides thetaiotaomicron VPI-5482	penicillin-binding protein 1C (PBP-1c) [Bacteroides thetaiotaomicron VPI- 5482] gb AAO75269.1 penicillin-binding protein 1C (PBP-1c) [Bacteroides thetaiotaomicron VPI-5482]				2.4.2.-
22063, 22064	48854895	59	2.00E-35	Cytophaga hutchinsonii	COG0491: Zn-dependent hydrolases, including glyoxylases (Cytophaga hutchinsonii)				
22065, 22066	48855782	26	9.00E-08	Cytophaga hutchinsonii	hypothetical protein Chut02000991 [Cytophaga hutchinsonii]				
22067, 22068	48856069	71	2.00E-32	Cytophaga hutchinsonii	COG3093: Plasmid maintenance system antidote protein [Cytophaga hutchinsonii]				
2207, 22071,	48856416	40	7.00E-51	Cytophaga hutchinsonii	hypothetical protein Chut02000134 [Cytophaga hutchinsonii]				
22072, 22073,	48856308	54	2.00E-58	Cytophaga hutchinsonii	COG0602: Organic radical activating enzymes [Cytophaga hutchinsonii]				
22074, 22075,	2281663	60	8.00E-30	Flavobacterium johnsoniae	gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding motility protein [Imported] - Flavobacterium johnsoniae				
22076	AAU3497	46	5.00E-53		Desc:Enterococcus faecalis cellular proliferation protein #265. Org:Enterococcus faecalis				2.1.1.61
22077, 22078	52007397	52	2.00E-42	Thiobacillus denitrificans ATCC 25259	COG1752: Predicted esterase of the alpha-beta hydrolase superfamily [Thiobacillus denitrificans ATCC 25259]				3.4.21.-
22079, 22080	31194819	54	3.00E-62	Anopheles gambiae	ENSANGP00000002020 [Anopheles gambiae]				
22085, 22086	26370741	32	5.00E-10	Mus musculus	unnamed protein product [Mus musculus]				
22087, 22088	21233748	46	2.00E-58	Proteus vulgaris	transposase [Proteus vulgaris] db BAB93648.1 transposase [Proteus vulgaris]				

22089, 22090	53714594	44	1.00E-37	Bacteroides fragilis YCH46	LacI family transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD50052.1 LacI family transcriptional regulator [Bacteroides fragilis YCH46]			
2209, 2210	48856118	50	2.00E-47	Cytophaga hutchinsonii	COG0242: N-formylmethionyl-tRNA deformylase [Cytophaga hutchinsonii] hypothetical protein PBPRB0095 [Photobacterium profundum SS9]			3.5.1.88
22091, 22092	54301775	45	3.00E-07	Photobacterium profundum SS9	emb CAG21968.1 hypothetical protein [Photobacterium profundum] Nin 221 (pept unknown;221) [Bacteriophage lambda] pir Q1BP1.L multiple specificity phosphoprotein phosphatase (EC 3.1.3.-) - phage lambda ref NP_040641.1 Nin protein [Bacteriophage lambda] sp P03772 PP_LAMBD Serine/threonine protein phosphatase transcription anti-termination protein [Bacteroides fragilis YCH46]	Bacteriophage lambda, complete genome	99	0 3.1.3.16
22093, 22094	215160	98	1.00E-108	bacteriophage lambda	dbj BAD50940.1 transcription anti-termination protein [Bacteroides fragilis YCH46]			
22095, 22096	53715482	36	1.00E-23	Bacteroides fragilis YCH46	putative peptidase [Bacteroides fragilis YCH46] dbj BAD47513.1 putative peptidase [Bacteroides fragilis YCH46]			3.5.1.-
22099, 22100	53712055	46	1.00E-55	Bacteroides fragilis YCH46	two-component system sensor histidine kinase [Bacteroides thetataoimicron VPI-5482] gb AAO76096.1 two-component system sensor histidine kinase [Bacteroides thetataoimicron VPI-5482]			2.7.3.-
22101, 22102	20088950	37	1.00E-21	Methanosarcina acetivorans C2A	hypothetical protein MA0051 [Methanosarcina acetivorans C2A] gb AAM03505.1 predicted protein [Methanosarcina acetivorans str. C2A]			
22103, 22104	11499143	39	3.00E-24	Archaeoglobus fulgidus DSM 4304	hypothetical protein AF1548 [Archaeoglobus fulgidus DSM 4304] gb AAB89701.1 A. fulgidus predicted coding region AF1548 [Archaeoglobus fulgidus DSM 4304] pir C69443 hypothetical protein AF1548 - Archaeoglobus fulgidus sp O28724 YF48_ARCFU Hypothetical protein AF1548			
22105, 22106	45657858	35	4.00E-15	Leptospira interrogans serovar Copenhageni str. Ficruz L1-130	hypothetical protein LIC12005 [Leptospira interrogans serovar Copenhageni str. Ficruz L1-130] ref NP_712075.1 hypothetical protein LA1894 [Leptospira interrogans serovar Lai str. 56601] gb AAN49093.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS70581.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Ficruz L1-130]			
22109, 22110	32476521	44	6.00E-27	Rhodopirellula baltica SH 1	iduronate-2-sulfatase [Rhodopirellula baltica SH 1] emb CAD78972.1 iduronate-2-sulfatase [Pirellula sp.]			3.1.6.6
22111, 22112	3093287	31	3.00E-18	Bacillus sphaericus	heat shock protein [Bacillus sphaericus] sp O69268 DNAK_BACSH Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70)			3.6.1.3
22117, 22118	48854288	42	6.00E-32	Cytophaga hutchinsonii	COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii]			

22123,	AAV3440	35	8.00E-43		Desc: Porphyromonas gingivalis protein PG67. Org: Porphyromonas gingivalis				
22124	3				RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO77291.1 RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482]				
22125,				Bacteroides thetaiotaomicron VPI-5482					
22126	29347594	44	1.00E-29						
22127,				Psychrobacter sp.					
22128	41690073	93	2.00E-89	273-4	COG0388: Predicted amidohydrolase [Psychrobacter sp. 273-4]				
22129,									
22130	53711667	59	4.00E-30	Bacteroides fragilis YCH46	hypothetical protein BF0376 [Bacteroides fragilis YCH46] db BAD47125.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
2213,									
2214	21674468	74	4.00E-43	Chlorobium tepidum TLS	leucyl-tRNA synthetase [Chlorobium tepidum TLS] gb AAM72875.1 leucyl-tRNA synthetase [Chlorobium tepidum TLS] sp Q8KBY2 SYL_CHL TE Leucyl-tRNA synthetase (Leucine-tRNA ligase) (LeuRS)				6.1.1.4
22131,				Cytophaga hutchinsonii					
22132	48854958	69	6.00E-52		COG1432: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
22135,				Haemophilus influenzae 86-028NP	COG2865: Predicted transcriptional regulator containing an HTH domain and an uncharacterized domain shared with the mammalian protein Schlaifen [Haemophilus influenzae 86-028NP]				
22136	48868353	54	7.00E-36						
22137,									
22138	53712434	58	3.00E-71	Bacteroides fragilis YCH46	type III restriction-modification system restriction subunit [Bacteroides fragilis YCH46] db BAD47892.1 type III restriction-modification system restriction subunit [Bacteroides fragilis YCH46]				
22139,				Cytophaga hutchinsonii	COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cytophaga hutchinsonii]				
22140	48853613	27	7.00E-16		COG0147: Anthranilate/para-aminobenzoate synthetases component I [Cytophaga hutchinsonii]				
22141,				Cytophaga hutchinsonii					
22142	48856398	53	1.00E-39		hypothetical protein ml5269 [Mesorhizobium loti MAFF303099]				4.1.3.-
22143,				Mesorhizobium loti MAFF303099	db BAB51748.1 ml5269 [Mesorhizobium loti MAFF303099]				
22144	13474394	47	6.00E-16		endopeptidase Clp ATP-binding chain B [Bacteroides thetaiotaomicron VPI-5482] sp Q89YY3 CLPB_BACTN Chaperone clpB gb AAO79702.1 endopeptidase Clp ATP-binding chain B [Bacteroides thetaiotaomicron VPI-5482]				
22145,									
22146	29350005	51	2.00E-41	Bacteroides thetaiotaomicron VPI-5482	S-adenosylmethionine synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78325.1 S-adenosylmethionine synthetase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A2T6 METK_BACTN S-adenosylmethionine synthetase (Methionine adenosyltransferase) (AdoMet synthetase) (MAT)				
22147,									
22148	29348628	66	2.00E-73	Bacteroides thetaiotaomicron VPI-5482	COG0389: Nucleotidyltransferase/DNA polymerase involved in DNA repair [Cytophaga hutchinsonii]				
22149,									
22150	48853782	57	3.00E-57	Cytophaga hutchinsonii					2.7.7.7

2215,	23098114	64	4.00E-42	Oceanobacillus ihayensis HTE831	hypothetical protein OB0659 [Oceanobacillus ihayensis HTE831] dbj BAC12615.1 hypothetical protein [Oceanobacillus ihayensis HTE831]			
2216					putative outer membrane protein [Bacteroides fragilis YCH46] dbj BAD48633.1 putative outer membrane protein [Bacteroides fragilis YCH46]			
22151,	53713175	31	2.00E-18	Bacteroides fragilis YCH46				
22152								
22153,	52853887	87	1.00E-122	Psychrobacter sp. 273-4	COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Psychrobacter sp. 273-4]			
22154								
22155,				Geobacter sulfurreducens	nucleoside diphosphate kinase regulator protein, putative [Geobacter sulfurreducens PCA] gb AAR34062.1 nucleoside diphosphate kinase regulator protein, putative [Geobacter sulfurreducens PCA]			
22156	39995838	34	2.00E-13	PCA				
22157,				Geobacter metallireducens GS-	COG3863: Uncharacterized distant relative of cell wall-associated hydrolases [Geobacter metallireducens GS-15]			
22158	48846570	26	1.00E-17	15				
22159,				Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]			
22160	48855258	36	8.00E-17					
22161,				Bacteroides thetataoiaomicon	hypothetical protein BT0909 [Bacteroides thetataoiaomicon VPI-5482] gb AAO76016.1 conserved hypothetical protein [Bacteroides thetataoiaomicon VPI-5482]			
22162	29346319	50	2.00E-45	VPI-5482				
22167,				Cytophaga hutchinsonii				
22168	48855120	48	5.00E-22		COG0495: Leucyl-tRNA synthetase [Cytophaga hutchinsonii]			6.1.1.4
22169,				Plasmodium yoelii				
22170	23479863	25	7.00E-07	yoelii	CCAAT-box DNA binding protein subunit B [Plasmodium yoelii yoelii] putative DNA mismatch repair protein [Streptomyces avermitilis MA-4680] dbj BAC75377.1 putative DNA mismatch repair protein [Streptomyces avermitilis]			
2217,				Streptomyces avermitilis MA-4680				
2218	29826536	25	3.00E-13					
22171,				Anopheles				
22172	31195649	48	5.00E-12	gambiae	ENSANGP00000000282 [Anopheles gambiae]			
22175,				Cytophaga hutchinsonii	COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases [Cytophaga hutchinsonii]			
22176	48855752	25	2.00E-17					
22177,				Bacteroides fragilis YCH46	valyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD47800.1 valyl-tRNA synthetase [Bacteroides fragilis YCH46]			6.1.1.9
22178	53712342	65	1.00E-111					
22179,				Cytophaga hutchinsonii	COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii]			2.7.3.-
22180	48855703	31	2.00E-29					
22183,				Bacteroides thetataoiaomicon	hypothetical protein BT2211 [Bacteroides thetataoiaomicon VPI-5482] gb AAO77318.1 conserved hypothetical protein [Bacteroides thetataoiaomicon VPI-5482]			
22184	29347621	52	2.00E-62	VPI-5482				
22185,				Bdellovibrio bacteriovorus	transcriptional regulator, LysR family [Bdellovibrio bacteriovorus HD100] emb CAE80411.1 transcriptional regulator, LysR family [Bdellovibrio bacteriovorus HD100]			
22186	42524039	41	7.00E-34	HD100				

22187,	48853606	39	2.00E-32	Cytophaga hutchinsonii	COG0497: ATPase involved in DNA repair [Cytophaga hutchinsonii]				
22188					much-desulfating sulfatase (N-acetylglucosamine-6-sulfatase)				
22189,				Rhodopirellula	[Rhodopirellula baltica SH 1] emb[CAD71852.1] much-desulfating sulfatase				
22190	32471182	63	3.00E-40	baltica SH 1	(N-acetylglucosamine-6-sulfatase) [Pirellula sp.]				3.1.6.4
22191,				Thermococcus	geranylgeranyl hydrogenase [Thermococcus kodakaraensis]				
22192	57159347	38	3.00E-12	kodakaraensis	ref YP_183501.1 geranylgeranyl hydrogenase [Thermococcus kodakaraensis]				
22193,				Microbulbifer					
22194	48863666	32	4.00E-07	degradans 2-40	COG3428: Predicted membrane protein [Microbulbifer degradans 2-40]				
22199,				Bacteroides fragilis	adenylosuccinate lyase [Bacteroides fragilis YCH46]				
22200	53715302	66	3.00E-72	YCH46	adenylosuccinate lyase [Bacteroides fragilis YCH46]				4.3.2.2
22201,				Bacteroides fragilis	putative chloride channel protein [Bacteroides fragilis YCH46]				
22202	53715188	49	3.00E-37	YCH46	dbj BAD50846.1 putative chloride channel protein [Bacteroides fragilis YCH46]				
22203,				Cytophaga	COG0389: Nucleotidyltransferase/DNA polymerase involved in DNA repair				
22204	48853782	52	3.00E-59	hutchinsonii	[Cytophaga hutchinsonii]				2.7.7.7
22207,				Porphyromonas	type I restriction-modification system, M subunit, putative [Porphyromonas				
22208	34397452	32	4.00E-22	gingivalis W83	gingivalis W83] ref NP_905615.1 type I restriction-modification system, M				2.1.1.72
22209,				Bacteroides	subunit, putative [Porphyromonas gingivalis W83]				
22210	29349518	60	1.00E-33	thetataoimicron	putative pectinesterase precursor [Bacteroides thetaiotaomicon VPI-5482]				
22211,				Porphyromonas	thetataoimicron VPI-5482]				
22212	34396714	40	1.00E-38	gingivalis W83	htrA protein [Porphyromonas gingivalis W83] ref NP_904880.1 htrA protein				3.4.21.-
22215,				Desulfotalea	related to 5' to 3' DNA helicase [Desulfotalea psychrophila LSv54]				
22216	51245839	37	3.00E-26	psychrophila LSv54	emb CAG36716.1 related to 5' to 3' DNA helicase [Desulfotalea psychrophila LSv54]				3.6.1.-
22217,				Bacteroides	DNA repair and recombination protein, putative helicase [Bacteroides				
22218	29346131	52	1.00E-76	thetataoimicron	thetataoimicron VPI-5482] gb AAO75828.1 DNA repair and recombination				
22219,				Cytophaga	protein, putative helicase [Bacteroides thetaiotaomicon VPI-5482]				
22220	48856044	58	2.00E-48	hutchinsonii	COG2908: Uncharacterized protein conserved in bacteria [Cytophaga				3.6.1.-
22221,				Bacteroides	hutchinsonii]				
22222	29346304	55	5.00E-48	thetataoimicron	DNA ligase [Bacteroides thetaiotaomicon VPI-5482] gb AAO76001.1 DNA				6.5.1.2
22223,				Bacteroides	ligase [Bacteroides thetaiotaomicon VPI-5482]				
22224	29348248	46	7.00E-18	thetataoimicron	ribosome-binding factor A [Bacteroides thetaiotaomicon VPI-5482]				
					gb AAO77945.1 ribosome-binding factor A [Bacteroides thetaiotaomicon				
					VPI-5482]				

22225,	53715757	32	1.00E-14	Bacteroides fragilis YCH46	hypothetical protein BF4478 [Bacteroides fragilis YCH46] dbj BAD51215.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
22226,	42630866	27	1.00E-09	Haemophilus influenzae R2866	COG0457: FOG: TPR repeat [Haemophilus influenzae R2866]				
22227,	42630866	27	1.00E-09	Bdellovibrio bacteriovorus HD100	hypothetical protein Bd3537 [Bdellovibrio bacteriovorus HD100]				
22228,	42524889	54	4.00E-28	Bdellovibrio bacteriovorus HD100	emb CAE78328.1 unnamed protein product [Bdellovibrio bacteriovorus HD100]				1.14.16.1
22229,	48854664	44	1.00E-58	Cytophaga hutchinsonii	COG2217: Cation transport ATPase [Cytophaga hutchinsonii]				3.6.3.4
22230,	48856095	34	2.00E-43	Cytophaga hutchinsonii	hypothetical protein Chut02001333 [Cytophaga hutchinsonii]				6.4.---
22231,	48855337	53	2.00E-61	Cytophaga hutchinsonii	COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii]				
22232,	29346568	33	4.00E-26	Bacteroides thetaiotaomicron VPI-5482	Na+-translocating NADH-quinone reductase subunit [Bacteroides thetaiotaomicron VPI-5482]				1.---
22233,	48856683	29	1.00E-22	Cytophaga hutchinsonii	COG4258: Predicted exporter [Cytophaga hutchinsonii]				
22234,	53712402	57	3.00E-59	Bacteroides fragilis YCH46	putative undecaprenyl-phosphate glycosyl-1-phosphate transferase [Bacteroides fragilis YCH46] gb AAD56746.1 putative undecaprenyl-phosphate glycosyl-1-phosphate transferase [Bacteroides fragilis] dbj BAD47860.1 putative undecaprenyl-phosphate glycosyl-1-phosphate transferase [Bacteroides fragilis YCH46]	Campylobacter jejuni waaC, galE, wia[B,C,D,E,F,G,H,I],K,L,M, cheY genes and orf1	85	7.00E-09	2.4.---
22235,	24379180	27	6.00E-15	Streptococcus mutans UA159	putative phosphoenolpyruvate carboxylase [Streptococcus mutans UA159] sp Q8DV10 CAPP_STRMU Phosphoenolpyruvate carboxylase (PEPC)				4.1.1.31
22236,	48854361	61	1.00E-93	Cytophaga hutchinsonii	COG0060: Isoleucyl-tRNA synthetase [Cytophaga hutchinsonii]				6.1.1.5
22237,	39997281	43	1.00E-65	Geobacter sulfurreducens PCA	fic family protein [Geobacter sulfurreducens PCA] gb AAR35559.1 fic family protein [Geobacter sulfurreducens PCA]				
22238,	53712139	40	1.00E-23	Bacteroides fragilis YCH46	mannan endo-1,4-beta-mannosidase [Bacteroides fragilis YCH46] dbj BAD47597.1 mannan endo-1,4-beta-mannosidase [Bacteroides fragilis YCH46]				
22239,									
22240,									
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22255,									
22256,	53713904	72	7.00E-98	Bacteroides fragilis YCH46	exonuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 exonuclease ABC subunit A [Bacteroides fragilis YCH46]	Bacillus cereus ATCC 14579 section 17 of 18 of the complete genome	93	9.00E-09	

22261, 22262	56460133	47	3.00E-49	Idiomarina loihlensis L2TR	Predicted extracellular metal-dependent peptidase [Idiomarina loihlensis L2TR] gb AAV81865.1 Predicted extracellular metal-dependent peptidase				
22263, 22264	9929259	43	3.00E-39	Lactobacillus reuteri	cystathionine beta-lyase [Lactobacillus reuteri]	Desc:Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1078.	86	4.00E-07	4.2.99.9
22269, 22270	30249527	50	1.00E-27	Nitrosomonas europaea ATCC 19718	putative transposase [Nitrosomonas europaea ATCC 19718] emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718]				
22273, 22274	27367704	44	1.00E-33	Vibrio vulnificus CMCP6	rRNA methylases [Vibrio vulnificus CMCP6] gb AAO08221.1 rRNA methylases [Vibrio vulnificus CMCP6]				2.1.1.-
22275, 22276	48854545	53	3.00E-62	Cytophaga hutchinsonii	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Cytophaga hutchinsonii]				2.1.1.-
22277, 22278	15896798	45	5.00E-48	Clostridium acetobutylicum ATCC 824	Mismatch repair protein MutS-like ATPase [Clostridium acetobutylicum ATCC 824] gb AAK81487.1 Mismatch repair protein MutS-like ATPase [Clostridium acetobutylicum ATCC 824] pir D97337 mismatch repair protein MutS-like ATPase [imported] - Clostridium acetobutylicum				
22279, 22280	28900414	33	3.00E-36	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VPA0559 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61902.1 conserved hypothetical protein [Vibrio parahaemolyticus]				
22281, 22282	48853718	30	3.00E-25	Cytophaga hutchinsonii	COG2120: Uncharacterized proteins, LmbE homologs [Cytophaga hutchinsonii]				
22285, 22286	34556624	50	2.00E-48	Wolinella succinogenes DSM 1740	[SOLEUCYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE09339.1 [SOLEUCYL-TRNA SYNTHETASE [Wolinella succinogenes]				6.1.1.5
22287, 22288	34558001	41	4.00E-17	Wolinella succinogenes DSM 1740	hypothetical protein WS1689 [Wolinella succinogenes DSM 1740] emb CAE10716.1 conserved hypothetical protein [Wolinella succinogenes]				
22289, 22290	27367083	20	2.00E-07	Vibrio vulnificus CMCP6	hypothetical protein VV20658 [Vibrio vulnificus CMCP6] gb AAO07600.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6]				
22295, 22296	48854535	53	5.00E-53	Cytophaga hutchinsonii	COG1674: DNA segregation ATPase FtsK/SpoIIIE and related proteins [Cytophaga hutchinsonii]				
22297, 22298	50255830	28	8.00E-16	Cryptococcus neoformans var. neoformans B-3501A	hypothetical protein CNBJ2030 [Cryptococcus neoformans var. neoformans B-3501A]				4.1.3.6

22299, 22300	34913154	25	1.00E-10	Oryza sativa (japonica cultivar- group)	putative oxidoreductase, FAD-binding [Oryza sativa (japonica cultivar- group)] dbj BAC07074.1 putative oxidoreductase, FAD-binding [Oryza sativa (japonica cultivar-group)]				
22301, 22302	54302756	39	4.00E-13	Photobacterium profundum SS9	hypothetical protein PPRB1077 [Photobacterium profundum SS9] emb CAG22949.1 conserved hypothetical protein [Photobacterium profundum]				
22303, 22304	33469585	43	3.00E-24	Alcaligenes faecalis	hypothetical protein [Alcaligenes faecalis]				
22305, 22306	54308287	46	4.00E-51	Photobacterium profundum SS9	putative signal transduction protein containing EAL and modified HD-GYP domains [Photobacterium profundum SS9] emb CAG19505.1 putative signal transduction protein containing EAL and modified HD-GYP domains [Photobacterium profundum]				
22307, 22308	53714565	28	4.00E-18	Bacteroides fragilis YCH46	hypothetical protein BF3279 [Bacteroides fragilis YCH46] dbj BAD50023.1 hypothetical protein [Bacteroides fragilis YCH46]				
22309, 22310	17231272	25	2.00E-10	Nostoc sp. PCC 7120	hypothetical protein all3780 [Nostoc sp. PCC 7120] pir AE2278 hypothetical protein all3780 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75479.1 all3780 [Nostoc sp. PCC 7120]				
22311, 22312	53712193	39	4.00E-15	Bacteroides fragilis YCH46	hypothetical protein BF0900 [Bacteroides fragilis YCH46] dbj BAD47651.1 hypothetical protein [Bacteroides fragilis YCH46]				2.7.3.-
22313, 22314	39935801	32	2.00E-11	Rhodopseudomonas palustris CGA009	possible epoxide hydrolase-related protein [Rhodopseudomonas palustris CGA009] emb CAE28176.1 possible epoxide hydrolase-related protein [Rhodopseudomonas palustris CGA009]				
22317, 22318	44004406	34	5.00E-36	Bacillus cereus ATCC 10987	transposase, IS605 OrfB family [Bacillus cereus ATCC 10987] gb AAAS44917.1 transposase, IS605 OrfB family [Bacillus cereus ATCC 10987]				
22319, 22320	53714063	34	2.00E-10	Bacteroides fragilis YCH46	hypothetical protein BF2771 [Bacteroides fragilis YCH46] dbj BAD49521.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
22321, 22322	ABP6083 8	36	1.00E-16		Desc:Treponema pallidum thioredoxin-like protein SEQ ID NO:187. Org: Treponema pallidum				
22323, 22324	31790565	59	8.00E-70	marine bacterium P99-3	phytoene desaturase [marine bacterium P99-3]				
22325, 22326	29346223	27	6.00E-18	Bacteroides thetaiotaomicron VPI-5482	TonB [Bacteroides thetaiotaomicron VPI-5482] gb AAO75920.1 TonB [Bacteroides thetaiotaomicron VPI-5482]				
22327, 22328	48854785	40	4.00E-46	Cytophaga hutchinsonii	COG0513: Superfamily II DNA and RNA helicases [Cytophaga hutchinsonii]				2.7.7.-
22329, 22330	49081478	31	1.00E-16	synthetic construct	PA1776 [synthetic construct]				

2233, 2234	18977094	57	3.00E-56	Pyrococcus furius DSM 3638	alkyl hydroperoxide reductase subunit c [Pyrococcus furiosus DSM 3638] gb AAL80846.1 alkyl hydroperoxide reductase subunit c [Pyrococcus furiosus DSM 3638]				1,6,4,-
22331, 22332	37528152	77	1.00E-111	Photobacterium luminescens subsp. laumondii TTO1	Type I site-specific deoxyribonuclease HsdR [Photobacterium luminescens subsp. laumondii TTO1] emb CAE16694.1 Type I site-specific deoxyribonuclease HsdR [Photobacterium luminescens subsp. laumondii TTO1]	Escherichia coli prfB, prfC and prfD genes	80	2.00E-40	3.1.21.3
22333, 22334	29347621	47	1.00E-25	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT2211 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77318.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
22337, 22338	48856102	39	1.00E-28	Cytophaga hutchinsonii	COG2353: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
22341, 22342	29349390	50	4.00E-45	Bacteroides thetaiotaomicron VPI-5482	ATP-dependent exoDNase (exonuclease V), alpha subunit - helicase superfamily I member [Bacteroides thetaiotaomicron VPI-5482] gb AAO79087.1 ATP-dependent exoDNase (exonuclease V), alpha subunit-helicase superfamily I member [Bacteroides thetaiotaomicron VPI-5482]				3.1.11.5
22343, 22344	54308172	52	1.00E-59	Photobacterium profundum SS9	putative transposase [Photobacterium profundum SS9]				
22345, 22346	53715189	47	5.00E-45	Bacteroides fragilis YCH46	putative translation factor [Bacteroides fragilis YCH46] dbj BAD50647.1 putative translation factor [Bacteroides fragilis YCH46]				
22349, 22350	14252939	40	3.00E-23	Escherichia coli	hypothetical protein [Escherichia coli]				
2235, 2236	15669750	44	1.00E-56	Methanocaldococcus jannaschii DSM 2661	aspartyl-tRNA synthetase (aspS) [Methanocaldococcus jannaschii DSM 2661] gb AAB99575.1 aspartyl-tRNA synthetase (aspS) [Methanocaldococcus jannaschii DSM 2661] pir B64494 aspartate-tRNA ligase (EC 6.1.1.12) - Methanocaldococcus jannaschii sp Q58950 SYD_METJA Aspartyl-tRNA synthetase (Aspartate-tRNA ligase) (AspRS)				6.1.1.12
22351, 22352	52549170	42	2.00E-48	uncultured archaeon GZfos26B2	two-component sensor histidine kinase [uncultured archaeon GZfos26B2] putative N-acyl-D-glucosamine 2-epimerase [Bacteroides fragilis YCH46]				2.7.3.-
22353, 22354	53712142	42	3.00E-38	Bacteroides fragilis YCH46	putative N-acyl-D-glucosamine 2-epimerase [Bacteroides fragilis YCH46]				2.7.7.22
22357, 22358	57241353	36	3.00E-14	Campylobacter lari RM2100	peptide ABC transporter, peptide-binding protein, putative [Campylobacter lari RM2100] protein, putative [Campylobacter lari RM2100]				
22359, 22360	29349895	43	6.00E-16	Bacteroides thetaiotaomicron VPI-5482	putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79592.1 putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicron VPI-5482]				

22361,	34397312	28	2.00E-10	Porphyromonas gingivalis W83	hypothetical protein PG1302 [Porphyromonas gingivalis W83]				
22362,				Porphyromonas gingivalis W83	ref NP_005476.1 hypothetical protein PG1302 [Porphyromonas gingivalis W83]				
22365,	48854193	37	1.00E-26	Cytophaga hutchinsonii	COG0451: Nucleoside-diphosphate-sugar epimerases [Cytophaga hutchinsonii]				1.1.1.21 ₉
22366									
22367,				Bacteroides fragilis YCH46	putative UDP-galactose 4-epimerase [Bacteroides fragilis YCH46]				
22368	53712842	47	1.00E-57	Bacteroides fragilis YCH46	dbj BAD48300.1 putative UDP-galactose 4-epimerase [Bacteroides fragilis YCH46]				5.1.3.-
22369,				Bacteroides fragilis YCH46	DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46]				
22370	53715439	59	3.00E-43	Bacteroides fragilis YCH46	dbj BAD50897.1 DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46]				2.7.7.6
2237,									
2238	21674733	33	4.00E-18	Chlorobium tepidum TLS	cysteine synthase/cystathionine beta-synthase family protein [Chlorobium tepidum TLS] gb AAM73140.1 cysteine synthase/cystathionine beta-synthase family protein [Chlorobium tepidum TLS]				4.2.1.22
22373,				Cytophaga hutchinsonii	COG0764: 3-hydroxymyristoyl-3-hydroxydecanoyl-(acyl carrier protein) dehydratases [Cytophaga hutchinsonii]				
22374	48853960	26	4.00E-17	Cytophaga hutchinsonii					
22375,				Cytophaga hutchinsonii	hypothetical protein Chut2002377 [Cytophaga hutchinsonii]				
22376	48854708	23	8.00E-15	Cytophaga hutchinsonii					
22377,				Nostoc punctiforme PCC 73102	COG0330: Membrane protease subunits, stomatin/prohibitin homologs [Nostoc punctiforme PCC 73102]				
22378	53688447	27	7.00E-19	Nostoc punctiforme PCC 73102					
22379,				Leptospira interrogans serovar Copenhageni str.	hypothetical protein LIC10638 [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130] gb AAS69259.1 conserved hypothetical protein				
22380	45656536	33	1.00E-24	Fio Cruz L1-130	[Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130] Likely secreted protein containing plastocyanin domain [Idiomarina loihiensis L2TR] gb AAV82057.1 Likely secreted protein containing plastocyanin domain [Idiomarina loihiensis L2TR]				
22381,				Idiomarina loihiensis L2TR	ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO78914.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482]				
22382	56460325	52	2.00E-30	Bacteroides thetaiotaomicron VPI-5482	deoxyribodipyrimidine photolyase, putative [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_231036.1 deoxyribodipyrimidine photolyase, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir A82205 probable deoxyribodipyrimidine photolyase VC1392 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				4.1.99.3
22385,				Vibrio cholerae O1 biovar eltor str.	hypothetical protein VPA1268 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62611.1 hypothetical protein [Vibrio parahaemolyticus]				
22386	29349217	49	9.00E-44	Vibrio cholerae O1 biovar eltor str. N16961					
22387,				Vibrio cholerae O1 biovar eltor str.					
22388	9655888	48	7.00E-60	Vibrio cholerae O1 biovar eltor str. N16961					
22389,				Vibrio parahaemolyticus RIMD 2210633					
22390	28901123	45	9.00E-38	Vibrio parahaemolyticus RIMD 2210633					

2239,	48856049	45	1.00E-31	Cytophaga hutchinsonii	hypothetical protein Chut02001282 [Cytophaga hutchinsonii]			
2240								
22391,	48855674	44	3.00E-45	Cytophaga hutchinsonii	hypothetical protein Chut02000868 [Cytophaga hutchinsonii]			
22392					COG2804: Type II secretory pathway, ATPase PufE/Tfp pilus assembly pathway, ATPase PilB [Cytophaga hutchinsonii]			
22393,	48855356	66	7.00E-13	Cytophaga hutchinsonii				
22394								
22395,	48855358	57	4.00E-38	Cytophaga hutchinsonii	hypothetical protein Chut02001689 [Cytophaga hutchinsonii]			
22396					COG1280: Putative threonine efflux protein [Pseudomonas fluorescens PfO-1]			
22403,	48730285	54	7.00E-59	Pseudomonas fluorescens PfO-1				
22404								
22407,	45516274	31	5.00E-11	Ralstonia eutropha JMP134	COG1335: Amidases related to nicotinamidase [Ralstonia eutropha JMP134]			
22408					COG3228: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
22409,	48855515	35	2.00E-11	Cytophaga hutchinsonii				
22410								
22411,				Vibrio cholerae O1	hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961]			
22412	9654639	45	2.00E-53	N16961	ref NP_229888.1 hypothetical protein VC0231 [Vibrio cholerae O1 biovar eltor str. N16961] pir J82349 hypothetical protein VC0231 [imported] - Vibrio cholerae (strain N16961 serogroup O1)			
22413,				Cytophaga hutchinsonii				
22414	48853635	57	5.00E-30	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-
22415,	31194159	48	4.00E-18	Anopheles gambiae				
22416					ENSANGP0000000346 [Anopheles gambiae]			
22417,				Bacteroides thetaiotaomicron	topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482]			
22418	29348988	46	1.00E-57	VPI-5482	gb AAO78685.1 topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482]			
22421,				Chlorobium tepidum TLS	hydrolase, alpha/beta hydrolase fold family [Chlorobium tepidum TLS]			
22422	21674076	60	6.00E-62	Chlorobium tepidum TLS	gb AAO72483.1 hydrolase, alpha/beta hydrolase fold family [Chlorobium tepidum TLS]			3.1.1.1
22423,				Bacteroides fragilis	seryl-tRNA synthetase [Bacteroides fragilis YCH46]			
22424	53712299	38	8.00E-16	YCH46	tRNA synthetase [Bacteroides fragilis YCH46]			6.1.1.11
22425,				Pseudomonas aeruginosa	unknown [Pseudomonas aeruginosa]			
22426	13183744	54	1.00E-44	aeruginosa				2.7.7.38
22427,				Cytophaga hutchinsonii				
22428	48855949	47	2.00E-07	Cytophaga hutchinsonii	hypothetical protein Chut02001173 [Cytophaga hutchinsonii]			
2243,				Bacteroides thetaiotaomicron	30S ribosomal protein S1 [Bacteroides thetaiotaomicron VPI-5482]			
2244	29349753	69	1.00E-125	VPI-5482	gb AAO79450.1 30S ribosomal protein S1 [Bacteroides thetaiotaomicron VPI-5482]			2.7.7.8
22435,				Bacteroides fragilis	hypothetical protein BF2134 [Bacteroides fragilis YCH46]			
22436	53713423	30	2.00E-07	YCH46	conserved hypothetical protein [Bacteroides fragilis YCH46]			

22437,	22438	45655699	31	1.00E-17	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	hypothetical protein LIC20117 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714691.1 conserved hypothetical protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51706.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				
22441,	22442	19879251	55	4.00E-57	Flavobacterium johnsoniae	hypothetical primosomal replication factor Y [Flavobacterium johnsoniae]				
22443,	22444	28897347	42	1.00E-32	Vibrio parahaemolyticus RIMD 2210633	polyphosphate kinase [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58836.1 polyphosphate kinase [Vibrio parahaemolyticus] sp Q87S51 PPK_VIBPA Polyphosphate kinase (Polyphosphoric acid kinase) (ATP-polyphosphate phosphotransferase)				2.7.4.1
22445,	22446	54307921	47	6.00E-37	Photobacterium profundum SS9	putative polyphosphate kinase [Photobacterium profundum SS9] emb CAG19139.1 putative polyphosphate kinase [Photobacterium profundum]				2.7.4.1
22447,	22448	48854784	61	5.00E-42	Cytophaga hutchinsonii	COG0044: Dihydroorotase and related cyclic amidohydrolases [Cytophaga hutchinsonii]				3.5.2.3
22457,	22458	54031509	38	5.00E-18	Polaromonas sp. JS666	hypothetical protein PJS6w01001889 [Polaromonas sp. JS666]				
22459,	22460	48855208	36	2.00E-26	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]				
22461,	22462	53713904	56	4.00E-56	Bacteroides fragilis YCH46	excinuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46]				
22463,	22464	51246763	35	3.00E-15	Desulfotalea psychrophila LSV54	hypothetical protein DP2911 [Desulfotalea psychrophila LSV54] emb CAG37640.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]				
22465,	22466	12024595	62	6.00E-78	Flavobacterium johnsoniae	GldE [Flavobacterium johnsoniae]				
22467,	22468	53715357	27	3.00E-27	Bacteroides fragilis YCH46	hypothetical protein BF4073 [Bacteroides fragilis YCH46] dbj BAD50815.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
22469,	22470	53715356	30	6.00E-29	Bacteroides fragilis YCH46	peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46] dbj BAD50814.1 peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46]				5.2.1.8
22473,	22474	48891870	42	1.00E-44	Trichodesmium erythraeum IMS101	COG0566: rRNA methylases [Trichodesmium erythraeum IMS101]				2.1.1.-
22475,	22476	56677793	42	7.00E-33	Silicibacter pomeroyi DSS-3	conserved domain protein [Silicibacter pomeroyi DSS-3] ref YP_166410.1 hypothetical protein SPO1160 [Silicibacter pomeroyi DSS-3]				

22477,	16119697	43	2.00E-39	Agrobacterium tumefaciens str. C58	hypothetical protein AGR_pAT_692 [Agrobacterium tumefaciens str. C58] gb AAK90844.1 AGR_pAT_692p [Agrobacterium tumefaciens str. C58] sp Q8UJK7 DP42_AGR_T5 DNA polymerase IV 2 (Pol IV 2)	2.7.7.7
22478	29346319	59	7.00E-94	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0909 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76016.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]	
22483,	6691651	40	2.00E-16	Moritella marina	ORF5 [Moritella marina]	
22484	54303381	36	1.00E-42	Photobacterium profundum SS9	hypothetical protein PBPRB1714 [Photobacterium profundum SS9] emb CAG32574.1 hypothetical protein [Photobacterium profundum]	1.14.-.-
22485,	54303381	36	1.00E-42	Photobacterium profundum SS9	hypothetical protein PBPRB1714 [Photobacterium profundum SS9] emb CAG32574.1 conserved hypothetical protein [Photobacterium profundum]	
22489,	54307658	30	4.00E-28	Microcystis aeruginosa	hypothetical protein BT0909 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76016.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]	6.3.2.-
22490	18920646	27	2.00E-15	Bacteroides thetaiotaomicron VPI-5482	putative transcription regulator [Bacteroides fragilis YCH46] db BAD48047.1 putative transcription regulator [Bacteroides fragilis YCH46]	
22493,	29346319	62	8.00E-56	Bacteroides fragilis YCH46	cation transport ATPase [Methanococcus maripaludis S2] emb CAF30076.1 cation transport ATPase [Methanococcus maripaludis S2]	3.6.1.-
22494	53712589	36	5.00E-13	Methanococcus maripaludis S2	COG0543: 2-polyphenylphenol hydroxylase and related flavodoxin oxidoreductases [Thiobacillus denitrificans ATCC 25259]	1.6.5.-
22495,	45358083	38	5.00E-37	Thiobacillus denitrificans ATCC 25259	ABC transporter, ATP-binding protein [Dehalococcoides ethenogenes 195] gb AAW39901.1 ABC transporter, ATP-binding protein [Dehalococcoides ethenogenes 195]	1.8.-.-
22496	52006884	41	4.00E-31	Dehalococcoides ethenogenes 195	hypothetical protein Chut02001830 [Cytophaga hutchinsonii]	
22497,	57234396	46	8.00E-19	Cytophaga hutchinsonii	hypothetical protein SAR2531 [Staphylococcus aureus subsp. aureus MRSA252] emb CAG41512.1 putative exported protein [Staphylococcus aureus subsp. aureus MRSA252]	3.5.2.6
22498	48855491	42	1.00E-43	Staphylococcus aureus subsp. aureus MRSA252	endonuclease [Tetrahymena thermophila]	
22499,	49484658	36	1.00E-10	Tetrahymena thermophila	phage-related protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM36364.1 phage-related protein [Xanthomonas axonopodis pv. citri str. 306]	
22500	18481487	25	3.00E-08	Xanthomonas axonopodis pv. citri str. 306		
22501,	21242246	36	1.00E-08	str. 306		

22509, 22510	17229899	38	8.00E-15	Nostoc sp. PCC 7120	hypothetical protein alr2407 [Nostoc sp. PCC 7120] pir AH2106 hypothetical protein alr2407 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB74106.1 alr2407 [Nostoc sp. PCC 7120]			3.1.2.6
2251, 2252	48854244	47	2.00E-31	Cytophaga hutchinsonii	COG0644: Dehydrogenases (flavoproteins) [Cytophaga hutchinsonii]			
22511, 22512	9655831	46	2.00E-25	Vibrio cholerae O1 biovar eltor str. N16961	prpE protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_230984.1 prpE protein [Vibrio cholerae O1 biovar eltor str. N16961] pir DB2213 prpE protein VC1340 [imported] - Vibrio cholerae (strain N16961 serogroup O1)			6.2.1.17
22515, 22516	23128539	31	7.00E-20	Nostoc punctiforme PCC 73102	COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102]			2.7.3.-
22517, 22518	16079944	30	4.00E-13	Bacillus subtilis subsp. subtilis str. 168	two-component response regulator [Bacillus subtilis subsp. subtilis str. 168] emb CAA9961.1 autolysin response regulator [Bacillus subtilis]			
22521, 22522	18309198	26	2.00E-08	Clostridium perfringens str. 13	emb CAB14852.1 two-component response regulator [Bacillus subtilis subsp. subtilis str. 168] pir B69655 two-component response regulator lyt-involved - Bacillus subtilis sp P94514 LYTT_BACSU Sensory transduction protein lytT			2.7.3.-
22523, 22524	48854404	44	2.00E-38	Cytophaga hutchinsonii	COG0881: Signal peptidase I [Cytophaga hutchinsonii]			3.1.11.-
22525, 22526	30248800	30	3.00E-15	Nitrosomonas europaea ATCC 19718	possible capK protein [Nitrosomonas europaea ATCC 19718] emb CAD84707.1 possible capK protein [Nitrosomonas europaea ATCC 19718]			3.4.21.8
22527, 22528	29170611	53	2.00E-52	Brevibacillus agri	b-alanine synthase [Brevibacillus agri]			3.5.1.6
22529, 22530	48855760	66	2.00E-80	Cytophaga hutchinsonii	COG1363: Cellulase M and related proteins [Cytophaga hutchinsonii]			3.2.1.4
22531, 22532	33864192	35	4.00E-37	Prochlorococcus marinus str. MIT 9313	Glycosyl transferase, group 1 [Prochlorococcus marinus str. MIT 9313] emb CAE22101.1 Glycosyl transferase, group 1 [Prochlorococcus marinus str. MIT 9313]			2.-.-.-
22533, 22534	29347385	63	4.00E-79	Bacteroides thetaiotaomicron VPI-5482	tRNA nucleotidyltransferase [Bacteroides thetaiotaomicron VPI-5482] gbl AAO77082.1 tRNA nucleotidyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.7.7.19
22535, 22536	37786088	40	2.00E-23	Escherichia coli	putative fucosyltransferase [Escherichia coli]			
22537, 22538	54309130	66	1.00E-24	Photobacterium profundum SS9	hypothetical protein PBPR1944 [Photobacterium profundum SS9] emb CAG20348.1 Conserved hypothetical protein [Photobacterium profundum]			

22541,	53797086	39	4.00E-41	Chloroflexus aurantiacus	COG0614: ABC-type Fe ³⁺ -hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus]			
22542,	48854815	51	2.00E-40	Cytophaga hutchinsonii	COG0719: ABC-type transport system involved in Fe-S cluster assembly, permease component [Cytophaga hutchinsonii]			
22543,	48854815	51	2.00E-40	Cytophaga hutchinsonii	thiol-disulfide oxidoreductase [Bacillus cereus ZK] gb/AAU18893.1 thiol-disulfide oxidoreductase [Bacillus cereus ZK]			
22544,	52143874	33	1.00E-06	Bacillus cereus ZK	hypothetical protein Chut02000024 [Cytophaga hutchinsonii]			
22545,	48856312	29	3.00E-10	Cytophaga hutchinsonii	COG2801: Transposase and inactivated derivatives [Psychrobacter sp. 273-4]			
22546,	52853441	77	5.00E-65	Psychrobacter sp. 273-4	Desc.N. gonorrhoeae amino acid sequence SEQ ID 2306. Org:Neisseria gonorrhoeae			
22547,	ABP7788	8	2.00E-33		putative nucleotide-diphosphate sugar epimerase [Bacteroides fragilis YCH46] dbj BAD49720.1 putative nucleotide-diphosphate sugar epimerase [Bacteroides fragilis YCH46]			4.2.1.-
22548,	53714262	35	9.00E-50	Bacteroides fragilis YCH46	Unclassified ABC-type transport system, ATPase component [Idiomarina loihiensis L2TR] gb/AAV81240.1 Unclassified ABC-type transport system, ATPase component [Idiomarina loihiensis L2TR]			
22549,	56459508	76	2.00E-74	Idiomarina loihiensis L2TR	type I restriction-modification system, M subunit [Desulfovibrio vulgaris subsp. vulgare str. Hildenborough] gb/AAO79669.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]			
22550,	46580119	72	1.00E-113	Desulfovibrio vulgaris subsp. vulgare str. Hildenborough	hypothetical protein BT2211 [Bacteroides thetaiotaomicron VPI-5482] gb/AAO77318.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			2.4.1.83
22551,	29349972	55	2.00E-38	Bacteroides thetaiotaomicron VPI-5482	two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj BAC48127.1 two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110]			2.7.3.-
22552,	29347621	50	3.00E-58	Bradyrhizobium japonicum USDA 110	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]			
22553,	27377973	51	2.00E-67	Cytophaga hutchinsonii	RfpB [Shigella dysenteriae]			2.4.1.-
22554,	48856381	47	1.00E-46	Cytophaga hutchinsonii	hypothetical protein Chut02002288 [Cytophaga hutchinsonii]			
22555,	18391088	62	8.00E-45	Shigella dysenteriae				
22556,	48855214	39	1.00E-35	Cytophaga hutchinsonii				
22557,								
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22583, 22584	16077689	29	1.00E-06	168	Bacillus subtilis subsp. subtilis str.	hypothetical protein BSU06220 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12441.1 ydJ [Bacillus subtilis subsp. subtilis str. 168] pir F69789 hypothetical protein ydjJ - Bacillus subtilis dbj BAA22765.1 function unknown [Bacillus subtilis]				
22585, 22586	29349251	74	1.00E-101	VPI-5482	Bacteroides thetataoamicon	ATP-dependent Cip protease ATP-binding subunit [Bacteroides thetataoamicon VPI-5482] gb AAO78948.1 ATP-dependent Cip protease ATP-binding subunit [Bacteroides thetataoamicon VPI-5482] sp Q8A128 CLPX_BACTN ATP-dependent Cip protease ATP-binding subunit clpX	Buchnera aphidicola str. Bp (Baizongia pistaciae), section 2 of 2 of the complete genome	83	6.00E-16	
22587, 22588	48853912	60	8.00E-30	Cytophaga hutchinsonii		COG1166: Arginine decarboxylase (spermidine biosynthesis) [Cytophaga hutchinsonii]				
22589, 22590	52853571	91	6.00E-97	Psychrobacter sp.		COG0784: FOG: CheY-like receiver [Psychrobacter sp. 273-4]				2.7.3.-
22591, 22592	38174845	36	5.00E-09	Melittangium lichenicola		hypothetical protein [Melittangium lichenicola]				
22593, 22594	42523322	36	3.00E-11	Bdellovibrio bacteriovorus HD100		oxidoeductase [Bdellovibrio bacteriovorus HD100] emb CAE79695.1 oxidoeductase [Bdellovibrio bacteriovorus HD100]				
22595, 22596	31194343	65	2.00E-51	Anopheles gambiae		ENSANGP00000000181 [Anopheles gambiae] GTP-binding elongation factor family protein TypA/BipA [Bacteroides fragilis YCH46] dbj BAD51200.1 GTP-binding elongation factor family protein TypA/BipA [Bacteroides fragilis YCH46]	Anopheles gambiae ENSANGP000000000 0181 (ENSANGG0000000 00177) mRNA, partial cds	87	1.00E-06	
22597, 22598	53715742	62	7.00E-55	Bacteroides fragilis YCH46		phosphoenolpyruvate carboxylase [Haloarcula marismortui ATCC 43049] gb AAV45577.1 phosphoenolpyruvate carboxylase [Haloarcula marismortui ATCC 43049]				4.1.1.31
22599, 22600	55377433	28	2.00E-14	Haloarcula marismortui ATCC 43049		hypothetical protein ECA3851 [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG76749.1 putative exported protein [Erwinia carotovora subsp. atroseptica SCRI1043]				2.7.3.-
22601, 22602	50122772	46	1.00E-37	Erwinia carotovora subsp. atroseptica SCRI1043		COG0629: Single-stranded DNA-binding protein [Cytophaga hutchinsonii] hypothetical protein BT3008 [Bacteroides thetataoamicon VPI-5482] gb AAO78114.1 conserved hypothetical protein [Bacteroides thetataoamicon VPI-5482]				
22603, 22604	48854352	50	3.00E-26	Cytophaga hutchinsonii						
22605, 22606	29348417	36	9.00E-31	Bacteroides thetataoamicon VPI-5482						

22607,	3329480	35	1.00E-18	Trichinella pseudospiralis	unknown [Trichinella pseudospiralis]				
22608				pseudospiralis					
22609,	5360168	53	2.00E-36	Flavobacterium johnsoniae	GidB [Flavobacterium johnsoniae]				
22610				johnsoniae					
2261,	48855091	41	6.00E-35	Cytophaga hutchinsonii	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii]				3.1.1.61
2262				hutchinsonii					
22611,	48855091	41	6.00E-35	Cytophaga hutchinsonii	COG0567: 2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, and related enzymes [Cytophaga hutchinsonii]				1.2.4.2
22612				hutchinsonii					
22613,	48853408	51	3.00E-40	Cytophaga hutchinsonii	COG0567: 2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, and related enzymes [Cytophaga hutchinsonii]				1.2.4.2
22614				hutchinsonii					
22615,	29347582	24	4.00E-07	Bacteroides thetaiotaomicron VPI-5482	putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482]				
22616				VPI-5482					
22617,	29348988	33	6.00E-38	Bacteroides thetaiotaomicron VPI-5482	topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482]				
22618				thetaiotaomicron					
22619,	53797086	38	1.00E-40	Chloroflexus aurantiacus	COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus]				
22620				aurantiacus					
22623,	22652003	43	2.00E-15	Synechococcus sp. PCC 7002	hypothetical protein [Synechococcus sp. PCC 7002]				
22624				PCC 7002					
22629,	49477771	31	2.00E-17	Bacillus thuringiensis serovar konkukian str. 97-27	conserved hypothetical protein, possible penicillin-binding protein [Bacillus thuringiensis serovar konkukian str. 97-27] gb AA759973.1 conserved hypothetical protein, possible penicillin-binding protein [Bacillus thuringiensis serovar konkukian str. 97-27]				3.4.16.4
22630				str. 97-27					
2263,	53730927	41	3.00E-30	Dechloromonas aromatica RCB	COG4585: Signal transduction histidine kinase [Dechloromonas aromatica RCB]				2.7.3.-
2264				aromatica RCB					
22631,	29349136	44	1.00E-11	Bacteroides thetaiotaomicron VPI-5482	riboflavin biosynthesis protein ribD [Bacteroides thetaiotaomicron VPI-5482]				
22632				thetaiotaomicron					
22633,	15793258	52	9.00E-42	Neisseria meningitidis Z2491	hypothetical protein NMA0240 [Neisseria meningitidis Z2491]				
22634				meningitidis Z2491					
22635,	48863717	24	7.00E-07	Rhodospirillum rubrum	COG1664: Integral membrane protein CcmA involved in cell shape determination [Rhodospirillum rubrum]				3.4.13.9
22636				degradans 2-40					
22637,	48764291	43	6.00E-19	Rhodospirillum rubrum					
22638				rubrum					

22639, 22640	15794870	51	1.00E-24	Neisseria meningitidis Z2491	integral membrane protein [Neisseria meningitidis Z2491] emb CAB85208.1 putative integral membrane protein [Neisseria meningitidis Z2491] gb AAAF42077.1 transporter, putative [Neisseria meningitidis MC58] pir JC81049 transporter, probable NMB1732 [imported] - Neisseria meningitidis (strain MC58 serogroup B, strain Z2491 serogroup A) ref NP_274735.1 transporter, putative [Neisseria meningitidis MC58]				
22641, 22642	48859645	41	2.00E-17	Clostridium thermocellum ATCC 27405	COG3587: Restriction endonuclease [Clostridium thermocellum ATCC 27405]				3.1.21.5
22643, 22644	48854463	56	4.00E-46	Cytophaga hutchinsonii	COG0193: Peptidyl-tRNA hydrolase [Cytophaga hutchinsonii]				3.1.1.29
22647, 22648	53713159	31	7.00E-21	Bacteroides fragilis YCH46	putative two-component system sensor protein without kinase domain [Bacteroides fragilis YCH46] db BAD48617.1 putative two-component system sensor protein without kinase domain [Bacteroides fragilis YCH46]				
22649, 22650	53714651	45	4.00E-56	Bacteroides fragilis YCH46	two-component system response regulator [Bacteroides fragilis YCH46] db BAD50109.1 two-component system response regulator [Bacteroides fragilis YCH46]				3.1.1.61
2265, 2266	15004787	33	7.00E-08	Clostridium acetobutylicum ATCC 824	SAM-dependent methyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK76829.1 SAM-dependent methyltransferase [Clostridium acetobutylicum ATCC 824]				
22653, 22654	34762717	26	2.00E-09	Fusobacterium nucleatum subsp. vincentii ATCC 49256	TETRA TRICOPEPTIDE REPEAT FAMILY PROTEIN [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24695.1 TETRA TRICOPEPTIDE REPEAT FAMILY PROTEIN [Fusobacterium nucleatum subsp. vincentii ATCC 49256]				
22659, 22660	45509650	39	7.00E-32	Anabaena variabilis ATCC 29413	COG0451: Nucleoside-diphosphate-sugar epimerases [Anabaena variabilis ATCC 29413]				5.1.3.-
22661, 22662	53714587	69	3.00E-28	Bacteroides fragilis YCH46	50S ribosomal protein L31 type B [Bacteroides fragilis YCH46] db BAD50045.1 50S ribosomal protein L31 type B [Bacteroides fragilis YCH46]				
22663, 22664	48855208	33	6.00E-23	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]				
22667, 22668	31195671	51	1.00E-32	Anopheles gambiae	ENSANGP00000000352 [Anopheles gambiae]				
2267, 2268	15605808	37	3.00E-18	Aquifex aeolicus VF5	hypothetical protein aq_268 [Aquifex aeolicus VF5] gb AAC06590.1 hypothetical protein [Aquifex aeolicus VF5] pir E70324 conserved				
22677, 22678	48766144	37	2.00E-32	Rhodospirillum rubrum	hypothetical protein aq_268 - Aquifex aeolicus COG2148: Sugar transferases involved in lipopolysaccharide synthesis [Rhodospirillum rubrum]				2.7.8.6

22681,	29345574	24	2.00E-16	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0164 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75271.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
22685,	53714651	45	2.00E-39	Bacteroides fragilis YCH46	two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD50109.1 two-component system response regulator [Bacteroides fragilis YCH46]				
22687,				Cytophaga hutchinsonii	COG0094: Ribosomal protein L5 [Cytophaga hutchinsonii]				
22688	48855309	67	5.00E-62	Bacteroides fragilis YCH46	hypothetical protein BF3562 [Bacteroides fragilis YCH46] dbj BAD50305.1 hypothetical protein [Bacteroides fragilis YCH46]			88	3.00E-08
22689,	53714847	29	2.00E-17	Bacteroides fragilis YCH46	COG0131: Imidazoleglycerol-phosphate dehydratase [Cytophaga hutchinsonii]				
22691,	48855137	57	1.00E-87	Cytophaga hutchinsonii	COG0365: Acyl-coenzyme A synthetases/AMP- (fatty) acid ligases [Cytophaga hutchinsonii]				3.1.3.15
22693,	48855752	26	7.00E-17	Cytophaga hutchinsonii	hypothetical protein PG0517 [Porphyromonas gingivalis W83] ref NP_904812.1 hypothetical protein PG0517 [Porphyromonas gingivalis W83]				
22695,				Porphyromonas gingivalis W83	COG0466: ATP-dependent Lon protease, bacterial type [Cytophaga hutchinsonii]				3.4.21.5
22696	34396645	31	3.00E-08	Cytophaga hutchinsonii	possible capK protein [Nitrosomonas europaea ATCC 19718] emb CAD84707.1 possible capK protein [Nitrosomonas europaea ATCC 19718]				3
22697,	48853586	52	5.00E-22	Nitrosomonas europaea ATCC 19718	hypothetical protein Chut02001282 [Cytophaga hutchinsonii]				
22699,				Cytophaga hutchinsonii	COG0845: Membrane-fusion protein [Cytophaga hutchinsonii]				
22700	30248800	36	2.00E-26	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]				
22705,	48856049	49	2.00E-48	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]				
22706				Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]				
22707,	48855612	33	9.00E-33	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]				
22708				Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]				
22709,	48856940	33	8.00E-15	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]				
22710				Anabaena variabilis ATCC 29413	COG0463: Glycosyltransferases involved in cell wall biogenesis [Anabaena variabilis ATCC 29413]				2.4.-.-
22711,	45509997	50	1.00E-23	Anabaena variabilis ATCC 29413	Desc:S. pneumoniae type 4 strain protein from coding region #1256. Org:Streptococcus pneumoniae type 4 strain				
22712	ABU0168								
22713,									
22714	0	46	1.00E-53						
22715,				Leptospira interrogans serovar Copenhageni str.	histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAST1873.1 histidine kinase sensor protein				
22716	45559150	34	1.00E-35	Flocruz L1-130	[Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				2.7.3.-

22717,	48854506	36	2.00E-15	Cytophaga hutchinsonii	hypothetical protein Chut02002705 [Cytophaga hutchinsonii]				3.6.1.-
22718				Cytophaga hutchinsonii	COG0719: ABC-type transport system involved in Fe-S cluster assembly, permease component [Cytophaga hutchinsonii]				
22719,	48854815	47	1.00E-54	Cytophaga hutchinsonii	DNA mismatch repair protein mutS [Bacteroides thetaiotaomicron VPI-5482]				
22720				Bacteroides thetaiotaomicron	gb AAO78227.1 DNA mismatch repair protein mutS [Bacteroides thetaiotaomicron VPI-5482] sp Q8A334 MUTS_BACTN DNA mismatch repair protein mutS				
22721,	29348530	48	3.00E-73	Bacteroides thetaiotaomicron VPI-5482	tRNA/rRNA methyltransferase [Bacteroides thetaiotaomicron VPI-5482]				
22722				Bacteroides thetaiotaomicron	gb AAO7827.1 tRNA/rRNA methyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.1.1.-
22723,	29348574	65	2.00E-60	Bacteroides thetaiotaomicron VPI-5482	type I restriction-modification system R subunit (endonuclease) [Geobacillus kaustophilus HTA426] db BAD74631.1 type I restriction-modification system R subunit (endonuclease) [Geobacillus kaustophilus HTA426]				3.1.21.3
22727,	56418881	30	6.00E-28	Geobacillus kaustophilus HTA426	COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii]				
22728				Cytophaga hutchinsonii	COG0242: N-formylmethionyl-tRNA deformylase [Cytophaga hutchinsonii]				3.5.1.88
22729,	48853984	38	7.00E-63	Cytophaga hutchinsonii	glucose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi Ty2] ref NP_458519.1 glucose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi str. CT18]				
22730				Cytophaga hutchinsonii	gb AAO71591.1 glucose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi Ty2] emb CAD09205.1 glucose-6-phosphate isomerase [Salmonella enterica subsp. enterica serovar Typhi] pirl AD1013				
2273,	48856118	46	8.00E-42	Salmonella enterica subsp. enterica serovar Typhi Ty2	glucose-6-phosphate isomerase (EC 5.3.1.9) [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)				5.3.1.9
2274				Cytophaga hutchinsonii	spiQ8Z1U7 G6PI_SALTI Glucose-6-phosphate isomerase (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI)				
22735,	29144389	55	6.00E-57	Salmonella enterica subsp. enterica serovar Typhi Ty2	ribonucleotide reductase [Porphyromonas gingivalis W83] ref NP_905338.1				1.17.4.1
22736				Salmonella enterica subsp. enterica serovar Typhi Ty2	ribonucleotide reductase [Porphyromonas gingivalis W83]				
22737,	34397173	44	2.00E-77	Porphyromonas gingivalis W83	ribonucleoside-diphosphate reductase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO77252.1 ribonucleoside-diphosphate reductase alpha chain [Bacteroides thetaiotaomicron VPI-5482]				
22738				Porphyromonas gingivalis W83	hypothetical protein BT1767 [Bacteroides thetaiotaomicron VPI-5482]				
22739,	29347555	56	1.00E-55	Bacteroides thetaiotaomicron VPI-5482	gb AAO76874.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
22740				Bacteroides thetaiotaomicron					
22741,	29347177	31	2.00E-34	Bacteroides thetaiotaomicron VPI-5482					
22742				Bacteroides thetaiotaomicron					

22743,	29349728	24	5.00E-09	Bacteroides [thetataoamlicron VPI-5482]	putative zinc protease [Bacteroides thetataoamlicron VPI-5482] gb AAO79425.1] putative zinc protease [Bacteroides thetataoamlicron VPI-5482]				
22744									
22747,									
22748	48856327	55	6.00E-36	Cytophaga hutchinsonii	COG3968: Uncharacterized protein related to glutamine synthetase [Cytophaga hutchinsonii]				6.3.1.2
22749,									
22750	48856043	27	8.00E-10	Cytophaga hutchinsonii	COG1556: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
2275,									
2276	28211428	54	5.00E-37	Clostridium tetani E88	D-hydantoinase [Clostridium tetani E88] [Clostridium tetani E88]				3.5.2.2
22751,									
22752	24373122	38	1.00E-35	Shewanella oneidensis MR-1	GGDEF domain protein [Shewanella oneidensis MR-1] gb AAN54608.1] GGDEF domain protein [Shewanella oneidensis MR-1]				2.7.3.-
22753,									
22754	48854312	38	1.00E-42	Cytophaga hutchinsonii	COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii]				
22755,									
22756	48856925	32	2.00E-17	Cytophaga hutchinsonii	COG1309: Transcriptional regulator [Cytophaga hutchinsonii]				
22757,									
22758	48844296	32	7.00E-07	Geobacter metallireducens GS-15	COG1858: Cytochrome c peroxidase [Geobacter metallireducens GS-15] hypothetical protein RB12645 [Rhodopirellula baltica SH 1] emb CAD77701.1] hypothetical protein [Pirellula sp.]				
22761,									
22762	32477630	36	3.00E-13	Rhodopirellula baltica SH 1					
22765,									
22766	29346648	63	1.00E-62	Bacteroides thetataoamlicron VPI-5482	putative RNA binding protein with S1 RNA-binding domain [Bacteroides thetataoamlicron VPI-5482] gb AAO76345.1] putative RNA binding protein with S1 RNA-binding domain [Bacteroides thetataoamlicron VPI-5482] hypothetical protein Bd3477 [Bdellovibrio bacteriovorus HD100] emb CAE78269.1] conserved hypothetical protein [Bdellovibrio bacteriovorus HD100]				2.7.7.8
22767,									
22768	42524830	26	5.00E-08	Bdellovibrio bacteriovorus HD100					
2277,									
2278	56675038	48	6.00E-20	uncultured bacterium	cellulase [uncultured bacterium]				
22771,									
22772	48855958	37	2.00E-10	Cytophaga hutchinsonii	hypothetical protein Chu02001184 [Cytophaga hutchinsonii]				
22773,									
22774	34557509	44	3.00E-31	Wolinella succinogenes DSM 1740	hypothetical protein WS1135 [Wolinella succinogenes DSM 1740] emb CAE10224.1] hypothetical protein [Wolinella succinogenes] COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus]				
22775,									
22776	53797086	39	4.00E-41	Chloroflexus aurantiacus					
22777,									
22778	28901123	46	5.00E-44	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VPA1268 [Vibrio parahaemolyticus RIMD 2210633] db BAC62611.1] hypothetical protein [Vibrio parahaemolyticus]				

22779, 22780	15668711	29	8.00E-09	Methanocaldococcus Jannaschii DSM 2661	hypothetical protein MJ0531 [Methanocaldococcus jannaschii DSM 2661] gblAAB98522.1 conserved hypothetical protein [Methanocaldococcus jannaschii DSM 2661] sp Q57951 Y531_METJA Hypothetical protein MJ0531 pir C64366 hypothetical protein homolog MJ0531 - Methanococcus jannaschii			
22781, 22782	32477622	41	4.00E-52	Rhodopirellula baltica SH 1	hypothetical protein-signal peptide and transmembrane prediction [Rhodopirellula baltica SH 1] emb CAD7693.1 hypothetical protein-signal peptide and transmembrane prediction [Pirellula sp.]			
22785, 22786	29349423	41	1.00E-14	Bacteroides thetaiotaomicron VPI-5482	transposase [Bacteroides thetaiotaomicron VPI-5482] gblAAO79120.1 transposase [Bacteroides thetaiotaomicron VPI-5482]			
22787, 22788	53712707	49	3.00E-26	Bacteroides fragilis YCH46	penicillin-binding protein 1C [Bacteroides fragilis YCH46] dbj BAD48165.1 penicillin-binding protein 1C [Bacteroides fragilis YCH46]			2.4.2.-
2279, 2280	48854863	55	3.00E-88	Cytophaga hutchinsonii	COG0358: DNA primase (bacterial type) [Cytophaga hutchinsonii] hypothetical protein PG0517 [Porphyromonas gingivalis W83] ref NP_904812.1 hypothetical protein PG0517 [Porphyromonas gingivalis W83]			2.7.7.-
22791, 22792	34396645	27	1.00E-25	Porphyromonas gingivalis W83	5'-nucleotidase precursor [Bacteroides fragilis YCH46] dbj BAD47314.1 5'- nucleotidase precursor [Bacteroides fragilis YCH46]			3.1.3.5
22793, 22794	53711856	40	5.00E-11	Bacteroides fragilis YCH46	histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gblAAS70606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			2.7.3.-
22799, 22800	45657883	51	2.00E-34	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	COG0096: Ribosomal protein S8 [Cytophaga hutchinsonii]			
22801, 22802	48855307	72	1.00E-49	Cytophaga hutchinsonii	COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii]			
22805, 22806	48856903	35	2.00E-37	Cytophaga hutchinsonii	COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii]			
22807, 22808	48856903	38	2.00E-39	Cytophaga hutchinsonii	COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii]			
22809, 22810	48854156	37	6.00E-32	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] cell division protein FtsQ [Bacteroides thetaiotaomicron VPI-5482] gblAAO78552.1 cell division protein FtsQ [Bacteroides thetaiotaomicron VPI-5482]			2.7.3.-
22811, 22812	29348855	30	7.00E-20	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein lpp0444 [Legionella pneumophila str. Paris] emb CAH11592.1 hypothetical protein [Legionella pneumophila str. Paris]			
22813, 22814	54296414	44	4.00E-48	Legionella pneumophila str. Paris				

22819,	15643161	32	6.00E-26	Thermotoga maritima MSB8	NADH oxidase, putative [Thermotoga maritima MSB8] gb AAD35480.1 NADH oxidase, putative [Thermotoga maritima MSB8] pir D72382 hypothetical protein TM0395 - Thermotoga maritima (strain MSB8)				1.6.-
22821,				Fusobacterium nucleatum subsp.	Probable quinovosaminephosphotransferase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93810.1 Probable quinovosaminephosphotransferase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]				2.7.8.6
22822,	19705016	31	1.00E-26	Dechloromonas aromatica RCB	COG0591: Na ⁺ /proline symporter [Dechloromonas aromatica RCB] putative zinc protease [Bacteroides thetaiotaomicron VPI-5482] gb AAO75853.1 putative zinc protease [Bacteroides thetaiotaomicron VPI- 5482]				2.7.3.-
22825,	53729687	35	2.00E-37	Bacteroides thetataomicron VPI-5482					3.4.99.-
22827,	29346156	35	1.00E-21	Vibrio parahaemolyticus RIMD 2210633	nucleotide sugar dehydrogenase [Vibrio parahaemolyticus RIMD 2210633] db BAC58499.1 nucleotide sugar dehydrogenase [Vibrio parahaemolyticus]			87 3.00E-17	1.1.1.22
22828,	28897010	76	3.00E-80	Cytophaga hutchinsonii	hypothetical protein Chut02003926 [Cytophaga hutchinsonii]				
22829,	48853339	40	7.00E-16	Microbulbifer degradans 2-40	hypothetical protein Mdeg02000551 [Microbulbifer degradans 2-40]				
22830,	48854178	31	1.00E-33	Legionella pneumophila subsp.	hypothetical protein lpg2561 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28621.1 hypothetical protein lpg2561 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]				
22831,	52842769	41	1.00E-17	Philadelphila 1	COG2220: Predicted Zn-dependent hydrolases of the beta-lactamase fold [Mesorhizobium sp. BNC1]				
22832,	45916344	52	3.00E-35	Mesorhizobium sp. BNC1					
22833,	48856049	50	5.00E-72	Cytophaga hutchinsonii	hypothetical protein Chut02001282 [Cytophaga hutchinsonii]				
22834,	48891870	43	3.00E-45	Trichodesmium erythraeum IMS101	COG0566: rRNA methylases [Trichodesmium erythraeum IMS101]				2.1.1.-
22835,	26246782	43	2.00E-56	Escherichia coli CFT073	Hypothetical protein ybIN [Escherichia coli CFT073] gb JAN79365.1 Hypothetical protein ybIN [Escherichia coli CFT073] O6-methylguanine-DNA methyltransferase [Bacillus cereus G9241] gb JAL14768.1 O6-methylguanine-DNA methyltransferase [Bacillus cereus G9241]				
22836,	47566806	51	1.00E-41	Bacillus cereus G9241					2.1.1.63

22849, 22850	53713280	72	1.00E-123	YCH46	Bacteroides fragilis	ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] dbj BAD48738.1 ABC transporter ATP-binding protein [Bacteroides fragilis YCH46]	Pasteurella multocida subsp. multocida str. Pm70 section 45 of 204 of the complete genome	84	3.00E-09	1.8.-
2285, 2286	48853339	40	7.00E-16	hutchinsonii	Cytophaga	hypothetical protein Chut02003926 [Cytophaga hutchinsonii]				
22851, 22852	18310442	33	6.00E-11	perfringens str. 13	Clostridium	hypothetical protein CPE1480 [Clostridium perfringens str. 13] dbj BAB81166.1 hypothetical protein [Clostridium perfringens str. 13]				
22853, 22854	27117221	33	2.00E-33	megaterium	Bacillus	glutaryl-tRNA-reductase [Bacillus megaterium] sp Q8GCB0 HEM1_BACME				1.2.1.-
22855, 22856	33149015	30	5.00E-09	ducreyi 35000HP	Haemophilus	cytochrome D ubiquinol oxidase, subunit II [Haemophilus ducreyi 35000HP] ref NP_874144.1 cytochrome D ubiquinol oxidase, subunit II [Haemophilus ducreyi 35000HP]				1.10.3.-
22859, 22860	22298886	62	5.00E-37	cus elongatus BP-1	Thermosynechococcus	hypothetical protein tlr1343 [Thermosynechococcus elongatus BP-1] dbj BAC08895.1 tlr1343 [Thermosynechococcus elongatus BP-1]				
22861, 22862	48856939	55	5.00E-24	hutchinsonii	Cytophaga	COG2884: Predicted ATPase involved in cell division [Cytophaga hutchinsonii]				1.8.-
22865, 22866	51893010	30	2.00E-22	14863	Symbiobacterium thermophilum IAM	8-amino-7-oxononanoate synthetase [Symbiobacterium thermophilum IAM 14863] dbj BAD40857.1 8-amino-7-oxononanoate synthetase [Symbiobacterium thermophilum IAM 14863]				2.3.1.47
22867, 22868	48853807	50	5.00E-57	hutchinsonii	Cytophaga	COG0793: Periplasmic protease [Cytophaga hutchinsonii]				
22869, 22870	56416952	32	6.00E-07	Maries	Anaplasma marginale str. St. Marie	hypothetical protein AM854 [Anaplasma marginale str. St. Marie] gb AAV86771.1 hypothetical protein AM854 [Anaplasma marginale str. St. Marie]				3.4.21.-
2287, 2288	50122086	55	6.00E-89	SCRI1043	Erwinia carotovora subsp. atroseptica	polyphosphate kinase [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG76062.1 polyphosphate kinase [Erwinia carotovora subsp. atroseptica SCRI1043]				
22873, 22874	AAO2094	9	4.00E-33			Desc:Protein of the BpmI endonuclease gene (BpmIRM). Org:Bacillus pumilus				2.7.4.1
22877, 22878	48855820	50	3.00E-37	hutchinsonii	Cytophaga	COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii]				2.1.1.72
22881, 22882	56498315	26	1.00E-09	berghei	Plasmodium	hypothetical protein PB000201.03.0 [Plasmodium berghei]				
22885, 22886	54302404	35	3.00E-30	profundum SS9	Photobacterium	hypothetical protein PBPRB0725 [Photobacterium profundum SS9] emb CAG22597.1 hypothetical protein [Photobacterium profundum]				

22887, 22888	55377565	28	7.00E-09	Haloarcula marismortui ATCC 43049	universal stress protein [Haloarcula marismortui ATCC 43049] gb AAV45709.1 universal stress protein [Haloarcula marismortui ATCC 43049]			
22891, 22892	57241727	31	5.00E-29	Campylobacter lari RM2100	iron(III) ABC transporter, ATP-binding protein [Campylobacter lari RM2100] gb EAL54397.1 iron(III) ABC transporter, ATP-binding protein [Campylobacter lari RM2100]			1.8.-
22893, 22894	23129686	26	1.00E-13	Nostoc punctiforme PCC 73102	COG2207: AraC-type DNA-binding domain-containing proteins [Nostoc punctiforme PCC 73102]			
22897, 22898	29347921	49	3.00E-29	Bacteroides thetataoamicron VPI-5482	putative transcription regulator [Bacteroides thetataoamicron VPI-5482] gb AAO77618.1 putative transcription regulator [Bacteroides thetataoamicron VPI-5482]			
22899, 22900	48856956	42	3.00E-42	Cytophaga hutchinsonii	COG0135: Phosphoribosylanthranilate isomerase [Cytophaga hutchinsonii]			5.3.1.24
22901, 22902	28211485	30	1.00E-13	Clostridium tetani E88	two-component sensor kinase yesM [Clostridium tetani E88] gb AAO36366.1 two-component sensor kinase yesM [Clostridium tetani E88]			2.7.3.-
22905, 22906	56477234	30	6.00E-16	Azoarcus sp. Ebn1 Ralstonia	hypothetical protein ebA3194 [Azoarcus sp. Ebn1] emb CAI07922.1 conserved hypothetical protein [Azoarcus sp. Ebn1]			
22907, 22908	48770184	25	5.00E-11	metallidurans CH34	COG0369: Sulfite reductase, alpha subunit (flavoprotein) [Ralstonia metallidurans CH34]			1.8.1.2
22909, 22910	9946545	41	2.00E-39	Pseudomonas aeruginosa PAO1	conserved hypothetical protein [Pseudomonas aeruginosa PAO1] pir B83563 conserved hypothetical protein PA0667 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_249358.1 hypothetical protein PA0667 [Pseudomonas aeruginosa PAO1]			3.5.1.-
2291, 2292	2947297	40	2.00E-26	Myxococcus xanthus	putative ECF sigma factor RpoE1 [Myxococcus xanthus]			
22917, 22918	53712491	35	1.00E-44	Bacteroides fragilis YCH46	putative nitrogen utilization substance protein [Bacteroides fragilis YCH46] db BAD47949.1 putative nitrogen utilization substance protein [Bacteroides fragilis YCH46]			
22919, 22920	15614651	39	1.00E-20	Bacillus halodurans C-125	hypothetical protein BH2088 [Bacillus halodurans C-125] db BAB05607.1 BH2088 [Bacillus halodurans C-125] pir H83910 hypothetical protein BH2088 [imported] - Bacillus halodurans (strain C-125) db BAA75367.1 Ydel [Bacillus halodurans]			
22923, 22924	19879252	72	4.00E-71	Flavobacterium johnsoniae	hypothetical pseudouridine synthase [Flavobacterium johnsoniae]			4.2.1.70
22929, 22930	32473830	55	3.00E-28	Rhodopirellula baltica SH 1	hypothetical protein RB5657 [Rhodopirellula baltica SH 1] emb CAD74364.1 conserved hypothetical protein [Rhodopirellula sp.]			

22931, 22932	46141353	91	7.00E-73	Psychrobacter sp. 273-4	COG0086: DNA-directed RNA polymerase, beta' subunit/160 kD subunit [Psychrobacter sp. 273-4]	Acinetobacter sp. ADP1 complete genome	92	1.00E-15	2.7.7.6
22933, 22934	29349121	38	1.00E-36	Bacteroides thetaitaomicron VPI-5482	D-alanine-D-alanine ligase [Bacteroides thetaitaomicron VPI-5482] gb AAO78818.1 D-alanine-D-alanine ligase [Bacteroides thetaitaomicron VPI-5482] sp Q8A1F3 DDL_BACTN D-alanine-D-alanine ligase (D- alanylalanine synthetase) (D-Ala-D-Ala ligase)			6.3.2.4	
22937, 22938	54308287	46	1.00E-59	Photobacterium profundum SS9	putative signal transduction protein containing EAL and modified HD-GYP domains [Photobacterium profundum SS9] emb CAG19505.1 putative signal transduction protein containing EAL and modified HD-GYP domains [Photobacterium profundum]				
22939, 22940	48856613	43	1.00E-31	Cytophaga hutchinsonii	COG0486: Predicted GTPase [Cytophaga hutchinsonii]				
22941, 22942	57158781	33	2.00E-23	Thermococcus kodakaraensis	carbohydrate esterase, family 1 [Thermococcus kodakaraensis] ref YP_182935.1 carbohydrate esterase, family 1 [Thermococcus kodakaraensis]			3.2.1.41	
22945, 22946	56416308	42	3.00E-35	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	subunit S of type I restriction-modification system [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] gb AAV80071.1 subunit S of type I restriction-modification system [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] ref NP_808151.1 subunit S of type I restriction-modification system [Salmonella enterica subsp. enterica serovar Typhi Ty2] ref NP_458948.1 subunit S of type I restriction- modification system [Salmonella enterica subsp. enterica serovar Typhi str. CT18] gb AAO72011.1 subunit S of type I restriction-modification system [Salmonella enterica subsp. enterica serovar Typhi Ty2] emb CAD03369.1 subunit S of type I restriction-modification system [Salmonella enterica subsp. enterica serovar Typhi] pir AB1069 chain S of type I restriction- modification system [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)			3.1.21.3	
22947, 22948	29349306	35	9.00E-10	Bacteroides thetaitaomicron VPI-5482	TonB [Bacteroides thetaitaomicron VPI-5482] gb AAO79003.1 TonB [Bacteroides thetaitaomicron VPI-5482]				
22949, 22950	42522703	47	5.00E-28	Bdellovibrio bacteriovorus HD100	hypothetical protein Bd1162 [Bdellovibrio bacteriovorus HD100] emb CAE79076.1 unnamed protein product [Bdellovibrio bacteriovorus HD100]			1.---	
22951, 22952	16127050	40	4.00E-22	Caulobacter crescentus CB15	TPR domain protein [Caulobacter crescentus CB15] gb AAK24782.1 TPR domain protein [Caulobacter crescentus CB15] pir B87598 TPR domain protein [imported] - Caulobacter crescentus				

22953, 22954	17936552	45	1.00E-29	Agrobacterium tumefaciens str. C58	protein tyrosine phosphatase [Agrobacterium tumefaciens str. C58] gb AAL43658.1 protein tyrosine phosphatase [Agrobacterium tumefaciens str. C58] pir JAD2905 protein tyrosine phosphatase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)				3.1.3.48
22955, 22956	20808235	33	2.00E-41	Thermoanaerobact er tengcongensis MB4	DNA polymerase III alpha subunit [Thermoanaerobacter tengcongensis MB4] gb AAM25010.1 DNA polymerase III alpha subunit [Thermoanaerobacter tengcongensis MB4]				2.7.7.7
22957, 22958	48854578	36	5.00E-38	Cytophaga hutchinsonii	COG0768: Cell division protein FtsI/penicillin-binding protein 2 [Cytophaga hutchinsonii]				
22959, 22960	22094882	58	2.00E-46	Flavobacterium johnsoniae	GldH [Flavobacterium johnsoniae]				
22961, 22962	13357977	38	4.00E-09	Ureaplasma parvum serovar 3 str. ATCC 700970	DNA polymerase III alpha chain 2 [Ureaplasma parvum serovar 3 str. ATCC 700970] gb AAF30826.1 DNA polymerase III alpha chain 2 [Ureaplasma parvum serovar 3 str. ATCC 700970] sp Q9PQ74 DP3A_UREPA DNA polymerase III alpha subunit pir D82895 DNA polymerase III alpha chain 2 UU415 [imported] - Ureaplasma urealyticum			2.7.7.7	
22963, 22964	23099733	46	1.00E-17	Oceanobacillus lheyensis HTE831	hypothetical protein OB2278 [Oceanobacillus lheyensis HTE831] dbj BAC14234.1 hypothetical conserved protein [Oceanobacillus lheyensis HTE831]				
22965, 22966	29350071	37	2.00E-16	Bacteroides thetalaotomicron VPI-5482	two-component system sensor histidine kinase/response [Bacteroides thetalaotomicron VPI-5482] gb AAO79768.1 two-component system sensor histidine kinase/response [Bacteroides thetalaotomicron VPI-5482]				
22967, 22968	46199940	36	4.00E-12	Thermus thermophilus HB27	porphobilinogen deaminase [Thermus thermophilus HB27] ref YP_143611.1 porphobilinogen deaminase [Thermus thermophilus HB8] gb AAS81980.1 porphobilinogen deaminase [Thermus thermophilus HB27] dbj BAD70168.1 porphobilinogen deaminase [Thermus thermophilus HB8] sp Q72H57 HEM3_THET2 Porphobilinogen deaminase (PBG) (Hydroxymethylbilane synthase) (HMBS) (Pre-uroporphyrinogen synthase)			4.3.1.8	
22969, 22970	53711360	49	2.00E-72	Bacteroides fragilis YCH46	putative Tricorn-like protease [Bacteroides fragilis YCH46] dbj BAD46818.1 putative Tricorn-like protease [Bacteroides fragilis YCH46]				3.4.21.-
22971, 22972	57234507	48	2.00E-28	Fe	[Fe] hydrogenase, HymA subunit, putative [Dehalococcoides ethenogenes 195] gb AAW40012.1 [Fe] hydrogenase, HymA subunit, putative [Dehalococcoides ethenogenes 195]				1.6.5.3
22973, 22974	29346842	53	2.00E-97	Bacteroides thetalaotomicron VPI-5482	mannonate dehydratase [Bacteroides thetalaotomicron VPI-5482] gb AAO76539.1 mannonate dehydratase [Bacteroides thetalaotomicron VPI- 5482] sp Q8A7U2 UXUA_BACTN Mannonate dehydratase (D-mannonate hydrolase)				4.2.1.8

22975,	53712512	31	2.00E-21	Bacteroides fragilis YCH46	iron(III) ABC transporter periplasmic iron-binding protein [Bacteroides fragilis YCH46] dbj BAD47970.1 iron(III) ABC transporter periplasmic iron-binding protein [Bacteroides fragilis YCH46]				
22976									
22979,	53713975	34	4.00E-10	Bacteroides fragilis YCH46	hypothetical protein BF2683 [Bacteroides fragilis YCH46] dbj BAD49433.1				
22980					hypothetical protein [Bacteroides fragilis YCH46]				
22981,				Legionella pneumophila str. Lens	hypothetical protein [Legionella pneumophila str. Lens]				2.3.1.51
22982	54295111	44	1.00E-31	Legionella pneumophila str. Lens	emb CAH1643.1 hypothetical protein [Legionella pneumophila str. Lens]				
22983,				Chloroflexus aurantiacus	COG4898: Uncharacterized protein conserved in bacteria [Chloroflexus aurantiacus]				
22984	53796261	72	1.00E-37	Chloroflexus aurantiacus					
22985,					similar to blackjack [Apis mellifera]				
22986	48127605	22	1.00E-07	Apis mellifera					
22989,				Cytophaga hutchinsonii	COG1284: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
22990	48856243	37	4.00E-23	Cytophaga hutchinsonii					
22993,				Cytophaga hutchinsonii	COG2353: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
22994	48855792	33	1.00E-13	Cytophaga hutchinsonii		Manhemia succiniciproducens MBEL55E, complete genome	84	1.00E-09	4.2.1.2
22995,				Haemophilus somnus 2336	COG0114: Fumarase [Haemophilus somnus 2336]				
22996	53728283	78	2.00E-38	Haemophilus somnus 2336					
22997,				Bacteroides fragilis YCH46	shikimate 5-dehydrogenase [Bacteroides fragilis YCH46] dbj BAD47667.1				1.1.1.25
22998	53712209	52	2.00E-31	Bacteroides fragilis YCH46	shikimate 5-dehydrogenase [Bacteroides fragilis YCH46]				
22999,				Cytophaga hutchinsonii	COG1999: Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems [Cytophaga hutchinsonii]				
23000	48855464	40	4.00E-22	Cytophaga hutchinsonii					
23001,				Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]				
23002	48853635	27	5.00E-07	Cytophaga hutchinsonii					
23005,				Clostridium thermocellum ATCC 27405	COG3328: Transposase and inactivated derivatives [Clostridium thermocellum ATCC 27405]				
23006	48859715	44	2.00E-31	Clostridium thermocellum ATCC 27405					
2301,				Xylella fastidiosa Temecula1	hypothetical protein PD2082 [Xylella fastidiosa Temecula1] gb AAO29905.1				
2302	28199942	31	2.00E-16	Xylella fastidiosa Temecula1	conserved hypothetical protein [Xylella fastidiosa Temecula1]				
23011,				Acinetobacter sp. ADP1	putative D-cysteine desulhydrase (DcyD) [Acinetobacter sp. ADP1]				
23012	50083970	48	1.00E-69	Acinetobacter sp. ADP1	emb CAG67658.1 putative D-cysteine desulhydrase (DcyD) [Acinetobacter sp. ADP1]				4.1.99.4
23013,				Cytophaga hutchinsonii	hypothetical protein Chut02003201 [Cytophaga hutchinsonii]				
23014	48854107	29	3.00E-12	Cytophaga hutchinsonii					

23015, 23016	32473146	41	5.00E-23	Rhodopirellula baltica SH 1	conserved hypothetical protein-putative membrane protein [Rhodopirellula baltica SH 1] emb CAD73826.1 conserved hypothetical protein-putative membrane protein [Pirellula sp.]			
23017, 23018	40643170	50	2.00E-76	Leptospira biflexa temperate bacteriophage LE1	unnamed protein product [Leptospira biflexa temperate bacteriophage LE1]			
23019, 23020	53713904	77	3.00E-81	Bacteroides fragilis YCH46	exonuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 exonuclease ABC subunit A [Bacteroides fragilis YCH46]			
23021, 23022	31194849	33	2.00E-20	Anopheles gambiae	ENSANGP0000001858 [Anopheles gambiae]			1.1.99.5
23023, 23024	29027481	59	3.00E-89	Aster yellows phytoplasma	threonine dehydratase [Aster yellows phytoplasma]			4.2.1.16
23025, 23026	46142301	64	1.00E-125	Methanococcoides burtonii DSM 6242	COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Methanococcoides burtonii DSM 6242]	Synthetic construct Francisella tularensis clone FLH156713.01X NT02FT0491 gene, complete cds	90	5.00E-17 3.1.21.3
23027, 23028	48862212	20	2.00E-09	Microbulbifer degradans 2-40	COG0419: ATPase involved in DNA repair [Microbulbifer degradans 2-40] conserved hypothetical protein [Silicibacter pomeroyi DSS-3] ref YP_168839.1 hypothetical protein SPO3644 [Silicibacter pomeroyi DSS- 3]			
23029, 23030	56680201	29	2.00E-17	Silicibacter pomeroyi DSS-3	COG2755: Lysophospholipase L1 and related esterases [Enterococcus faecium]			
2303, 2304	48824677	36	5.00E-29	Enterococcus faecium	putative haloacid dehalogenase-like family hydrolase [Bacteroides fragilis YCH46] dbj BAD50300.1 putative haloacid dehalogenase-like family hydrolase [Bacteroides fragilis YCH46]			
23031, 23032	53714842	47	1.00E-30	Bacteroides fragilis YCH46	shikimate 5-dehydrogenase [Bacteroides fragilis YCH46] dbj BAD47667.1 shikimate 5-dehydrogenase [Bacteroides fragilis YCH46]			1.1.1.25
23035, 23036	53712209	50	1.00E-45	Bacteroides fragilis YCH46	hypothetical protein Chut02002554 [Cytophaga hutchinsonii]			
23037, 23038	48854871	31	1.00E-13	Cytophaga hutchinsonii				

23041, 23042	16330995	56	2.00E-41	Synechocystis sp. PCC 6803	fructose-bisphosphate aldolase [Synechocystis sp. PCC 6803] sp P74309 ALF1_SYNY3 Fructose-bisphosphate aldolase class I (FBP aldolase) dbj BAA18403.1 fructose-bisphosphate aldolase [Synechocystis sp. PCC 6803] pir S76144 hypothetical protein - Synechocystis sp. (strain PCC 6803)				4.1.2.13
23045, 23046	9955888	52	5.00E-55	Vibrio cholerae O1 biovar eltor str. N16961	deoxyribodipyrimidine photolyase, putative [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_231036.1 deoxyribodipyrimidine photolyase, putative [Vibrio cholerae O1 biovar eltor str. N16961] pir A82205 probable deoxyribodipyrimidine photolyase VC1392 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				4.1.99.3
23047, 23048	18309705	41	8.00E-24	Clostridium perfringens str. 13	hypothetical protein CPE0723 [Clostridium perfringens str. 13] dbj BAB80429.1 conserved hypothetical protein [Clostridium perfringens str. 13]				
23049, 23050	48854027	30	5.00E-18	Cytophaga hutchinsonii	COG0747: ABC-type dipeptide transport system, periplasmic component [Cytophaga hutchinsonii]				
23051, 23052	48853539	38	2.00E-12	Cytophaga hutchinsonii	COG3021: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
23053, 23054	37519590	36	2.00E-38	Gloeobacter violaceus PCC 7421	Hyb/Msba family ABC transporter [Gloeobacter violaceus PCC 7421] dbj BAC87962.1 Hyb/Msba family ABC transporter [Gloeobacter violaceus PCC 7421]				1.8.-.-
23055, 23056	48854085	36	1.00E-17	Cytophaga hutchinsonii	COG0607: Rhodanese-related sulfurtransferase [Cytophaga hutchinsonii]				3.1.2.6
23057, 23058	48855702	38	6.00E-42	Cytophaga hutchinsonii	COG3279: Response regulator of the LytR/AIGR family [Cytophaga hutchinsonii]				3.1.4.17
23059, 23060	58543155	33	1.00E-14	Zymomonas mobilis subsp. mobilis ZM4	conserved hypothetical protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_162420.1 hypothetical protein ZMO0685 [Zymomonas mobilis subsp. mobilis ZM4]				
23061, 23062	6691651	41	6.00E-25	Moritella marina	ORF5 [Moritella marina]				3.4.21.-
23063, 23064	42524257	43	1.00E-15	Bdellovibrio bacteriovorus HD100	sensor histidine kinase/response regulator [Bdellovibrio bacteriovorus HD100] emb CAE80630.1 sensor histidine kinase/response regulator [Bdellovibrio bacteriovorus HD100]				2.7.3.-
23067, 23068	48855243	41	3.00E-15	Cytophaga hutchinsonii	hypothetical protein Chut02001571 [Cytophaga hutchinsonii]				
23069, 23070	32473409	30	2.00E-22	Rhodopirellula baltica SH 1	probable aminopeptidase [Rhodopirellula baltica SH 1] emb CAD78184.1 probable aminopeptidase [Pirellula sp.]				3.4.21.-
23073, 23074	48854978	72	8.00E-98	Cytophaga hutchinsonii	COG1410: Methionine synthase I, cobalamin-binding domain [Cytophaga hutchinsonii]	Acinetobacter sp. ADP1 complete genome	89	1.00E-10	2.1.1.13

23077,	53714415	64	3.00E-74	Bacteroides fragilis YCH46	dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46]				2.4.1.83
23078					fragilis YCH46]				
23079,				Chlorobium	glycosyl transferase [Chlorobium tepidum TLS]				2.4.-.-
23080	21674237	41	5.00E-35	tepidum TLS	transferase [Chlorobium tepidum TLS]				
23081,				Cytophaga	COG0540: Aspartate carbamoyltransferase, catalytic chain [Cytophaga			Bartonella henselae	
23082	48853820	76	4.00E-94	hutchinsonii	hutchinsonii]			strain Houston-1,	92 3.00E-08 2.1.3.2
23083,				Cytophaga	COG0571: dsRNA-specific ribonuclease [Cytophaga hutchinsonii]				3.1.26.3
23084	48855014	37	2.00E-24	hutchinsonii					
23087,				Cytophaga	COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii]				2.7.7.24
23088	48854175	56	1.00E-68	hutchinsonii					
23089,				Cytophaga	COG3781: Predicted membrane protein [Cytophaga hutchinsonii]				
23090	48856121	40	1.00E-57	hutchinsonii					
2309,				Pseudomonas	COG1943: Transposase and inactivated derivatives [Pseudomonas syringae				
2310	46187901	34	4.00E-23	syringae pv.	pv. syringae B728a] ref ZP_00205512.1 COG1943: Transposase and				
23093,				syringae B728a	inactivated derivatives [Pseudomonas syringae pv. syringae B728a]				
23094	48863739	39	7.00E-20	Microbulifer	COG2202: FOG: PAS/PAC domain [Microbulifer degradans 2-40]				2.7.3.-
23095,				degradans 2-40	ABC transporter, ATP-binding protein [Porphyromonas gingivalis W83]				
23096	34397012	60	3.00E-35	Porphyromonas	ref NP_905177.1 ABC transporter, ATP-binding protein [Porphyromonas				1.8.-.-
				gingivalis W83	gingivalis W83]				
23099,				Photobacterium	hypothetical protein PBPRB1077 [Photobacterium profundum SS9]				
23100	54302756	38	1.00E-11	profundum SS9	emb CAG22949.1 conserved hypothetical protein [Photobacterium				
23101,					profundum]				
23102	79387	41	2.00E-13		clindamycin resistance transfer factor btgB - Bacteroides fragilis plasmid				
					pBFTM10 gb AAA22903.1 putative				
23103,				Cupriavidus	NAD-reducing hydrogenase diaphorase moiety small subunit [Cupriavidus				
23104	38637754	46	7.00E-57	necator	necator] gb AAP85842.1 NAD-reducing hydrogenase diaphorase moiety				1.6.5.3
23105,				Methanosarcina	small subunit [Ralstonia eutropha] pir B35385 hydrogen dehydrogenase (EC				
23106	48839250	32	1.00E-20	barkeri str. fusaro	1.12.1.2) gamma chain - Alcaligenes eutrophus gb AAC0614.1 NAD-				
					reducing hydrogenase [Ralstonia eutropha] sp P22318 HOXU_ALCEU NAD-				
					reducing hydrogenase hoxS gamma subunit				
23109,				Porphyromonas	COG2202: FOG: PAS/PAC domain [Methanosarcina barkeri str. fusaro]				2.7.3.-
23110	34396251	41	1.00E-46	gingivalis W83	conserved hypothetical protein [Porphyromonas gingivalis W83]				
					ref NP_904419.1 hypothetical protein PG0069 [Porphyromonas gingivalis				
					W83]				

2311,	2311,	46187901	34	4.00E-23	Pseudomonas syringae pv. syringae B728a	COG1943: Transposase and inactivated derivatives [Pseudomonas syringae pv. syringae B728a] ref JP_00205512.1 COG1943: Transposase and inactivated derivatives [Pseudomonas syringae pv. syringae B728a]			
2312,	2312,	48854716	46	8.00E-27	Cytophaga hutchinsonii	COG0009: Putative translation factor (SUA5) [Cytophaga hutchinsonii]			
2313,	2313,	56543618	28	6.00E-08	Zymomonas mobilis subsp. mobilis ZM4	outer membrane protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_162883.1 outer membrane protein [Zymomonas mobilis subsp. mobilis ZM4]			
2314,	2314,	AA1168	25	2.00E-08		Desc:Sulfated fucose-containing polysaccharide degrading polypeptide. Org:Flavobacterium sp			
2315,	2315,	52549170	34	6.00E-16	uncultured archaeon	two-component sensor histidine kinase [uncultured archaeon GZfos26B2]			2.7.3.-
2316,	2316,	48858974	54	2.00E-43	Cytophaga hutchinsonii	COG1778: Low specificity phosphatase (HAD superfamily) [Cytophaga hutchinsonii]			3.1.3.29
2317,	2317,	46141620	58	8.00E-28	Psychrobacter sp. 273-4	COG3335: Transposase and inactivated derivatives [Psychrobacter sp. 273-4]			
2318,	2318,	54302404	35	1.00E-16	Photobacterium profundum SS9	hypothetical protein PBPBR0725 [Photobacterium profundum SS9] emb CAG22597.1 hypothetical protein [Photobacterium profundum]			
2319,	2319,	21674236	37	3.00E-29	Chlorobium tepidum TLS	hypothetical protein CT1415 [Chlorobium tepidum TLS] gb AAM72643.1 conserved hypothetical protein [Chlorobium tepidum TLS]			
2320,	2320,	48854514	49	4.00E-68	Cytophaga hutchinsonii	COG1216: Predicted glycosyltransferases [Cytophaga hutchinsonii]			2.4.1.-
2321,	2321,	48855191	48	4.00E-53	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-
2322,	2322,	53713687	43	1.00E-31	Bacteroides fragilis YCH46	hypothetical protein BF2396 [Bacteroides fragilis YCH46] dbj BAD49145.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
2323,	2323,	20092576	55	5.00E-55	Methanosarcina acetivorans C2A	dTDP-4-dehydrothamnose 3,5-epimerase [Methanosarcina acetivorans C2A] gb AAM07131.1 dTDP-4-dehydrothamnose 3,5-epimerase [Methanosarcina acetivorans str. C2A]			5.1.3.13
2324,	2324,	48854901	29	1.00E-08	Cytophaga hutchinsonii	COG3696: Putative silver efflux pump [Cytophaga hutchinsonii]			
2325,	2325,	53715245	48	3.00E-73	Bacteroides fragilis YCH46	ATP-dependent DNA helicase RecG [Bacteroides fragilis YCH46] dbj BAD50703.1 ATP-dependent DNA helicase RecG [Bacteroides fragilis YCH46]			3.6.1.-
2326,	2326,	AAB4698	1			Desc:H. influenzae MurB protein SEQ ID 9. Org:Haemophilus influenzae			1.1.1.15
2327,	2327,		48	2.00E-29					8

23141,	48854182	36	4.00E-38	Cytophaga hutchinsonii	COG1472: Beta-glucosidase-related glycosidases [Cytophaga hutchinsonii]				
23142				Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0820 [Bacteroides thetaiotaomicron VPI-5482]				
23147,	29346230	54	1.00E-29	Anopheles gambiae	gb AAO75927.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
23148				Cytophaga hutchinsonii	ENSANGP00000000218 [Anopheles gambiae]				6.3.2.-
23149,	31195713	63	2.00E-94	Anopheles gambiae	COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii]				
23150	48855186	36	8.00E-11	Cytophaga hutchinsonii	ENSANGP00000000095 [Anopheles gambiae str. PEST] ref XP_561483.1				
23151,	55247361	48	3.00E-36	Anopheles gambiae str. PEST	ENSANGP00000000095 [Anopheles gambiae str. PEST]				
23152				Bacillus thuringiensis serovar konkukian str. 97-27	uoporphyrinogen-III synthase [Bacillus thuringiensis serovar konkukian str. 97-27] gb AA160847.1 uroporphyrinogen-III synthase [Bacillus thuringiensis serovar konkukian str. 97-27]				
23157,	49478645	32	3.00E-08	Cytophaga hutchinsonii	COG0373: Glutaryl-tRNA reductase [Cytophaga hutchinsonii]				1.2.1.-
23158				Acinetobacter sp. ADP1	putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1]				
23159,	48855777	33	5.00E-31	Geobacter sulfurreducens PCA	emb CAG67658.1 putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1]				4.1.99.4
23160	50083970	49	1.00E-48	Geobacter sulfurreducens PCA	thioredoxin family protein [Geobacter sulfurreducens PCA] gb AAR34697.1				
23161,	39986423	32	2.00E-17	Bdellovibrio bacteriovorus HD100	thioredoxin family protein [Geobacter sulfurreducens PCA]				
23162				Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	major anaerobically induced transmembrane protein [Bdellovibrio bacteriovorus HD100] emb CAE80401.1 major anaerobically induced transmembrane protein [Bdellovibrio bacteriovorus HD100]				1.7.99.3
23165,	42524028	43	7.00E-19	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_710808.1 Putative glycosyl transferase [Leptospira interrogans serovar Lai str. 56601] gb AAN47826.1 Putative glycosyl transferase [Leptospira interrogans serovar lai str. 56601] gb AAS71510.1				
23166				Cytophaga hutchinsonii	glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				
23167,	45658787	32	4.00E-37	Cytophaga hutchinsonii	COG2932: Predicted transcriptional regulator [Cytophaga hutchinsonii]				
23168				Bacteroides thetaiotaomicron VPI-5482	putative RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79825.1 putative RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482]				
23169,	48856470	35	2.00E-16	Bacteroides thetaiotaomicron VPI-5482					
23170									
23171,	29350128	38	2.00E-26						
23172									

23177, 23178	48856945	48	1.00E-43	Cytophaga hutchinsonii	COG2801: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00309595.1 COG2801: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00308310.1 COG2801: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00308305.1 COG2801: Transposase and inactivated derivatives [Cytophaga hutchinsonii]				
23183, 23184	29349785	29	8.00E-09	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT4377 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79482.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482]				
23187, 23188	27364673	28	4.00E-09	Vibrio vulnificus CMCP6	Transcriptional regulator [Vibrio vulnificus CMCP6] ref NP_935886.1 transcriptional regulator [Vibrio vulnificus YJ016] gb AAO09728.1 transcriptional regulator [Vibrio vulnificus CMCP6] dbj BAC95857.1 transcriptional regulator [Vibrio vulnificus YJ016]				
2319, 2320	48856489	45	5.00E-61	Cytophaga hutchinsonii	COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii]				2.7.3.-
23193, 23194	12024595	56	6.00E-87	Flavobacterium johnsoniae	GidE [Flavobacterium johnsoniae]				
23195, 23196	48855328	73	1.00E-65	Cytophaga hutchinsonii	COG0085: DNA-directed RNA polymerase, beta subunit/140 kD subunit [Cytophaga hutchinsonii]			92	1.00E-10/2.7.7.6
23197, 23198	48786803	36	2.00E-24	Burkholderia fungorum LB400	COG0438: Glycosyltransferase [Burkholderia fungorum LB400] related to MCBG protein (microcin resistance protein) [Desulfotalea psychrophila Lsv54] emb CAG35262.1 related to MCBG protein (microcin resistance protein) [Desulfotalea psychrophila Lsv54]				
23199, 23200	51244385	37	3.00E-30	Desulfotalea psychrophila Lsv54	ATP-independent RNA helicase [Bacteroides fragilis YCH46] dbj BAD48764.1 ATP-independent RNA helicase [Bacteroides fragilis YCH46]				2.7.7.-
23203, 23204	53713306	48	1.00E-39	Bacteroides fragilis YCH46	similar to cell wall-associated protein precursor wapA [Bdellovibrio bacteriovorus HD100] emb CAE77783.1 similar to cell wall-associated protein precursor wapA [Bdellovibrio bacteriovorus HD100]				
23205, 23206	42521749	31	6.00E-10	Bdellovibrio bacteriovorus HD100	putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79669.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.4.1.83
23209, 23210	29349972	64	1.00E-106	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein Chut02003580 [Cytophaga hutchinsonii] phosphohydrolase [Bacteroides fragilis YCH46] dbj BAD47659.1 phosphohydrolase [Bacteroides fragilis YCH46]				
2321, 2322	48853721	51	3.00E-22	Cytophaga hutchinsonii					
23211, 23212	53712201	39	2.00E-19	Bacteroides fragilis YCH46					

23213, 23214, 23215, 23216	29349615 45524044	50 49	7.00E-41 8.00E-71	3-hydroxymyristoyl Crocosphaera watsonii WH 8501 Bacteroides thetaitaomicron VPI-5482	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79312.1 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.3.1.-
23217, 23218	29347921	50	3.00E-31		COG0280: Phosphotransacetylase [Crocosphaera watsonii WH 8501] putative transcription regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO77618.1 putative transcription regulator [Bacteroides thetaiotaomicron VPI-5482]				2.3.1.8
23219, 23220 23223, 23224	9947830 48856903	49 33	4.00E-64 2.00E-35	Pseudomonas aeruginosa PAO1 Cytophaga hutchinsonii	methionine synthase [Pseudomonas aeruginosa PAO1] ref NP_250534.1 methionine synthase [Pseudomonas aeruginosa PAO1] pir E83415 methionine synthase PA1843 [Imported] - Pseudomonas aeruginosa (strain PAO1) COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii]				2.1.1.13
23227, 23228	48855349	58	8.00E-76	Cytophaga hutchinsonii Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	COG0320: Lipote synthase [Cytophaga hutchinsonii]		Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis DNA, complete genome	93	5.00E-07
23229, 23230	56416279	27	9.00E-18		hypothetical protein SPA4314 [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] gb AAV80042.1 orf, hypothetical protein [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] gb AAO79565.1 putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482]				
2323, 2324	29349868	36	2.00E-11	Bacteroides thetaitaomicron VPI-5482 Vibrio parahaemolyticus RIMD 2210633					
23235, 23236	28901124	61	6.00E-60		hypothetical protein VPA1269 [Vibrio parahaemolyticus RIMD 2210633] db BAC62612.1 hypothetical protein [Vibrio parahaemolyticus]				
23237, 23238	48772259	30	1.00E-10	Ralstonia metallidurans CH34	hypothetical protein Reut02001021 [Ralstonia metallidurans CH34]				
23239, 23240	27366889	56	6.00E-32	Vibrio vulnificus CMCP6	hypothetical protein VV20452 [Vibrio vulnificus CMCP6] gb AAO07406.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6]				
23243, 23244	585368	40	5.00E-22		Phosphoribulokinase (Phosphopentokinase) (PRK) gb AAA27293.1 phosphoribulokinase				2.7.1.19

23247, 23248	52842769	41	1.00E-17	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	hypothetical protein lpg2561 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] hypothetical protein lpg2561 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]				
2325, 2326	52425394	53	5.00E-11	Mannheimia succiniciproducens MBEL55E	hypothetical protein MS1339 [Mannheimia succiniciproducens MBEL55E] gb AAU37946.1 unknown [Mannheimia succiniciproducens MBEL55E]				
23255, 23256	53714706	56	7.00E-31	Bacteroides fragilis YCH46	adenylosuccinate synthetase [Bacteroides fragilis YCH46] dbj BAD50164.1				6.3.4.4
23259, 23260	48854535	49	9.00E-53	Cytophaga hutchinsonii	adenylosuccinate synthetase [Bacteroides fragilis YCH46] COG1674: DNA segregation ATPase FtsK/SpoIIIE and related proteins [Cytophaga hutchinsonii]				
23261, 23262	48855642	28	4.00E-24	Cytophaga hutchinsonii	COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii] histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482]				
23263, 23264	29347250	63	3.00E-90	Bacteroides thetaitaomicron VPI-5482	gb AAO76947.1 histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A6N7 SYH_BACTN Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HisRS)				6.1.1.21
23265, 23266	31790570	41	7.00E-32	marine bacterium P99-3	lycopene beta-monoxygenase [marine bacterium P99-3]				
23269, 23270	23125566	27	1.00E-15	Nostoc punctiforme PCC 73102	COG0457: FOG: TPR repeat [Nostoc punctiforme PCC 73102]				
2327, 2328	48854348	52	4.00E-68	Cytophaga hutchinsonii	COG1530: Ribonucleases G and E [Cytophaga hutchinsonii]				3.1.4.-
23271, 23272	53712308	47	1.00E-60	Bacteroides fragilis YCH46	ATP-binding protein [Bacteroides fragilis YCH46] dbj BAD47766.1 ATP-binding protein [Bacteroides fragilis YCH46]				1.8.-
23273, 23274	53715023	49	2.00E-32	Bacteroides fragilis YCH46	hypothetical protein BF3739 [Bacteroides fragilis YCH46] dbj BAD50481.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
23275, 23276	29348700	27	5.00E-23	Bacteroides thetaitaomicron VPI-5482	hypothetical protein BT3291 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78397.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
23277, 23278	48863715	23	8.00E-08	Microbulifer degradans 2-40	COG0845: Membrane-fusion protein [Microbulifer degradans 2-40]				
23285, 23286	48854655	27	8.00E-10	Cytophaga hutchinsonii	hypothetical protein Chui02002321 [Cytophaga hutchinsonii]				
23287, 23288	34396743	25	2.00E-07	Porphyromonas gingivalis W83	hypothetical protein PG0624 [Porphyromonas gingivalis W83] ref NP_904909.1 hypothetical protein PG0624 [Porphyromonas gingivalis W83]				

23289,	48853745	29	1.00E-14	Cytophaga hutchinsonii	hypothetical protein Chut02003390 [Cytophaga hutchinsonii]				
23290				hutchinsonii	Probable cysteine desulfurase (Nifs protein homolog) gb AAG01802.1				
2329,	13431585	48	3.00E-60	Methanosarcina thermophila	cysteine desulfurase Nifs [Methanosarcina thermophila]				4.4.1.-
2330				thermophila	Uncharacterized conserved secreted protein [Idiomarina loihiensis L2TR]				
23291,	56459184	53	5.00E-42	Idiomarina loihiensis L2TR	gb AAV80916.1 Uncharacterized conserved secreted protein [Idiomarina loihiensis L2TR]				
23292				Idiomarina loihiensis L2TR					
23295,	31195677	62	1.00E-91	Anopheles gambiae	ENSANGP00000000375 [Anopheles gambiae]				6.1.1.18
23296				Anopheles gambiae	replication protein - Pseudomonas syringae plasmid pPS10				
23297,	95009	31	1.00E-23	Pseudomonas syringae	emb CAA41700.1 replication protein [Pseudomonas syringae]				
23298				Pseudomonas syringae					
23299,	46321450	29	5.00E-17	Burkholderia cepacia R1808	COG5135: Uncharacterized conserved protein [Burkholderia cepacia R1808]				
23300				Burkholderia cepacia R1808					
233,				Methanococcoides burtonii DSM 6242					
234	53731213	48	3.00E-44	Methanococcoides burtonii DSM 6242	hypothetical protein Mbur03001560 [Methanococcoides burtonii DSM 6242]				
23301,				Ralstonia solanacearum					
23302	17548499	46	1.00E-13	GMI1000	hypothetical protein RS03686 [Ralstonia solanacearum GMI1000]				
23303,				Bacteroides fragilis	emb CAD17429.1 HYPOTHETICAL PROTEIN [Ralstonia solanacearum]				
23304	53715185	28	9.00E-17	YCH46	competence protein [Bacteroides fragilis YCH46] db BAD50643.1				
23305,				Bacteroides thetaiotaomicron	competence protein [Bacteroides fragilis YCH46]				
23306	29346570	49	9.00E-62	VPI-5482	Na ⁺ -translocating NADH-quinone reductase subunit [Bacteroides thetaiotaomicron VPI-5482] gb AAO76267.1 Na ⁺ -translocating NADH-quinone reductase subunit [Bacteroides thetaiotaomicron VPI-5482]				1.6.5.-
23309,				Rhizobium etli	probable ABC transporter (ATPase component). [Rhizobium etli]				
23310	21467398	56	9.00E-39	Rhizobium etli	ref NP_660060.1 probable ABC transporter (ATPase component). [Rhizobium etli]				3.4.21.-
2331,				Thermosynechococcus elongatus BP-1					
2332	22298131	47	3.00E-24	Thermosynechococcus elongatus BP-1	hypothetical protein trf0588 [Thermosynechococcus elongatus BP-1] db BAC08140.1 trf0588 [Thermosynechococcus elongatus BP-1]				
23311,				Desulfotalea psychrophila Lsv54					
23312	51245771	88	1.00E-122	Desulfotalea psychrophila Lsv54	hypothetical protein DP-1919 [Desulfotalea psychrophila Lsv54] emb CAG36648.1 hypothetical protein [Desulfotalea psychrophila Lsv54]			81	3.00E-80
23313,				Pseudomonas fluorescens PfO-1					
23314	48728488	40	4.00E-34	fluorescens PfO-1	hypothetical protein Pfu02005424 [Pseudomonas fluorescens PfO-1]				
23317,				Bacteroides fragilis YCH46	transcription-repair coupling factor [Bacteroides fragilis YCH46]				
23318	53714414	56	1.00E-102	YCH46	db BAD49872.1 transcription-repair coupling factor [Bacteroides fragilis YCH46]				3.6.1.-
23319,				Cytophaga hutchinsonii					
23320	48854452	56	1.00E-67	Cytophaga hutchinsonii	COG0034: Glutamine phosphoribosylpyrophosphate amidotransferase [Cytophaga hutchinsonii]				2.4.2.14

23321,	48854240	62	1.00E-66	Cytophaga hutchinsonii	COG3145: Alkylated DNA repair protein [Cytophaga hutchinsonii]				
23322					ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83]				
23327,				Porphyromonas	ref NP_904660.1 ATP-dependent DNA helicase RecG [Porphyromonas				3.6.1.-
23328	34396493	45	1.00E-73	gingivalis W83					
23329,				Cytophaga	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]				
23330	48855778	26	6.00E-13	hutchinsonii					
23331,				Cytophaga	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]				2.7.3.-
23332	48855778	47	9.00E-36	hutchinsonii	Desc: Streptococcus polypeptide SEQ ID NO 4360. Org: Streptococcus				2.4.1.21
23333,	ABP2759	2	2.00E-28		agalactiae				
23334		33	2.00E-28		peptidase M20/M25/M40 family protein [Caulobacter crescentus CB15]				3.4.17.2
23335,				Caulobacter	gb AAK24473.1 peptidase M20/M25/M40 family protein [Caulobacter				1
23336	16126741	43	2.00E-45	crescentus CB15	crescentus CB15] pir E87559 peptidase M20/M25/M40 family protein				
23337,				Cytophaga	[Imported] - Caulobacter crescentus				
23338	48853326	42	1.00E-32	hutchinsonii	COG1485: Predicted ATPase [Cytophaga hutchinsonii]				
23339,				Bacillus subtilis	hypothetical protein BSU13010 [Bacillus subtilis subsp. subtilis str. 168]				
23340	16078366	38	6.00E-27	subsp. subtilis str. 168	emb CAA05581.1 YkgB [Bacillus subtilis] emb CAB13158.1 ykgB [Bacillus				
23341,				Psychrobacter sp.	subtilis subsp. subtilis str. 168] pir D98856 conserved hypothetical protein				
23342	46141524	59	8.00E-72	273-4	ykgB - Bacillus subtilis sp O34499 YKGB_BACSU Hypothetical protein ykgB				3.1.21.4
23343,				Pseudomonas	hypothetical protein Psc03000453 [Psychrobacter sp. 273-4]				
23344	9946150	36	2.00E-38	aeruginosa PAO1	hypothetical protein PA0305 [Pseudomonas aeruginosa PAO1] pir B83608				
23345,				Cytophaga	hypothetical protein PA0305 [Imported] - Pseudomonas aeruginosa (strain				3.5.1.11
23346	48853805	51	1.00E-45	hutchinsonii	PAO1) ref NP_248996.1 hypothetical protein PA0305 [Pseudomonas				
23347,				Bacillus clausii	aeruginosa PAO1]				
23348	56965532	31	5.00E-13	KSM-K16	COG0166: Glucose-6-phosphate isomerase [Cytophaga hutchinsonii]				6.3.4.6
2335,				Bacteroides fragilis	hypothetical protein ABC3772 [Bacillus clausii KSM-K16] dbj BAD66304.1				
2336	53715357	26	1.00E-11	YCH46	conserved hypothetical protein [Bacillus clausii KSM-K16]				
23353,				Vibrio	hypothetical protein BF4073 [Bacteroides fragilis YCH46] dbj BAD50815.1				
23354	28901124	44	2.00E-48	parahaemolyticus	conserved hypothetical protein [Bacteroides fragilis YCH46]				
				RIMD 2210633	hypothetical protein VPA1269 [Vibrio parahaemolyticus RIMD 2210633]				
					dbj BAC62612.1 hypothetical protein [Vibrio parahaemolyticus]				

23355,	30249527	48	2.00E-27	19718	Nitrosomonas europaea ATCC 19718	putative transposase [Nitrosomonas europaea ATCC 19718]				
23356					emb CAD85469.1 putative transposase [Nitrosomonas europaea ATCC 19718]					
23357,					Crocospaera	COG1252: NADH dehydrogenase, FAD-containing subunit [Crocospaera watsonii WH 8501]				1.6.99.3
23358	53735983	50	2.00E-57	19718	Bacteroides fragilis	hypothetical protein BF3562 [Bacteroides fragilis YCH46] dbj BAD50305.1				
23359,					YCH46	hypothetical protein [Bacteroides fragilis YCH46]				
23360	53714847	25	9.00E-14	YCH46						
23361,					Bacteroides fragilis	putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD46977.1				2.4.1.16
23362	53711519	32	6.00E-30	YCH46		putative glycosyltransferase [Bacteroides fragilis YCH46]				6
23363,					Cytophaga	COG0159: Tryptophan synthase alpha chain [Cytophaga hutchinsonii]				
23364	48856725	66	4.00E-47	hutchinsonii						
23367,					Cytophaga	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]				2.7.3.-
23368	48856487	38	3.00E-39	hutchinsonii		lipopolysaccharide biosynthesis [Oceanobacillus theyensis HTE831]				
23373,					Oceanobacillus	lipopolysaccharide biosynthesis [Oceanobacillus theyensis HTE831]				2.4.1.-
23374	23099221	26	4.00E-16	theyensis HTE831		phenylalanine 4-monooxygenase (phenylalanine-4-hydroxylase) [Bacillus thuringiensis serovar konkukian str. 97-27] gb AA163620.1 phenylalanine 4-monooxygenase (phenylalanine-4-hydroxylase) [Bacillus thuringiensis serovar konkukian str. 97-27]				
23375,					Bacillus					
23376	49481418	38	2.00E-35	thuringiensis serovar konkukian str. 97-27						
					Nostoc sp. PCC 7120	transcriptional regulator [Nostoc sp. PCC 7120] dbj BAB74294.1				
23379,						transcriptional regulator [Nostoc sp. PCC 7120] pir AD2130 transcription regulator alr2595 [imported] - Nostoc sp. (strain PCC 7120)				
23380	17230087	32	2.00E-19	7120						
					Cytophaga	COG0504: CTP synthase (UTP-ammonia lyase) [Cytophaga hutchinsonii]				
23381,					hutchinsonii	hypothetical protein BT3321 [Bacteroides thetaiotaomicron VPI-5482]				
23382	48856944	64	8.00E-69	Bacteroides thetaiotaomicron VPI-5482		hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			83	4.00E-07 6.3.4.2
23385,						cycle control [Cytophaga hutchinsonii]				
23386	29348730	43	3.00E-43	Cytophaga	COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cytophaga hutchinsonii]					
23387,					hutchinsonii	hydrogenase expression/formation protein HypD [Chlorobium tepidum TLS]				
23388	48853613	45	3.00E-33	hutchinsonii		hydrogenase expression/formation protein HypD [Chlorobium tepidum TLS]				
23389,					Chlorobium	hypothetical protein BF0900 [Bacteroides fragilis YCH46] dbj BAD47651.1				
23390	21674608	55	3.00E-26	tepidum TLS		hypothetical protein [Bacteroides fragilis YCH46]				
23393,					Bacteroides fragilis					
23394	53712193	25	1.00E-19	YCH46						2.7.3.-

23395,	30248905	38	2.00E-12	Nitrosomonas europaea ATCC 19718	PDZ domain (also known as DHR or GLGF) [Nitrosomonas europaea ATCC 19718] emb CAD84812.1 PDZ domain (also known as DHR or GLGF) [Nitrosomonas europaea ATCC 19718]				
23396	32473915	30	9.00E-17	Rhodopirellula baltica SH 1	alpha-L-fucosidase [Rhodopirellula baltica SH 1] emb CAD74450.1 alpha-L-fucosidase [Pirellula sp.]				3.2.1.51
23399,	23119926	35	2.00E-18	Desulfotobacterium hafniense DCB-2	COG3669: Alpha-L-fucosidase [Desulfotobacterium hafniense DCB-2]				3.2.1.51
23400	23003108	27	3.00E-07	Lactobacillus gasseri	COG2755: Lysophospholipase L1 and related esterases [Lactobacillus gasseri]				
23401,	56962028	29	1.00E-14	Bacillus clausii KSM-K16	transcriptional regulator, AraC/XylS family [Bacillus clausii KSM-K16]				
23402	53714987	63	1.00E-62	Bacteroides fragilis YCH46	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacteroides fragilis YCH46] dbj BAD50445.1 UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Bacteroides fragilis YCH46]				2.5.1.7
23403,					COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00310901.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00309724.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00309596.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00309379.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00308324.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00308306.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] outer membrane efflux protein [Bacteroides thetaiotaomicron VPI-5482] gbl AAO75667.1 outer membrane efflux protein [Bacteroides thetaiotaomicron VPI-5482]				
23409,	48856946	31	4.00E-07	Cytophaga hutchinsonii	COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00310901.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00309724.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00309596.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00309379.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00308324.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] ref ZP_00308306.1 COG2963: Transposase and inactivated derivatives [Cytophaga hutchinsonii] outer membrane efflux protein [Bacteroides thetaiotaomicron VPI-5482] gbl AAO75667.1 outer membrane efflux protein [Bacteroides thetaiotaomicron VPI-5482]				
23410	29345970	26	3.00E-19	Bacteroides thetaiotaomicron VPI-5482	putative helicase family protein [Burkholderia pseudomallei K96243] emb CAH34757.1 putative helicase family protein [Burkholderia pseudomallei K96243]				
23411,					adenylate cyclase-related protein [Shewanella oneidensis MR-1] gbl AAN54394.1 adenylate cyclase-related protein [Shewanella oneidensis MR-1]				4.6.1.1
23412	53718404	36	8.00E-29	Shewanella oneidensis MR-1	hypothetical protein BT0164 [Bacteroides thetaiotaomicron VPI-5482] gbl AAO75271.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
23413,	24372907	31	4.00E-41	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0164 [Bacteroides thetaiotaomicron VPI-5482] gbl AAO75271.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
23414	29345574	44	2.00E-68						

23421,	48853385	41	2.00E-12	Cytophaga hutchinsonii	hypothetical protein Chut02003884 [Cytophaga hutchinsonii]				
23422,				Shewanella	GGDEF domain protein [Shewanella oneidensis MR-1] gb AAN54609.1]				
23423,	24373122	36	4.00E-52	oneidensis MR-1	GGDEF domain protein [Shewanella oneidensis MR-1]				2.7.3.-
23425,				Anopheles					
23426,	31194223	40	3.00E-47	gambiae	ENSANGP0000015562 [Anopheles gambiae]				2.7.6.5
23433,				Bacteroides fragilis	O-succinylbenzoic acid-CoA ligase [Bacteroides fragilis YCH46]				
23434,	53712612	38	2.00E-23	YCH46	dbj BAD48070.1] O-succinylbenzoic acid-CoA ligase [Bacteroides fragilis YCH46]				
23435,				Thermotoga	hypothetical protein TM0358 [Thermotoga maritima MSB8] gb AAD35445.1]				
23436	15643126	26	2.00E-21	maritima MSB8	conserved hypothetical protein [Thermotoga maritima MSB8] pir F72386				
					conserved hypothetical protein - Thermotoga maritima (strain MSB8)				
23437,				Nostoc sp. PCC	two-component response regulator [Nostoc sp. PCC 7120] dbj BAB75465.1]				
23438	17231258	35	4.00E-17	7120	two-component response regulator [Nostoc sp. PCC 7120] pir AG2276 two-				2.7.3.-
					component response regulator all3766 [imported] - Nostoc sp. (strain PCC 7120)				
23441,				Cytophaga	COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases				6.2.1.1
23442	48856843	60	3.00E-47	hutchinsonii	[Cytophaga hutchinsonii]				
23443,				Caulobacter	hypothetical protein CC0341 [Caulobacter crescentus CB15]				
23444	16124596	34	4.00E-30	crescentus CB15	gb AAK22328.1] hypothetical protein [Caulobacter crescentus CB15]				3.2.1.41
					pir D87291 hypothetical protein CC0341 [imported] - Caulobacter crescentus				
23447,				Synechocystis sp.	hybrid sensory kinase [Synechocystis sp. PCC 6803] dbj BAA17056.1]				
23448	16329648	45	3.00E-44	PCC 6803	hybrid sensory kinase [Synechocystis sp. PCC 6803] pir S75142 sensory				2.7.3.-
					transduction histidine kinase sir1759 - Synechocystis sp. (strain PCC 6803)				
23449,				Bacteroides fragilis	adenylosuccinate synthetase [Bacteroides fragilis YCH46] dbj BAD50164.1]				
23450	53714706	56	7.00E-34	YCH46	adenylosuccinate synthetase [Bacteroides fragilis YCH46]				6.3.4.4
2345,				uncultured	hypothetical protein [uncultured crenarchaeote]				
2346	42557719	60	3.00E-29	crenarchaeote					
				Pseudomonas					
23451,				aeruginosa UC8PP	COG2808: Transcriptional regulator [Pseudomonas aeruginosa UC8PP-				
23452	32039397	35	6.00E-18	PA14	PA14]				
23455,				Chlorobium	hypothetical protein CT2083 [Chlorobium tepidum TLS] gb AAM73300.1]				
23456	21674893	37	7.00E-20	tepidum TLS	conserved hypothetical protein [Chlorobium tepidum TLS]				
23457,				uncultured					
23458	22596896	43	6.00E-51	bacterium	polyposphate kinase [uncultured bacterium]				2.7.4.1

23459, 23460	45658362	51	3.00E-44	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	pyridoxamine 5'-phosphate oxidase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_711347.1 Pyridoxamine 5'-phosphate oxidase [Leptospira interrogans serovar lai str. 56601] gb AA48365.1 Pyridoxamine 5'-phosphate oxidase [Leptospira interrogans serovar lai str. 56601] gb AAS71085.1 pyridoxamine 5'-phosphate oxidase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]	1.4.3.5
23461, 23462	15678496	43	7.00E-16	Methanothermobacter thermautotrophicus str. Delta H	sensory transduction histidine kinase [Methanothermobacter thermotrophicus str. Delta H] gb AAB84974.1 sensory transduction histidine kinase [Methanothermobacter thermotrophicus str. Delta H] pir C69161 sensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain Delta H)	2.7.3.-
23463, 23464	48855925	40	6.00E-16	Cytophaga hutchinsonii	COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family [Cytophaga hutchinsonii]	5.2.1.8
23465, 23466	53712193	30	5.00E-19	Bacteroides fragilis YCH46	hypothetical protein BF0900 [Bacteroides fragilis YCH46] dbj BAD47651.1 hypothetical protein [Bacteroides fragilis YCH46]	2.7.3.-
23467, 23468	48853591	50	6.00E-23	Cytophaga hutchinsonii	COG1021: Peptide arylation enzymes [Cytophaga hutchinsonii]	
23469, 23470	53714985	39	3.00E-46	Bacteroides fragilis YCH46	putative membrane peptidase [Bacteroides fragilis YCH46] dbj BAD50443.1 putative membrane peptidase [Bacteroides fragilis YCH46]	3.5.1.-
2347, 2348	ABJ18796	41	9.00E-12		Desc:Pseudomonas aeruginosa biofilm formation-related protein #60. Org:Pseudomonas aeruginosa	
23471, 23472	52548588	23	4.00E-16	uncultured archaeon GZfos17F1	FOG TPR repeat [uncultured archaeon GZfos17F1]	
23473, 23474	48854351	58	3.00E-32	Cytophaga hutchinsonii	COG1194: A/G-specific DNA glycosylase [Cytophaga hutchinsonii]	3.2.2.-
23475, 23476	48854348	54	2.00E-74	Cytophaga hutchinsonii	COG1530: Ribonucleases G and E [Cytophaga hutchinsonii]	3.1.4.-
23477, 23478	41725492	34	5.00E-14	Dechloromonas aromatica RCB	COG0232: dGTP triphosphohydrolase [Dechloromonas aromatica RCB]	3.1.5.1
23479, 23480	48854329	39	4.00E-51	Cytophaga hutchinsonii	COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii]	
23481, 23482	48856501	40	5.00E-42	Cytophaga hutchinsonii	COG1234: Metal-dependent hydrolases of the beta-lactamase superfamily III [Cytophaga hutchinsonii]	
23483, 23484	53714728	67	3.00E-45	Bacteroides fragilis YCH46	dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] dbj BAD50186.1 dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46]	2.4.1.83

23487, 23488	29346648	62	1.00E-96	Bacteroides thetaiotaomicron VPI-5482	putative RNA binding protein with S1 RNA-binding domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76345.1 putative RNA binding protein with S1 RNA-binding domain [Bacteroides thetaiotaomicron VPI-5482]				2.7.7.8
23489, 23490	53711885	42	5.00E-44	Bacteroides fragilis YCH46	GTP cyclohydrolase II [Bacteroides fragilis YCH46] dbj BAD47343.1 GTP cyclohydrolase II [Bacteroides fragilis YCH46]				3.5.4.25
2349, 2350	48854812	55	4.00E-44	Cytophaga hutchinsonii	COG1522: Transcriptional regulators [Cytophaga hutchinsonii]				
23491, 23492				Porphyromonas gingivalis W83	hypothetical protein PG0598 [Porphyromonas gingivalis W83] ref NP_904885.1 hypothetical protein PG0598 [Porphyromonas gingivalis W83]				
23493, 23494	34396719	38	4.00E-17	Cytophaga hutchinsonii	COG0770: UDP-N-acetylmuramyl pentapeptide synthase [Cytophaga hutchinsonii]				5.1.1.1
23495, 23496	48854314	43	5.00E-61	Cytophaga hutchinsonii	hypothetical protein Chut02001715 [Cytophaga hutchinsonii]				
23499, 23500	48855383	64	8.00E-61	Dechloromonas aromatica RCB	COG0493: NADPH-dependent glutamate synthase beta chain and related oxidoreductases [Dechloromonas aromatica RCB]				1.4.1.13
	41726215	56	2.00E-86		type I restriction-modification system restriction subunit [Methanosarcina mazei Go1] gb AAM31357.1 type I restriction-modification system restriction subunit [Methanosarcina mazei Go1]				
235, 236	21227763	50	3.00E-57	Methanosarcina mazei Go1	conserved hypothetical protein [Bacillus cereus G9241] gb EAL16872.1 conserved hypothetical protein [Bacillus cereus G9241]				3.1.21.3
23501, 23502	47564397	39	1.00E-23	Bacillus cereus G9241					
				Legionella pneumophila subsp. pneumophila str. Philadelphia 1	transposase (resolvase, DNA Invertase) [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28632.1 transposase (resolvase, DNA Invertase) [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]				
23503, 23504	52842780	54	8.00E-22	Philadelphia 1	hypothetical protein LIC20117 [Leptospira interrogans serovar Copenhageni str. Floccruz L1-130] ref NP_714691.1 conserved hypothetical protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51706.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS72145.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Floccruz L1-130]				
23507, 23508	45655699	25	3.00E-09	Leptospira interrogans serovar Copenhageni str. Floccruz L1-130					
23509, 23510	48854949	26	3.00E-28	Cytophaga hutchinsonii	COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii] conserved hypothetical protein-putative sodium:solute symporter [Rhodopirellula baltica SH 1] emb CAD73139.1 conserved hypothetical protein-putative sodium:solute symporter [Pirellula sp.]				
2351, 2352	32472461	32	2.00E-18	Rhodopirellula baltica SH 1					

23511,	29349999	35	6.00E-47	Bacteroides thetaiotaomicron	putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79696.1 putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482]			
23512								
23513,				Desulfitobacterium	COG1012: NAD-dependent aldehyde dehydrogenases [Desulfitobacterium			1.2.1.3
23514	23112449	52	6.00E-89	hafnense DCB-2	hafnense DCB-2]			
23521,				Bacteroides fragilis	putative translation factor [Bacteroides fragilis YCH46] dbj BAD50647.1			
23522	53715189	44	2.00E-38	YCH46	putative translation factor [Bacteroides fragilis YCH46]			
23525,				Cytophaga	COG0537: Diadenosine tetraphosphate (Ap4A) hydrolase and other HIT			
23526	48853966	58	4.00E-33	hutchinsonii	family hydrolases [Cytophaga hutchinsonii]			3.6.1.17
23527,				Bacteroides fragilis	IS110 family transposase [Bacteroides fragilis YCH46] dbj BAD48521.1			
23528	53713063	32	1.00E-23	YCH46	IS110 family transposase [Bacteroides fragilis YCH46]			
23529,				Bacteroides	ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]			
23530	29349346	34	2.00E-44	thetaiotaomicron	gb AAO79043.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]			3.6.1.-
2353,				Caulobacter	hypothetical protein CC0890 [Caulobacter crescentus CB15]			
2354	16125143	30	4.00E-13	crescentus CB15	gb AAK22875.1 hypothetical protein [Caulobacter crescentus CB15]			
23531,				Mesorhizobium sp.	pir G87359 hypothetical protein CC0890 [Imported] - Caulobacter			
23532	45681660	32	3.00E-14	BNC1	crescentus			
23533,				Cytophaga	COG3911: Predicted ATPase [Mesorhizobium sp. BNC1]			
23534	48855358	57	4.00E-38	hutchinsonii	hypothetical protein Chut02001689 [Cytophaga hutchinsonii]			
23535,				Cytophaga				
23536	48854812	44	3.00E-31	hutchinsonii	COG1522: Transcriptional regulators [Cytophaga hutchinsonii]			
23539,				Anopheles				
23540	31195963	68	3.00E-83	gambiae	ENSANGP00000000454 [Anopheles gambiae]			4.2.1.22
23541,				Anabaena variabilis				
23542	53764144	50	4.00E-41	ATCC 29413	COG1770: Protease II [Anabaena variabilis ATCC 29413]			3.4.21.8
23543,				Gluconobacter				3
23544	58002517	42	5.00E-24	oxydans 621H	ApaG protein [Gluconobacter oxydans 621H]			
23545,				Cytophaga	COG0589: Universal stress protein UspA and related nucleotide-binding			
23546	48854662	24	7.00E-12	hutchinsonii	proteins [Cytophaga hutchinsonii]			
2355,				Xanthomonas	hypothetical protein XCC4074 [Xanthomonas campestris pv. campestris str.			
2356	21233496	33	2.00E-30	ATCC 33913	ATCC 33913] gb AAM43295.1 conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913]			

23555, 23556 23557, 23558	53715557 29 3.00E-15 20	29 3.00E-15 20	Bacteroides fragilis YCH46 Cystobacter fuscus	tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] dbj BAD51015.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] hypothetical protein [Cystobacter fuscus]			
23559, 23560	34398043 27 1.00E-15 27	27 1.00E-15 27	Porphyromonas gingivalis W83	LysM domain protein [Porphyromonas gingivalis W83] ref NP_906204.1 LysM domain protein [Porphyromonas gingivalis W83]			3.2.1.-
23561, 23562	53712371 31 4.00E-37 31	31 4.00E-37 31	Bacteroides fragilis YCH46	hypothetical protein BF1079 [Bacteroides fragilis YCH46] dbj BAD47829.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
23563, 23564	29348968 49 1.00E-26 49	49 1.00E-26 49	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3559 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78665.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
23567, 23568	48855142 32 1.00E-26 32	32 1.00E-26 32	Cytophaga hutchinsonii	COG4585: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-
23569, 23570 23575, 23576	15613273 37 3.00E-45 37 48854288 36 2.00E-33 36	37 3.00E-45 37 2.00E-33 36	Bacillus halodurans C-125 Cytophaga hutchinsonii	hypothetical protein BH0710 [Bacillus halodurans C-125] dbj BAB04429.1 BH0710 [Bacillus halodurans C-125] pir F83738 hypothetical protein BH0710 [imported] - Bacillus halodurans (strain C-125) COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii]			1.1.1.18
23583, 23584	55379638 33 1.00E-08 33	33 1.00E-08 33	Haloarcula marismortui ATCC 43049	homoserine O-acetyltransferase [Haloarcula marismortui ATCC 43049] gb AAV47782.1 homoserine O-acetyltransferase [Haloarcula marismortui ATCC 43049]			2.3.1.31
23585, 23586	34556468 44 2.00E-39 44	44 2.00E-39 44	Wolinella succinogenes DSM 1740	CYTA PROTEIN PRECURSOR [Wolinella succinogenes DSM 1740] emb CAE09183.1 CYTA PROTEIN PRECURSOR [Wolinella succinogenes] emb CAC50081.1 CyfA protein [Wolinella succinogenes]			
23587, 23588	20808837 37 1.00E-27 37	37 1.00E-27 37	Thermoanaerobact er tengcongensis MB4	Membrane-associated lipoprotein involved in thiamine biosynthesis [Thermoanaerobacter tengcongensis MB4] gb AAM25612.1 Membrane-associated lipoprotein involved in thiamine biosynthesis [Thermoanaerobacter tengcongensis MB4]			
23589, 23590 23591, 23592	46141805 52 2.00E-82 52 48856061 38 1.00E-12 38	52 2.00E-82 52 1.00E-12 38	Psychrobacter sp. 273-4 Cytophaga hutchinsonii	COG3328: Transposase and inactivated derivatives [Psychrobacter sp. 273-4] hypothetical protein Chut02001296 [Cytophaga hutchinsonii]			82 1.00E-29

23593, 23594	34396861	42	2.00E-35	Porphyromonas gingivalis W83	trigger factor, putative [Porphyromonas gingivalis W83] ref[NP_905027.1] trigger factor, putative [Porphyromonas gingivalis W83]			
23595, 23596	9657128	63	2.00E-25	Vibrio cholerae O1 biovar eltor str. N16961	fructose-1,6-bisphosphatase [Vibrio cholerae O1 biovar eltor str. N16961] ref[NP_232172.1] fructose-1,6-bisphosphatase [Vibrio cholerae O1 biovar eltor str. N16961] pir[B82064 fructose-1,6-bisphosphatase VC2544 [imported] - Vibrio cholerae (strain N16961 serogroup O1)]			3.1.3.11
23597, 23598	29346223	28	5.00E-21	Bacteroides thetaiotaomicron VPI-5482	TonB [Bacteroides thetaiotaomicron VPI-5482] gb AAO75920.1 TonB [Bacteroides thetaiotaomicron VPI-5482]			
23599, 23600	53711581	60	1.00E-33	Bacteroides fragilis YCH46	ribonuclease HII [Bacteroides fragilis YCH46] dbj BAD47039.1 ribonuclease HII [Bacteroides fragilis YCH46]			3.1.26.4
23603, 23604	29347298	31	7.00E-11	Bacteroides thetaiotaomicron VPI-5482	transcriptional regulator, LuxR family [Bacteroides thetaiotaomicron VPI- 5482] gb AAO76995.1 transcriptional regulator, LuxR family [Bacteroides thetaiotaomicron VPI-5482]			
23605, 23606	37520392	34	1.00E-37	Gloeobacter violaceus PCC 7421	hypothetical protein glr0823 [Gloeobacter violaceus PCC 7421] dbj BAC88764.1 glr0823 [Gloeobacter violaceus PCC 7421]			
23607, 23608	41152672	37	1.00E-34	Geobacter sulfurreducens PCA	glycosyl transferase, group 2 family protein [Geobacter sulfurreducens PCA] helicase [Shewanella oneidensis MR-1] gb AAN53453.1 helicase [Shewanella oneidensis MR-1]			2.4.--
23611, 23612	24371966	44	8.00E-49	Shewanella oneidensis MR-1	hypothetical protein Bd3175 [Bdellovibrio bacteriovorus HD100] emb CAE80931.1 ptrB [Bdellovibrio bacteriovorus HD100]			3.4.21.8 3
23613, 23614	42524558	41	4.00E-69	Bdellovibrio bacteriovorus HD100	transposase [Riemerella anatipestifer] gb AAD33096.1 transposase [Riemerella anatipestifer]			
23615, 23616	10956806	63	2.00E-78	Riemerella anatipestifer	Acyl-CoA synthetase [Idiomarina loihiensis L2TR] gb AAV82659.1 Acyl-CoA synthetase [Idiomarina loihiensis L2TR]			6.2.1.3
23617, 23618	56460927	67	3.00E-92	Idiomarina loihiensis L2TR	COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
23619, 23620	48854285	32	2.00E-26	Cytophaga hutchinsonii				

23621, 23622	16129122	40	2.00E-12	K12	Escherichia coli	e14 prophage; restriction of DNA at 5-methylcytosine residues [Escherichia coli K12] emb CAA79520.1 methyl cytosine restriction enzyme [Escherichia coli] gb AAC74243.1 restriction of DNA at 5-methylcytosine residues; at locus of e14 element; e14 prophage; restriction of DNA at 5-methylcytosine residues [Escherichia coli K12] dbj BAA35995.1 Modified cytosine restriction protein a [Escherichia coli K12] pir A41424 5-methylcytosine-specific restriction enzyme A (EC 3.1.21.-) - Escherichia coli (strain K-12) sp P24200 MCRA_ECOLI 5-methylcytosine-specific restriction enzyme A (EcoKMcra) gb AAA69481.1 mcrA gene product				3.1.21.-
23623, 23624	29348486	53	2.00E-36	VPI-5482	Bacteroides thetaiotaomicron	ribonuclease R [Bacteroides thetaiotaomicron VPI-5482] gb AAO78183.1 ribonuclease R [Bacteroides thetaiotaomicron VPI-5482]				3.1.-
23625, 23626	20093240	27	3.00E-11	acetivorans C2A	Methanosarcina acetivorans C2A	hypothetical protein MA4454 [Methanosarcina acetivorans C2A] gb AAM07795.1 predicted protein [Methanosarcina acetivorans str. C2A]				
23627, 23628	48855337	57	8.00E-81	hutchinsonii	Cytophaga hutchinsonii	COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii]				
23629, 23630	34397767	52	6.00E-61	gingivalis W83	Porphyromonas gingivalis W83	glycogen synthase-related protein [Porphyromonas gingivalis W83] ref NP_905929.1 glycogen synthase-related protein [Porphyromonas gingivalis W83]				2.4.1.21
2363, 2364	15616225	23	1.00E-12	C-125	Bacillus halodurans C-125	[lipopolysaccharide biosynthesis [Bacillus halodurans C-125] dbj BAB07382.1 lipopolysaccharide biosynthesis [Bacillus halodurans C-125] pir G84107 lipopolysaccharide biosynthesis BH3663 [imported] - Bacillus halodurans (strain C-125)]				
23631, 23632	53712371	33	2.00E-26	YCH46	Bacteroides fragilis YCH46	hypothetical protein BF1079 [Bacteroides fragilis YCH46] dbj BAD47829.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
23633, 23634	54302415	49	5.00E-31	profundum SS9	Photobacterium profundum SS9	hypothetical protein PBPRB0736 [Photobacterium profundum SS9] emb CAG22608.1 hypothetical protein [Photobacterium profundum]				
23635, 23636	48854645	36	3.00E-31	hutchinsonii	Cytophaga hutchinsonii	COG3358: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
23637, 23638	52853520	94	4.00E-81	273-4	Psychrobacter sp. 273-4	COG0160: 4-aminobutyrate aminotransferase and related aminotransferases [Psychrobacter sp. 273-4]				2.6.1.19
23639, 23640	23485476	23	1.00E-11	yoelii	Plasmodium yoelii	hypothetical protein [Plasmodium yoelii yoelii]				3.1.11.-
23641, 23642	21228523	28	2.00E-17	mazei Go1	Methanosarcina mazei Go1	Chaperone protein [Methanosarcina mazei Go1] gb AAM32117.1 Chaperone protein [Methanosarcina mazei Go1]				
23643, 23644	48856104	37	4.00E-25	hutchinsonii	Cytophaga hutchinsonii	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii]				

23645,	30020660	54	3.00E-49	Bacillus cereus ATCC 14579	Methyltransferase [Bacillus cereus ATCC 14579] gb AAP09492.1				
23646					Methyltransferase [Bacillus cereus ATCC 14579]				
23647,									
23648	48854412	46	9.00E-33	Cytophaga hutchinsonii	COG0492: Thioredoxin reductase [Cytophaga hutchinsonii]				1,6,4,5
2365,					COG0610: Type I site-specific restriction-modification system, R (restriction)				
2366	22995174	50	2.00E-35	Xylella fastidiosa Dixon	subunit and related helicases [Xylella fastidiosa Dixon]				3,1,21,3
23651,									
23652	53714775	35	3.00E-31	Bacteroides fragilis YCH46	transcription regulator [Bacteroides fragilis YCH46] dbj BAD50233.1				
23653,					transcription regulator [Bacteroides fragilis YCH46]				
23654	54307397	58	4.00E-29	Photobacterium profundum SS9	hypothetical protein PBPR0176 [Photobacterium profundum SS9]				
					emb CAG18615.1 hypothetical protein [Photobacterium profundum]				
				Legionella					
				pneumophila subsp.					
23655,				pneumophila str.	hypothetical protein lpg1074 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27160.1 hypothetical protein lpg1074 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]				
23656	52841308	42	1.00E-22	Philadelphia 1					
23657,				Bacteroides					
23658	1066445	38	9.00E-13	vulgatus	mobB [Bacteroides vulgatus]				
23659,				Microbulbifer	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Microbulbifer degradans 2-40]				
23660	48864587	27	2.00E-20	degradans 2-40					
				Bacteroides					
23661,				thetaiotaomicron	hypothetical protein BT3291 [Bacteroides thetaiotaomicron VPI-5482]				
23662	29348700	26	2.00E-22	VPI-5482	gb AAO78397.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
23663,				Methanococcus					
23664	46141914	65	4.00E-52	burtonii DSM 6242	COG0450: Peroxiredoxin [Methanococcus burtonii DSM 6242]				1,6,4,-
23667,				Mesorhizobium sp.					
23668	45915228	38	1.00E-55	BNC1	COG1236: Predicted exonuclease of the beta-lactamase fold involved in RNA processing [Mesorhizobium sp. BNC1]				
				Legionella					
23669,				pneumophila str.	hypothetical protein lpp2210 [Legionella pneumophila str. Paris]				
23670	54298153	52	3.00E-50	Paris	emb CAH13362.1 hypothetical protein [Legionella pneumophila str. Paris]				
2367,				Sulfolobus	Aminotransferase [Sulfolobus solfataricus P2] gb AAK42830.1				
2368	15899435	38	1.00E-19	solfataricus P2	Aminotransferase [Sulfolobus solfataricus P2] pir [G90446 aminotransferase [Imported] - Sulfolobus solfataricus]				2,6,1,-
23671,					Type I restriction enzyme EcoEI R protein [Vibrio vulnificus CMCP6]				
23672	27365375	86	1.00E-138	CMCP6	gb AAO10430.1 Type I restriction enzyme EcoEI R protein [Vibrio vulnificus CMCP6]				
				Vibrio vulnificus					
					Desc:E. coli				
					CFT073 genomic				
					sequence #225.				
					Org:Escherichia coli				
						82	8,00E-22	3,1,21,3	

23673, 23674	53714874	56	5.00E-59	Bacteroides fragilis YCH46	putative outer membrane protein [Bacteroides fragilis YCH46] dbj BAD50332.1 putative outer membrane protein [Bacteroides fragilis YCH46]			
23675, 23676	48858283	57	2.00E-76	Clostridium thermocellum ATCC 27405	COG2304: Uncharacterized protein containing a von Willebrand factor type A (VWA) domain [Clostridium thermocellum ATCC 27405]			
23677, 23678	48864000	34	2.00E-20	Microbulbifer degradans 2-40	COG1428: Deoxynucleoside kinases [Microbulbifer degradans 2-40]			2.7.1.11
23679, 23680	48854772	60	9.00E-62	Cytophaga hutchinsonii	COG2234: Predicted aminopeptidases [Cytophaga hutchinsonii]			3
23681, 23682	45656536	32	1.00E-16	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	hypothetical protein LIC10638 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS69259.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			
23683, 23684	20806551	57	5.00E-27	Thermoanaerobact er tengcongensis MB4	EMAP domain [Thermoanaerobacter tengcongensis MB4] gb AAM23326.1 EMAP domain [Thermoanaerobacter tengcongensis MB4]			6.1.1.10
23685, 23686	56421039	35	1.00E-34	Geobacillus kaustophilus HTA426	chaperone protein (heat shock protein 70) (HSP70) [Geobacillus kaustophilus HTA426] dbj BAD76789.1 chaperone protein (heat shock protein 70) (HSP70) [Geobacillus kaustophilus HTA426]			3.6.1.3
2369, 2370	45657908	30	4.00E-17	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70631.1 histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			
23691, 23692	29349119	33	1.00E-13	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3711 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78816.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			2.7.1.37
23693, 23694	48854504	27	1.00E-25	Cytophaga hutchinsonii	COG1072: Panthothenate kinase [Cytophaga hutchinsonii]			
23695, 23696	29348158	30	1.00E-10	Bacteroides thetaiotaomicron VPI-5482	putative membrane-associated HD superfamily hydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO7855.1 putative membrane-associated HD superfamily hydrolase [Bacteroides thetaiotaomicron VPI-5482]			
23697, 23698	53715492	25	2.00E-16	Bacteroides fragilis YCH46	putative membrane-associated HD superfamily hydrolase [Bacteroides fragilis YCH46] dbj BAD50950.1 putative membrane-associated HD superfamily hydrolase [Bacteroides fragilis YCH46]			
23699, 23700	48853783	26	7.00E-16	Cytophaga hutchinsonii	COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii]			

237, 238	23125015	54	2.00E-27	Nostoc punctiforme PCC 73102	COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102]			2.7.3.-
23701, 23702	29348771	44	8.00E-35	Bacteroides thetaiotaomicron VPI-5482	heptosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78468.1 heptosyltransferase [Bacteroides thetaiotaomicron VPI-5482]			
23703, 23704	53715600	56	3.00E-18	Bacteroides fragilis YCH46	hypothetical protein BF4320 [Bacteroides fragilis YCH46] db BAD51058.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
23705, 23706	34762436	43	6.00E-40	Fusobacterium nucleatum subsp. Vincentii ATCC 49256	3-deoxy-manno-octulosonate cytidylyltransferase [Fusobacterium nucleatum subsp. Vincentii ATCC 49256] cytidylyltransferase [Fusobacterium nucleatum subsp. Vincentii ATCC 49256]			2.7.7.38
23707, 23708	16329450	36	2.00E-31	Synechocystis sp. PCC 6803	regulatory components of sensory transduction system [Synechocystis sp. PCC 6803] db BAA16858.1 regulatory components of sensory transduction system [Synechocystis sp. PCC 6803] pir S74707 nitrogen fixation positive activator protein - Synechocystis sp. (strain PCC 6803)			2.7.3.-
23709, 23710	29654894	42	8.00E-40	Coxiella burnetii RSA 493	hypothetical protein CBU1603 [Coxiella burnetii RSA 493] gb AAO91100.1 conserved hypothetical protein [Coxiella burnetii RSA 493]			
2371, 2372	29349869	42	1.00E-24	Bacteroides thetaiotaomicron VPI-5482	RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79566.1 RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482]			
23711, 23712	23465361	44	2.00E-18	Bifidobacterium longum NCC2705	possible alpha beta hydrolase [Bifidobacterium longum NCC2705] gb AAN24600.1 possible alpha beta hydrolase [Bifidobacterium longum NCC2705]			3.8.1.2
23713, 23714	48856184	34	3.00E-13	Cytophaga hutchinsonii	hypothetical protein Chut02001428 [Cytophaga hutchinsonii]			
23717, 23718	48856007	35	8.00E-34	Cytophaga hutchinsonii	COG0308: Aminopeptidase N [Cytophaga hutchinsonii]			3.4.11.-
23719, 23720	57234123	58	4.00E-98	Dehalococcoides ethenogenes 195	helicase domain/SNF2 family domain protein [Dehalococcoides ethenogenes 195] gb AAW39628.1 helicase domain/SNF2 family domain protein [Dehalococcoides ethenogenes 195]			
23721, 23722	48856110	61	1.00E-74	Cytophaga hutchinsonii	COG0031: Cysteine synthase [Cytophaga hutchinsonii]			4.2.99.8
23723, 23724	48856125	44	9.00E-31	Cytophaga hutchinsonii	COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii]			

23725, 23726	29349412	51	9.00E-50	[Bacteroides thetataoamlicron VPI-5482]	lipid-A-disaccharide synthase [Bacteroides thetataoamlicron VPI-5482] gb AAO79109.1 lipid-A-disaccharide synthase [Bacteroides thetataoamlicron VPI-5482]				2.4.1.18 2
23727, 23728	29347827	25	3.00E-20	[Bacteroides thetataoamlicron VPI-5482]	hypothetical protein BT2417 [Bacteroides thetataoamlicron VPI-5482] gb AAO77524.1 conserved hypothetical protein [Bacteroides thetataoamlicron VPI-5482]				
23729, 23730	16127932	47	8.00E-19	Caulobacter crescentus CB15	peptidyl-dipeptidase Dcp [Caulobacter crescentus CB15] gb AAK25664.1 peptidyl-dipeptidase Dcp [Caulobacter crescentus CB15] pir D87708 peptidyl-dipeptidase Dcp [imported] - Caulobacter crescentus				3.4.15.5
2373, 2374	48854680	25	4.00E-16	Cytophaga hutchinsonii	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii]				
23731, 23732	48855925	35	6.00E-21	Cytophaga hutchinsonii	COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family [Cytophaga hutchinsonii]				5.2.1.8
23733, 23734	31194279	38	3.00E-17	Anopheles gambiae	ENSANGP00000023840 [Anopheles gambiae]				
23735, 23736	48854578	46	1.00E-61	Cytophaga hutchinsonii	COG0768: Cell division protein FtsI/penicillin-binding protein 2 [Cytophaga hutchinsonii]				2.3.2.-
23737, 23738	32473118	34	4.00E-13	Rhodopirellula ballica SH 1	hypothetical protein RB4459 [Rhodopirellula ballica SH 1] emb CAD73798.1 conserved hypothetical protein [Pirellula sp.]				
23739, 23740	53711839	38	7.00E-38	Bacteroides fragilis YCH46	putative mutS-like mismatch repair protein [Bacteroides fragilis YCH46] db BAD47297.1 putative mutS-like mismatch repair protein [Bacteroides fragilis YCH46]				
23743, 23744	15614794	40	1.00E-35	Bacillus halodurans C-125	hypothetical protein BH2231 [Bacillus halodurans C-125] db BAB05950.1 BH2231 [Bacillus halodurans C-125] pir G83928 hypothetical protein BH2231 [imported] - Bacillus halodurans (strain C-125)				2.-.-.-
23745, 23746	28897175	23	4.00E-07	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VP0401 [Vibrio parahaemolyticus RIMD 2210633] db BAC58664.1 hypothetical protein [Vibrio parahaemolyticus]				
23749, 23750	47826743	42	3.00E-31	Streptomyces sp. AP77	beta-1,3-glucanase [Streptomyces sp. AP77]				3.2.1.-
23751, 23752	50083970	49	1.00E-48	Acinetobacter sp. ADP1	putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1] emb CAG67658.1 putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1]				4.1.99.4
23753, 23754	53712069	31	5.00E-22	Bacteroides fragilis YCH46	hypothetical protein BF0776 [Bacteroides fragilis YCH46] db BAD47527.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				

23755,	54297099	50	2.00E-21	Legionella pneumophila str. Paris	hypothetical protein lpp1144 [Legionella pneumophila str. Paris]				
23756				Paris	emb CAH112295.1 hypothetical protein [Legionella pneumophila str. Paris]				
23759,	53797086	39	1.00E-28	Chloroflexus aurantiacus	COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus]				
23760					hypothetical protein all8075 [Nostoc sp. PCC 7120] pir AD2560 hypothetical protein all8075 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120gamma dbj BAB77405.1 ORF_ID:all8075--probable helicase [Nostoc sp. PCC 7120]				3.1.21.3
23761,	17227449	31	4.00E-17	Nostoc sp. PCC 7120	D-lactate dehydrogenase [Synechococcus elongatus PCC 6301]				
23762				Synechococcus elongatus PCC 6301	dbj BAD78396.1 D-lactate dehydrogenase [Synechococcus elongatus PCC 6301] ref ZP_00164440.1 COG1052: Lactate dehydrogenase and related dehydrogenases [Synechococcus elongatus PCC 7942]				1.1.1.28
23763,	56750215	53	9.00E-48	Bacteroides thetaiotaomicron VPI-5482	penicillin-binding protein 1C (PBP-1c) [Bacteroides thetaiotaomicron VPI-5482] gb AAO75269.1 penicillin-binding protein 1C (PBP-1c) [Bacteroides thetaiotaomicron VPI-5482]				2.4.2.-
23764	29345572	51	3.00E-78	Bacillus halodurans C-125	hypothetical protein BH2088 [Bacillus halodurans C-125] dbj BAB05807.1 BH2088 [Bacillus halodurans C-125] pir H83910 hypothetical protein BH2088 [imported] - Bacillus halodurans (strain C-125) dbj BAA75367.1 Ydel [Bacillus halodurans]				
23765,	15614651	39	8.00E-32	Chlorobium	glycosyl transferase [Chlorobium tepidum TLS] gb AAM72644.1 glycosyl transferase [Chlorobium tepidum TLS]				2.4.1.83
23766	21674237	36	2.00E-28	Sulfolobus	hypothetical protein SSO3050 [Sulfolobus solfataricus P2] gb AAK43150.1				
2377,	15899755	27	3.00E-11	Sulfolobus solfataricus P2	Hypothetical protein SSO3050 [Sulfolobus solfataricus P2] pir G90486				
23771,	48855208	36	3.00E-26	Cytophaga hutchinsonii	hypothetical protein SSO3050 [imported] - Sulfolobus solfataricus				
23772					COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]				
23773,				Bacteroides thetaiotaomicron VPI-5482	putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482]				
23774	29349387	40	1.00E-30	Porphyromonas gingivalis W83	gb AAO79084.1 putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.1.1.-
23775,				Porphyromonas gingivalis W83	DNA polymerase III, gamma and tau subunits [Porphyromonas gingivalis W83] ref NP_905573.1 DNA polymerase III, gamma and tau subunits [Porphyromonas gingivalis W83]				
23776	34397409	62	1.00E-26	Cytophaga hutchinsonii	COG0635: Coproporphyrinogen III oxidase and related Fe-S oxidoreductases [Cytophaga hutchinsonii]				2.7.7.7
23777,	48854653	59	5.00E-83	Methanosarcina mazei Go1	glycosyltransferase [Methanosarcina mazei Go1] gb AAM30838.1				1.-.-.
23778					conserved hypothetical protein-putative acetyltransferase [Rhodopirellula ballica SH 1] emb CAD72907.1 conserved hypothetical protein-putative acetyltransferase [Pirellula sp.]				2.4.1.-
23779,	21227244	29	8.00E-17	Rhodopirellula ballica SH 1	glycosyltransferase [Methanosarcina mazei Go1]				2.3.1.12
23780,					conserved hypothetical protein-putative acetyltransferase [Rhodopirellula ballica SH 1] emb CAD72907.1 conserved hypothetical protein-putative acetyltransferase [Pirellula sp.]				8
23781,	32472229	43	9.00E-25	Rhodopirellula ballica SH 1					

2379, 2380	17229774	48	2.00E-26	7120	Nostoc sp. PCC 7120	serine/threonine kinase with two-component sensor domain [Nostoc sp. PCC 7120] pir AC2091 serine/threonine kinase with two-component sensor domain all 2282 [Imported] - Nostoc sp. (strain PCC 7120) dbj BAB73981.1 serine/threonine kinase with two-component sensor domain [Nostoc sp. PCC 7120]				2.7.3.-
23791, 23792	53714606	47	1.00E-73	YCH46	Bacteroides fragilis YCH46	excinuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD50064.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46]				
23793, 23794	48854339	65	9.00E-67		Cytophaga hutchinsonii	COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii]	Desc:Restriction enzyme AccII gene.			
23795, 23796	53711964	44	4.00E-65	YCH46	Bacteroides fragilis YCH46	aminopeptidase N [Bacteroides fragilis YCH46]	Org:Acinetobacter calcoaceticus	87	1.00E-07	3.4.21.-
23797, 23798	48855486	53	7.00E-38		Cytophaga hutchinsonii	aminopeptidase N [Bacteroides fragilis YCH46]				3.4.11.-
23799, 23800	53711964	43	2.00E-24	YCH46	Bacteroides fragilis YCH46	COG1721: Uncharacterized conserved protein (some members contain a von Willebrand factor type A (vWA) domain) [Cytophaga hutchinsonii]				
23801, 23802	52858290	28	9.00E-09		Lactobacillus gasserii	aminopeptidase N [Bacteroides fragilis YCH46]				
23803, 23804	48869750	35	2.00E-13		acyl-carrier-protein	COG2352: Phosphoenolpyruvate carboxylase [Lactobacillus gasserii]				4.1.1.31
2381, 2382	15899755	27	2.00E-10		Sulfolobus solfataricus P2	COG0332: 3-oxoacyl-acyl-carrier-protein synthase III [Pediococcus pentosaceus ATCC 25745]				2.3.1.38
23811, 23812	53711614	42	1.00E-59		Bacteroides fragilis YCH46	hypothetical protein SSO3050 [Sulfolobus solfataricus P2] gb AAK43150.1 Hypothetical protein SSO3050 [Sulfolobus solfataricus P2] pir G90486				
23813, 23814	29350001	26	1.00E-07		Bacteroides thetaiotaomicron VPI-5482	hypothetical protein SSO3050 [Imported] - Sulfolobus solfataricus				3.1.5.1
23815, 23816	52853363	82	6.00E-66		Psychrobacter sp. 273-4	dGTP triphosphohydrolase [Bacteroides fragilis YCH46] dbj BAD47072.1 dGTP triphosphohydrolase [Bacteroides fragilis YCH46]				
23817, 23818	52853382	78	6.00E-55		Psychrobacter sp. 273-4	hypothetical protein BT4593 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79698.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
23819, 23820	53713702	62	7.00E-99		Bacteroides fragilis YCH46	COG0569: K+ transport systems, NAD-binding component [Psychrobacter sp. 273-4]				
23821, 23822	48855500	48	2.00E-55		Cytophaga hutchinsonii	hypothetical protein Pyc03002036 [Psychrobacter sp. 273-4]				
						DNA gyrase A subunit [Bacteroides fragilis YCH46] dbj BAD49160.1 DNA gyrase A subunit [Bacteroides fragilis YCH46]				5.99.1.3
						COG0249: Mismatch repair ATPase (MutS family) [Cytophaga hutchinsonii]				

23823, 23824	48854545	57	1.00E-38	Cytophaga hutchinsonii	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Cytophaga hutchinsonii]			2.1.1.-
23825, 23826	29346224	27	3.00E-18	Bacteroides thetaiotaomicron VPI-5482	conserved hypothetical protein, putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482] gblAAO75921.1] conserved hypothetical protein, putative outer membrane protein [Bacteroides thetaiotaomicron VPI-5482]			
2383, 2384	22855032	34	1.00E-36	Bacteriophage phi- 105	ORF8 [Bacteriophage phi-105] pir T13548 hypothetical protein 8 - Bacillus phage phi-105 dbj BAA36665.1] ORF8 [Bacteriophage phi-105]			
23831, 23832	46141389	38	3.00E-15	Psychrobacter sp. 273-4	COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Psychrobacter sp. 273-4]			
23835, 23836	28379927	36	6.00E-09	Lactobacillus plantarum WCFS1	sorbitol-6-phosphate 2-dehydrogenase [Lactobacillus plantarum WCFS1] emb CAD65697.1] sorbitol-6-phosphate 2-dehydrogenase [Lactobacillus plantarum WCFS1]			1.1.1.14 0
23837, 23838	28852358	37	4.00E-41	Pseudomonas syringae pv. tomato str. DC3000	oxidoreductase, short chain dehydrogenase/reductase family [Pseudomonas syringae pv. tomato str. DC3000] ref NP_791737.1] oxidoreductase, short chain dehydrogenase/reductase family [Pseudomonas syringae pv. tomato str. DC3000]			1.1.1.10 0
23843, 23844	48854525	69	1.00E-138	Cytophaga hutchinsonii	COG0143: Methionyl-tRNA synthetase [Cytophaga hutchinsonii]	Bacteroides fragilis YCH46 DNA, complete genome	82 3.00E-12	6.1.1.10
23845, 23846	56460315	37	5.00E-23	Idiomarina loihlensis L2TR	Predicted metal-dependent amidohydrolase with the TIM-barrel fold [Idiomarina loihlensis L2TR] gblAAV82047.1] Predicted metal-dependent amidohydrolase with the TIM-barrel fold [Idiomarina loihlensis L2TR]			
23847, 23848	29346648	67	1.00E-114	Bacteroides thetaiotaomicron VPI-5482	putative RNA binding protein with S1 RNA-binding domain [Bacteroides thetaiotaomicron VPI-5482] gblAAO76345.1] putative RNA binding protein with S1 RNA-binding domain [Bacteroides thetaiotaomicron VPI-5482]	Streptococcus mutans UA159 section 65 of 185 of the complete genome	85 7.00E-07	
23849, 23850	48853628	51	6.00E-15	Cytophaga hutchinsonii	COG0006: Xaa-Pro aminopeptidase [Cytophaga hutchinsonii]			
2385, 2386	16125286	51	2.00E-87	Caulobacter crescentus CB15	GTP-binding protein LepA [Caulobacter crescentus CB15] gblAAK23018.1] GTP-binding protein LepA [Caulobacter crescentus CB15] pir F87377 GTP- binding protein LepA [imported] - Caulobacter crescentus			3.6.1.48
23851, 23852	48863907	41	9.00E-28	Microbulbifer degradans 2-40	COG5651: PPE-repeat proteins [Microbulbifer degradans 2-40]			
23853, 23854	57236797	54	5.00E-96	Flavobacterium johnsoniae	SprA [Flavobacterium johnsoniae]			

23855, 23856	27363755	75	8.00E-46	Vibrio vulnificus CMCP6	hypothetical protein VV10277 [Vibrio vulnificus CMCP6] gb AAO08810.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6]				
23857, 23858	9654540	47	3.00E-32	Vibrio cholerae O1 biovar eltor str. N16961	DPS family protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229797.1 DPS family protein [Vibrio cholerae O1 biovar eltor str. N16961] pir B82359 DPS family protein VC0139 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				
23859, 23860	32140459	62	3.00E-37	Polaribacter filamentus	tryptophan 2,3-dioxygenase [Polaribacter filamentus]				
23861, 23862	53715627	38	2.00E-24	Bacteroides fragilis YCH46	putative haloacid dehalogenase-like hydrolase [Bacteroides fragilis YCH46] dbj BAD51085.1 putative haloacid dehalogenase-like hydrolase			84	1.00E-09
23863, 23864	53711798	53	2.00E-68	Bacteroides fragilis YCH46	riboflavin biosynthesis protein RibD [Bacteroides fragilis YCH46] dbj BAD47256.1 riboflavin biosynthesis protein RibD [Bacteroides fragilis YCH46]				1.1.1.19 3
23865, 23866	48855258	29	3.00E-20	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]				
23867, 23868	53714264	45	3.00E-71	Bacteroides fragilis YCH46	folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 folypolyglutamate synthase [Bacteroides fragilis YCH46]				6.3.2.17
23869, 23870	45657718	48	2.00E-26	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	d-alanine-d-alanine ligase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70441.1 d-alanine-d-alanine ligase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				6.3.2.4
2387, 2388	53714487	56	3.00E-44	Bacteroides fragilis YCH46	SsrA-binding protein [Bacteroides fragilis YCH46] dbj BAD49945.1 SsrA- binding protein [Bacteroides fragilis YCH46]				
23871, 23872	48856909	60	8.00E-44	Cytophaga hutchinsonii	COG4276: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
23873, 23874	48854192	28	3.00E-12	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]				
23875, 23876	34396999	56	3.00E-38	Porphyromonas gingivalis W83	response regulator [Porphyromonas gingivalis W83] ref NP_905164.1 response regulator [Porphyromonas gingivalis W83]				
23877, 23878	21674076	59	2.00E-69	Chlorobium tepidum TLS	hydrolase, alpha/beta hydrolase fold family [Chlorobium tepidum TLS] gb AAM72483.1 hydrolase, alpha/beta hydrolase fold family [Chlorobium tepidum TLS]				3.1.1.1

23883,	53715650	26	6.00E-13	Bacteroides fragilis YCH46	putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD51108.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46]				
23884,				Cytophaga					
23885,	48854506	41	2.00E-18	hutchinsonii	hypothetical protein Chut0202705 [Cytophaga hutchinsonii]				
23886					biotin-acetyl-CoA-carboxylase ligase [Porphyromonas gingivalis W83] ref NP_905731.1 biotin-acetyl-CoA-carboxylase ligase [Porphyromonas gingivalis W83]				6.3.4.15
23887,	34397568	37	7.00E-33	Porphyromonas gingivalis W83	COG0188: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit [Cytophaga hutchinsonii]				5.99.1.3
23891,	48853785	58	1.00E-105	Cytophaga hutchinsonii	hypothetical protein RPA2762 [Rhodopseudomonas palustris CGA009]				
23892				Rhodopseudomonas palustris CGA009	emb CAE28204.1 conserved hypothetical protein [Rhodopseudomonas palustris CGA009]				
23899,	39935829	32	8.00E-07	s palustris CGA009	3-dehydroquininate synthase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79080.1 3-dehydroquininate synthase [Bacteroides thetaiotaomicron VPI-5482]				4.2.3.4
239,	29349383	43	4.00E-28	Bacteroides thetaiotaomicron VPI-5482	COG0030: Dimethyladenosine transferase (RNA methylation) [Cytophaga hutchinsonii]				2.1.1.-
23903,	48853962	58	8.00E-75	Cytophaga hutchinsonii	DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46] dbj BAD50897.1 DNA-directed RNA polymerase alpha chain [Bacteroides fragilis YCH46]				2.7.7.6
23905,	53715439	69	5.00E-80	Bacteroides fragilis YCH46	COG1482: Phosphomannose isomerase [Cytophaga hutchinsonii]				5.3.1.8
23906				Cytophaga	COG0179: 2-keto-4-pentenolate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase (catechol pathway) [Cytophaga hutchinsonii]				3.7.1.5
23907,	48855901	51	9.00E-60	hutchinsonii	serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130] gb AAS70895.1 serine/threonine kinase with GAF domain [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130]				
23908				Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130	DNA polymerase IV (family X) [Thermoanaerobacter tengcongensis MB4] gb AAM25645.1 DNA polymerase IV (family X) [Thermoanaerobacter tengcongensis MB4]				2.7.7.7
23909,	48856479	54	5.00E-44	hutchinsonii	conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_900602.1 hypothetical protein CV0932 [Chromobacterium violaceum ATCC 12472]				
23910					putative sugar hydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79068.1 putative sugar hydrolase [Bacteroides thetaiotaomicron VPI-5482]				
23911,	45658172	33	2.00E-34	Thermoanaerobacter tengcongensis MB4					
23912	20808870	35	5.00E-22	Chromobacterium violaceum ATCC 12472					
23913,									
23914	34102240	44	1.00E-20	Bacteroides thetaiotaomicron VPI-5482					
23915,									
23916	29349371	52	3.00E-74	Bacteroides thetaiotaomicron VPI-5482					

23917,	37222111	75	5.00E-90	uncultured bacterium	Uvs062 [uncultured bacterium]				
23918	32475352	29	6.00E-20	Rhodopirellula baltica SH 1	hypothetical protein RB8406 [Rhodopirellula baltica SH 1] emb CAD78624.1				
23919,				Bacteroides thetaiotaomicron VPI-5482	ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]				
23920	29349252	49	6.00E-72	Bacteroides thetaiotaomicron VPI-5482	gb AAO78949.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]				3.6.1.-
23921,	53713725	62	1.00E-79	Bacteroides fragilis YCH46	prolyl-tRNA synthetase [Bacteroides fragilis YCH46]				6.1.1.15
23922,				Chloroflexus aurantiacus	COG4898: Uncharacterized protein conserved in bacteria [Chloroflexus aurantiacus]				
23923,	53796261	72	4.00E-39						
23924									
23925,									
23926									
23927,									3.1.31.1
23928									
2393,	48856599	44	6.00E-33	Cytophaga hutchinsonii	COG0848: Biopolymer transport protein [Cytophaga hutchinsonii]				
2394									
23931,	48893454	58	1.00E-26	Trichodesmium erythraeum IMS101	COG1012: NAD-dependent aldehyde dehydrogenases [Trichodesmium erythraeum IMS101]				1.2.1.16
23932									
23933,									
23934	46142168	48	6.00E-63	Methanococcoides burtonii DSM 6242	COG1012: NAD-dependent aldehyde dehydrogenases [Methanococcoides burtonii DSM 6242]				1.2.1.16
23939,	31194225	51	8.00E-41	Anopheles gambiae	ENSANGP00000000349 [Anopheles gambiae]				1.5.1.3
23940									
23947,	29347921	51	1.00E-31	Bacteroides thetaiotaomicron VPI-5482	putative transcription regulator [Bacteroides thetaiotaomicron VPI-5482]				
23948									
2395,	48833666	29	4.00E-19	Magnetococcus sp. MC-1	COG0702: Predicted nucleoside-diphosphate-sugar epimerases [Magnetococcus sp. MC-1]				5.1.3.13
2396									
23951,	48856392	40	3.00E-25	Cytophaga hutchinsonii	COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii]				
23952,									
23953,	24371625	50	9.00E-38	Shewanella oneidensis MR-1	hypothetical flavodoxin [Shewanella oneidensis MR-1] gb AAAN53112.1 conserved hypothetical protein [Shewanella oneidensis MR-1]				1.3.3.4
23954									
23955,	17229665	48	5.00E-19	Nostoc sp. PCC 7120	hypothetical protein air2173 [Nostoc sp. PCC 7120] pir JAG2077 hypothetical protein air2173 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73872.1				
23956									
23957,	48854368	60	3.00E-52	Cytophaga hutchinsonii	COG1137: ABC-type (unclassified) transport system, ATPase component [Cytophaga hutchinsonii]				1.8.-.-
23958									

23959, 23960	28897146	37	3.00E-38	Vibrio parahaemolyticus RIMD 2210633	putative hemolysin [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58635.1 putative hemolysin [Vibrio parahaemolyticus] conserved domain protein [Porphyromonas gingivalis W83] ref NP_906133.1 hypothetical protein PG2071 [Porphyromonas gingivalis W83]					2.3.1.51
23961, 23962	34397972	35	5.00E-36	Porphyromonas gingivalis W83	exodeoxyribonuclease III [Porphyromonas gingivalis W83] ref NP_904590.1 exodeoxyribonuclease III [Porphyromonas gingivalis W83] COG4753: Response regulator containing CheY-like receiver domain and AraC-type DNA-binding domain [Cytophaga hutchinsonii]					3.1.11.2
23963, 23964	34396422	57	1.00E-87	Porphyromonas gingivalis W83	hypothetical protein LIC13303 [Leptospira interrogans serovar Copenhagen] str. Flocruz L1-130] gb AA571845.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130] glutamine amidotransferase, class II/dipeptidase [Porphyromonas gingivalis W83] ref NP_905813.1 glutamine amidotransferase, class II/dipeptidase [Porphyromonas gingivalis W83]					3.4.13.1 9
23965, 23966	48856986	36	3.00E-14	Cytophaga hutchinsonii	Eps6E [Streptococcus thermophilus] unknown [uncultured bacterium] COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii]					2.7.8.6
23967, 23968	45659122	31	3.00E-07	Leptospira interrogans serovar Copenhagen str. Flocruz L1-130	conserved hypothetical protein-putative integral membrane protein [Rhodopirellula ballica SH 1] emb CAD77840.1 conserved hypothetical protein-putative integral membrane protein [Pirellula sp.] COG0438: Glycosyltransferase [Pseudomonas fluorescens PfO-1]					
23969, 23970	34397650	35	1.00E-48	Porphyromonas gingivalis W83	COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii] (3R)-hydroxymyristoyl-(acyl-carrier-protein) dehydratase, putative [Coxiella burnetii RSA 493] gb AAO89605.1 (3R)-hydroxymyristoyl-(acyl-carrier- protein) dehydratase, putative [Coxiella burnetii RSA 493] COG0627: Predicted esterase [Microbulifer degradans 2-40]					4.2.1.-
2397, 2398	24637443	32	3.00E-15	Streptococcus thermophilus	putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD49534.1 putative glycosyltransferase [Bacteroides fragilis YCH46]					2.4.1.-
23975, 23976	29611405	26	7.00E-08	uncultured bacterium						
23977, 23978	48857000	37	3.00E-15	Cytophaga hutchinsonii						
23981, 23982	32477769	56	4.00E-69	Rhodopirellula ballica SH 1						
23983, 23984	48731496	42	2.00E-50	Pseudomonas fluorescens PfO-1						
23985, 23986	48856125	46	7.00E-35	Cytophaga hutchinsonii						
23987, 23988	29653399	35	8.00E-23	Coxiella burnetii RSA 493						
23989, 23990	48863772	31	7.00E-30	Microbulifer degradans 2-40						
2399, 2400	53714076	27	1.00E-14	Bacteroides fragilis YCH46						

23993,	53711313	52	4.00E-63	Bacteroides fragilis YCH46	L-aspartate oxidase [Bacteroides fragilis YCH46] dbj BAD46771.1 L-aspartate oxidase [Bacteroides fragilis YCH46]	1.4.3.16
23994						
23995,	48863242	33	1.00E-24	Microbulbifer degradans 2-40	hypothetical protein Mdeg02001316 [Microbulbifer degradans 2-40]	2.4.1.-
23996				Vibrio vulnificus	putative hemolysin [Vibrio vulnificus YJ016] dbj BAC93559.1 putative hemolysin [Vibrio vulnificus YJ016]	
24000	37678979	33	3.00E-34	Vibrio	putative hemolysin [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58635.1 putative hemolysin [Vibrio parahaemolyticus]	
24001,				parahaemolyticus	hypothetical spermidine synthase [Shewanella oneidensis MR-1]	
24002	28897146	38	1.00E-21	RIMD 2210633	hypothetical protein [Shewanella oneidensis MR-1]	
24007,				Shewanella	tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]	2.5.1.16
24008	24372547	29	1.00E-08	oneidensis MR-1	COG0438: Glycosyltransferase [Geobacter metallireducens GS-15]	
2401,				Geobacter	tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]	2.4.1.-
2402	48847339	34	2.00E-12	metallireducens GS	hypothetical protein BT4619 [Bacteroides thetaiotaomicron VPI-5482]	
24011,				Bacteroides fragilis YCH46	glycosyltransferase [Bacillus clausii KSM-K16] dbj BAD65698.1	
24012	53713347	27	2.00E-22	YCH46	hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]	
24013,				Bacteroides	COG0307: Riboflavin synthase alpha chain [Cytophaga hutchinsonii]	2.5.1.9
24014	29350027	42	3.00E-21	VPI-5482	glycosyltransferase [Bacillus clausii KSM-K16] dbj BAD65698.1	
24015,				Cytophaga	glycosyltransferase [Bacillus clausii KSM-K16]	
24016	48856513	55	1.00E-26	hutchinsonii	hypothetical protein PG1492 [Porphyromonas gingivalis W83]	
24017,				Bacillus clausii	ref NP_905638.1 hypothetical protein PG1492 [Porphyromonas gingivalis W83]	
24018	56964929	52	9.00E-11	KSM-K16	ENSANGP000000000334 [Anopheles gambiae]	
24019,				Porphyromonas	COG0034: Glutamine phosphoribosylpyrophosphate amidotransferase [Cytophaga hutchinsonii]	2.4.2.14
24020	34397475	31	3.00E-08	gingivalis W83	aminotransferase, DegT/DnrJ/EryC1 family [Treponema denticola ATCC 35405] gb AAS11943.1 aminotransferase, DegT/DnrJ/EryC1 family [Treponema denticola ATCC 35405]	
24021,				Anopheles	Trk system K+ uptake protein TrkA [Bacteroides fragilis YCH46]	
24022	31194161	54	3.00E-43	gambiae	dbj BAD47623.1 Trk system K+ uptake protein TrkA [Bacteroides fragilis YCH46]	
24025,				Cytophaga		
24026	48854452	51	5.00E-93	hutchinsonii		
24027,				Treponema		
24028	42526934	53	3.00E-44	denticola ATCC 35405		
24029,				Bacteroides fragilis		
24030	53712165	38	2.00E-41	YCH46		

2403, 2404	29349121	41	3.00E-49	Bacteroides thetaitaomicron VPI-5482	D-alanine-D-alanine ligase [Bacteroides thetaitaomicron VPI-5482] gb AAO78818.1 D-alanine-D-alanine ligase [Bacteroides thetaitaomicron VPI-5482] sp Q8A1F3 DDL_BACTN D-alanine-D-alanine ligase (D- alanylalanine synthetase) (D-Ala-D-Ala ligase)				6.3.2.4	
24033, 24034	48854117	51	1.00E-32	Cytophaga hutchinsonii	COG1846: Transcriptional regulators [Cytophaga hutchinsonii]					
24035, 24036	52548776	44	4.00E-70	uncultured archaeon GZfos18F2	asparagine synthetase protein [uncultured archaeon GZfos18F2] dbj BAD49154.1 chloramphenicol acetyltransferase (CAT-III) [Bacteroides fragilis YCH46]				6.3.5.4	
24037, 24038	53713696	41	3.00E-34	Bacteroides fragilis YCH46	hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_232756.1 hypothetical protein VCA0361 [Vibrio cholerae O1 biovar eltor str. N16961] pir H82467 hypothetical protein VCA0361 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				2.3.1.28	
24039, 24040	9657761	32	3.00E-17	N16961	repAC1 [Buchnera aphidicola]					
24043, 24044	4160158	25	2.00E-07	Buchnera aphidicola		Desc:Listeria monocytogenes 4b contig DNA sequence #786. Org:Listeria monocytogenes 4b	87	3.00E-12		
24045, 24046	48854713	54	2.00E-85	Cytophaga hutchinsonii	COG0542: ATPases with chaperone activity, ATP-binding subunit [Cytophaga hutchinsonii] hypothetical protein PBPRB1077 [Photobacterium profundum SS9] emb CAG22949.1 conserved hypothetical protein [Photobacterium profundum]					
24047, 24048	54302756	39	2.00E-13	Photobacterium profundum SS9	D-alanine-D-alanine ligase [Bacteroides thetaitaomicron VPI-5482] gb AAO78818.1 D-alanine-D-alanine ligase [Bacteroides thetaitaomicron VPI-5482] sp Q8A1F3 DDL_BACTN D-alanine-D-alanine ligase (D- alanylalanine synthetase) (D-Ala-D-Ala ligase)				6.3.2.4	
2405, 24055, 24056	29349121	41	2.00E-25	Bacteroides thetaitaomicron VPI-5482	COG5587: Uncharacterized conserved protein [Cytophaga hutchinsonii] ABC transporter ATP-binding protein [Bacteroides thetaitaomicron VPI- 5482] gb AAO77281.1 ABC transporter ATP-binding protein [Bacteroides thetaitaomicron VPI-5482] COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii]					
24057, 24058	48856669	47	8.00E-54	Cytophaga hutchinsonii						
24059, 24060	29347584	32	7.00E-25	Bacteroides thetaitaomicron VPI-5482						
24061, 24062	48856477	33	3.00E-12	Cytophaga hutchinsonii						
	48856922	45	5.00E-24	Cytophaga hutchinsonii	COG0841: Cation/multidrug efflux pump [Cytophaga hutchinsonii]					

24063, 24064	17229898	33	1.00E-07	Nostoc sp. PCC 7120	hypothetical protein alr2407 [Nostoc sp. PCC 7120] pir AH2106 hypothetical protein alr2407 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB74106.1 alr2407 [Nostoc sp. PCC 7120]				
24065, 24066	9658341	30	7.00E-24	Vibrio cholerae O1 biovar eltor str. N16961	methyl-accepting chemotaxis protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_233291.1 methyl-accepting chemotaxis protein [Vibrio cholerae O1 biovar eltor str. N16961] pir H82402 methyl-accepting chemotaxis protein VCA0906 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				
24067, 24068	48856487	40	2.00E-43	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]				2.7.3.-
24069, 24070	53714999	38	1.00E-09	Bacteroides fragilis YCH46	polyphosphate kinase [Bacteroides fragilis YCH46] dbj BAD50457.1				2.7.4.1
24071, 24072	52627365	46	8.00E-40	Prevotella intermedia	phosphorylase family protein [Prevotella intermedia]				2.4.2.3
24073, 24074	34396629	31	6.00E-31	Porphyromonas gingivalis W83	conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_904796.1 hypothetical protein PG0501 [Porphyromonas gingivalis W83]				
24075, 24076	29347634	30	4.00E-23	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT2224 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77331.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
24083, 24084	48855830	52	3.00E-36	Cytophaga hutchinsonii	hypothetical protein Chut02001042 [Cytophaga hutchinsonii]				
24087, 24088	52698755	34	7.00E-33	Rickettsia akari str. Hartford	COG2194: Predicted membrane-associated, metal-dependent hydrolase [Rickettsia akari str. Hartford]				
24089, 24090	24374921	35	3.00E-48	Shewanella oneidensis MR-1	protease, putative [Shewanella oneidensis MR-1] gb AAN56408.1 protease, putative [Shewanella oneidensis MR-1]				3.4.21.-
2409, 2410	48854462	46	7.00E-26	Cytophaga hutchinsonii	COG0796: Glutamate racemase [Cytophaga hutchinsonii]				5.1.1.3
24091, 24092	4164093	25	1.00E-09	Bacteroides fragilis	BfmC [Bacteroides fragilis]				
24095, 24096	53711532	36	2.00E-23	Bacteroides fragilis YCH46	RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD46990.1 RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46]				
24097, 24098	53715046	48	1.00E-58	Bacteroides fragilis YCH46	acetylactate synthase large subunit [Bacteroides fragilis YCH46] dbj BAD50504.1 acetylactate synthase large subunit [Bacteroides fragilis YCH46]				4.1.3.18
24099, 24100	53712708	43	5.00E-71	Bacteroides fragilis YCH46	hypothetical protein BF1415 [Bacteroides fragilis YCH46] dbj BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
24103, 24104	AAE3396	39	2.00E-39		Desc:Acetobacter turbidans alpha-amino ester hydrolase mutant protein #4. Org:Acetobacter turbidans				

24105, 24106	53691878	31	2.00E-22	Desulfovibrio desulfuricans G20	COG0739: Membrane proteins related to metalloendopeptidases [Desulfovibrio desulfuricans G20]				
24109, 24110	15893313	41	7.00E-25	Clostridium acetobutylicum ATCC 824	D-3-phosphoglycerate dehydrogenase [Clostridium acetobutylicum ATCC 824] gb AAK78002.1 D-3-phosphoglycerate dehydrogenase [Clostridium acetobutylicum ATCC 824] pir G96901 D-3-phosphoglycerate dehydrogenase [imported] - Clostridium acetobutylicum				1.1.1.95
24111, 24112	48853533	48	1.00E-40	Cytophaga hutchinsonii	COG2825: Outer membrane protein [Cytophaga hutchinsonii]				
24111, 24112	34397297	42	2.00E-53	Porphyromonas gingivalis W83	conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_905461.1 hypothetical protein PG1280 [Porphyromonas gingivalis W83]				
24117, 24118	48853461	37	1.00E-27	Cytophaga hutchinsonii	COG3839: ABC-type sugar transport systems, ATPase components [Cytophaga hutchinsonii]				
24121, 24122	48856700	54	1.00E-40	Cytophaga hutchinsonii	COG1541: Coenzyme F390 synthetase [Cytophaga hutchinsonii]				
24123, 24124	9654589	46	2.00E-72	Vibrio cholerae O1 blovar eltor str. N16961	transposase, putative [Vibrio cholerae O1 blovar eltor str. N16961] ref NP_229842.1 transposase, putative [Vibrio cholerae O1 blovar eltor str. N16961] pir D82355 probable transposase VC0185 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				
24125, 24126	15895127	45	2.00E-56	Clostridium acetobutylicum ATCC 824	Magnesium and cobalt transport protein [Clostridium acetobutylicum ATCC 824] gb AAK79816.1 Magnesium and cobalt transport protein [Clostridium acetobutylicum ATCC 824] pir E97128 magnesium and cobalt transport protein CAC1852 [imported] - Clostridium acetobutylicum				
24127, 24128	53713469	56	6.00E-40	Bacteroides fragilis YCH46	putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1 putative helicase [Bacteroides fragilis YCH46]				
24129, 24130	29653396	36	2.00E-08	Coxiella burnetii RSA 493	hypothetical protein CBU0033 [Coxiella burnetii RSA 493] gb AAO89602.1 hypothetical protein CBU0033 [Coxiella burnetii RSA 493]				
2413, 2414	53766201	42	1.00E-49	Rubrobacter xylanophilus DSM 9941	COG2141: Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases [Rubrobacter xylanophilus DSM 9941]				1.5.99.9
24131, 24132	23126057	22	9.00E-07	Nostoc punctiforme PCC 73102	COG0457: FOG: TPR repeat [Nostoc punctiforme PCC 73102]				
24133, 24134	48860822	59	2.00E-36	Microbubifer degradans 2-40	COG0229: Conserved domain frequently associated with peptide methionine sulfoxide reductase [Microbubifer degradans 2-40]				1.8.4.6
24135, 24136	24371966	74	1.00E-118	Shewanella oneidensis MR-1	helicase [Shewanella oneidensis MR-1] gb AAN53453.1 helicase [Shewanella oneidensis MR-1]				

24137, 24138	18311295	64	7.00E-77	Clostridium perfringens str. 13	hypothetical protein CPE2313 [Clostridium perfringens str. 13] dbj BAB82019.1 conserved hypothetical protein [Clostridium perfringens str. 13]			4.2.1.70
24143, 24144	56965587	28	7.00E-16	Bacillus clausii KSM-K16	nuclease inhibitor [Bacillus clausii KSM-K16] dbj BAD66360.1 nuclease inhibitor [Bacillus clausii KSM-K16]			
24145, 24146	52549170	40	6.00E-43	uncultured archaeon GZfos26B2	two-component sensor histidine kinase [uncultured archaeon GZfos26B2]			2.7.3.-
24149, 24150	48893909	44	4.00E-25	Trichodesmium erythraeum IMS101	COG4251: Bacteriophytochrome (light-regulated signal transduction histidine kinase) [Trichodesmium erythraeum IMS101]			2.7.3.-
2415, 2416	48858507	30	2.00E-07	Clostridium thermocellum ATCC 27405	COG3507: Beta-xylosidase [Clostridium thermocellum ATCC 27405]			
24151, 24152	15643773	52	1.00E-36	Thermotoga maritima MSB8	glutamate dehydrogenase [Thermotoga maritima MSB8] gb AAD36092.1 glutamate dehydrogenase [Thermotoga maritima MSB8] sp P96110 DHE3_THEME Glutamate dehydrogenase (GDH) pir G72305 glutamate dehydrogenase - Thermotoga maritima (strain MSB8)		1.4.1.3	
24155, 24156	48854139	62	4.00E-59	Cytophaga hutchinsonii	COG1066: Predicted ATP-dependent serine protease [Cytophaga hutchinsonii]			
24159, 24160	37675978	55	5.00E-45	Vibrio vulnificus YJ016	bacterial lipocalin [Vibrio vulnificus YJ016] dbj BAC96344.1 bacterial lipocalin [Vibrio vulnificus YJ016]			
24161, 24162	21232979	32	6.00E-21	Xanthomonas campestris pv. campestris str. ATCC 33913	hypothetical protein XCC3550 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM42820.1 conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913]			
24163, 24164	27363931	42	5.00E-35	Vibrio vulnificus CMCP6	Polyphosphate kinase [Vibrio vulnificus CMCP6] gb AAO08986.1 Polyphosphate kinase [Vibrio vulnificus CMCP6] sp Q8DEW2 PPK_VIBVU Polyphosphate kinase (Polyphosphoric acid kinase) (ATP-polyphosphate phosphotransferase)			2.7.4.1
24165, 24166	54307921	55	2.00E-38	Photobacterium profundum SS9	putative polyphosphate kinase [Photobacterium profundum SS9] emb CAG19139.1 putative polyphosphate kinase [Photobacterium profundum]			2.7.4.1
24167, 24168	17231523	35	1.00E-33	Nostoc sp. PCC 7120	periplasmic-binding protein of ABC transporter [Nostoc sp. PCC 7120] pir AH2309 periplasmic-binding protein of ABC transporter alr4031 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75730.1 periplasmic- binding protein of ABC transporter [Nostoc sp. PCC 7120]			
24169, 24170	56460557	48	4.00E-47	Idiomarina loihensis L2TR	Alpha/beta superfamily hydrolase [Idiomarina loihensis L2TR] gb AAV82289.1 Alpha/beta superfamily hydrolase [Idiomarina loihensis L2TR]			

2417, 2418	39996605	63	2.00E-91	Geobacter sulfurreducens PCA	ABC transporter, ATP-binding protein [Geobacter sulfurreducens PCA] gb AAR34879.1 ABC transporter, ATP-binding protein [Geobacter sulfurreducens PCA]			1.8.-
24171, 24172	21673717	38	1.00E-43	Chlorobium tepidum TLS	phosphoglycolate phosphatase [Chlorobium tepidum TLS] gb AAM72124.1 phosphoglycolate phosphatase [Chlorobium tepidum TLS]			3.1.3.18
24173, 24174	53715107	33	4.00E-26	Bacteroides fragilis YCH46	putative N-acetylmuramoyl-L-alanine amidase AmiA [Bacteroides fragilis YCH46] db BAD50565.1 putative N-acetylmuramoyl-L-alanine amidase AmiA [Bacteroides fragilis YCH46]			3.5.1.28
24175, 24176	56962411	28	9.00E-07	Bacillus clausii KSM-K16	hypothetical protein ABC0637 [Bacillus clausii KSM-K16] db BAD63176.1 hypothetical protein [Bacillus clausii KSM-K16]			
24177, 24178	48838149	30	5.00E-36	Methanosarcina barkeri str. fusaro	COG2202: FOG: PAS/PAC domain [Methanosarcina barkeri str. fusaro]			2.7.3.-
24179, 24180	45659150	43	2.00E-38	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS71873.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			2.7.3.-
24181, 24182	21231194	38	6.00E-10	Xanthomonas campestris pv. campestris str. ATCC 33913	2-oxo-3-deoxygalactonate kinase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM41035.1 2-oxo-3-deoxygalactonate kinase [Xanthomonas campestris pv. campestris str. ATCC 33913]			2.7.1.58
24183, 24184	52425546	59	5.00E-71	Mannheimia succiniciproducens MBEL55E	CarB protein [Mannheimia succiniciproducens MBEL55E] gb AAU38098.1 CarB protein [Mannheimia succiniciproducens MBEL55E]			
24185, 24186	48854285	32	1.00E-19	Cytophaga hutchinsonii	COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
24187, 24188	29349036	43	1.00E-45	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3628 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78733.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
24189, 24190	56460695	47	3.00E-26	Idiomarina lohiensis L2TR	Glyoxalase/dioxygenase superfamily protein [Idiomarina lohiensis L2TR] gb AAV82427.1 Glyoxalase/dioxygenase superfamily protein [Idiomarina lohiensis L2TR]			
2419, 2420	2511751	58	1.00E-29	Rhodobacter capsulatus	tyrosine-phenol-lyase [Rhodobacter capsulatus] sp O30971 TNAA_RHOCA Tryptophanase (L-tryptophan indole-lyase) (TNase) pir T45297 tyrosine phenol-lyase (EC 4.1.99.2) [Imported] - Rhodobacter capsulatus			4.1.99.2
24191, 24192	46321822	34	1.00E-10	Burkholderia cepacia R1808	COG1522: Transcriptional regulators [Burkholderia cepacia R1808]			
24193, 24194	48854355	64	1.00E-66	Cytophaga hutchinsonii	COG1200: RecG-like helicase [Cytophaga hutchinsonii]			3.6.1.-

24197, 24198, 24199, 24200	48855120 48856384	70 22	1.00E-109 3.00E-10	Cytophaga hutchinsonii Cytophaga hutchinsonii	COG0495: Leucyl-tRNA synthetase [Cytophaga hutchinsonii] hypothetical protein Chut02000101 [Cytophaga hutchinsonii]	Flavobacterium johnsoniae LeuS (leuS) gene, partial cds; and Fjo12 (fjo12), FtsX (ftsX), Fjo13 (fjo13), BacA (bacA), and TruB (truB) genes, complete cds	80 4.00E-17	6.1.1.4
24201, 24202	28855211	34	4.00E-14	Pseudomonas syringae pv. tomato str. DC3000	esterase/lipase/thioesterase family protein [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794577.1 esterase/lipase/thioesterase family protein [Pseudomonas syringae pv. tomato str. DC3000]			
24203, 24204	56480140	34	2.00E-07	Shigella flexneri 2a str. 301	hypothetical protein SF2623 [Shigella flexneri 2a str. 301] gb AA44120.2 orf, conserved hypothetical protein [Shigella flexneri 2a str. 301] ref NP_838134.1 hypothetical protein S2796 [Shigella flexneri 2a str. 24577] gb AAP17944.1 hypothetical protein S2796 [Shigella flexneri 2a str. 24577]			
24208, 24210	29346727	53	2.00E-35	Bacteroides thetaiotaomicron VPI-5482	riboflavin synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO76424.1 riboflavin synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482]			2.5.1.9
2421, 2422	4049885	33	3.00E-26	Melanoplus sanguinipes entomopoxvirus	ORF MSV027 tryptophan repeat gene family protein [Melanoplus sanguinipes entomopoxvirus] pir T28188 hypothetical protein ORF29 - Melanoplus sanguinipes entomopoxvirus (isolate Tuscon) ref NP_048098.1 ORF MSV027 tryptophan repeat gene family protein [Melanoplus sanguinipes entomopoxvirus]			
24211, 24212	23501247	28	4.00E-08	Brucella suis 1330	DNA-binding response regulator, LuxR family [Brucella suis 1330] ref NP_540499.1 TRANSCRIPTIONAL REGULATORY PROTEIN DEGU [Brucella melitensis 16M] gb AAN29289.1 DNA-binding response regulator, LuxR family [Brucella suis 1330] gb AAL52763.1 two-component response regulator [Brucella melitensis 16M] pir AH3449 transcription regulatory protein degU [imported] - Brucella melitensis (strain 16M)			
24213, 24214	53712193	23	1.00E-20	Bacteroides fragilis YCH46	hypothetical protein BF0900 [Bacteroides fragilis YCH46] db BAD47651.1 hypothetical protein [Bacteroides fragilis YCH46]			2.7.3.-
24215, 24216	48856044	50	7.00E-74	Cytophaga hutchinsonii	COG2908: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			3.6.1.-

24217, 24218	29348158	53	5.00E-49	Bacteroides thetaiotaomicron VPI-5482	putative membrane-associated HD superfamily hydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77855.1 putative membrane-associated HD superfamily hydrolase [Bacteroides thetaiotaomicron VPI-5482]				
24219, 24220	29348158	28	4.00E-20	Bacteroides thetaiotaomicron VPI-5482	putative membrane-associated HD superfamily hydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77855.1 putative membrane-associated HD superfamily hydrolase [Bacteroides thetaiotaomicron VPI-5482]				
24221, 24222	34397011	29	8.00E-25	Porphyromonas gingivalis W83	ABC transporter, permease protein, putative [Porphyromonas gingivalis W83] ref NP_905176.1 ABC transporter, permease protein, putative [Porphyromonas gingivalis W83]				
24225, 24226	48856113	36	2.00E-30	Cytophaga hutchinsonii	COG0212: 5-formyltetrahydrofolate cyclo-ligase [Cytophaga hutchinsonii] probable transmembrane protein [Chromobacterium violaceum ATCC 12472] ref NP_903091.1 probable transmembrane protein [Chromobacterium violaceum ATCC 12472]	6.3.3.2			
24227, 24228	34332880	56	1.00E-29	Chromobacterium violaceum ATCC 12472	COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii]				
24229, 24230	48853602	49	5.00E-53	Cytophaga hutchinsonii	hypothetical protein Chut02002705 [Cytophaga hutchinsonii] putative transposase [Yersinia pestis] ref YP_071802.1 putative transposase [Yersinia pseudotuberculosis IP 32953] ref YP_070613.1 putative transposase [Yersinia pseudotuberculosis IP 32953] ref YP_069318.1 putative transposase-like protein [Yersinia pseudotuberculosis IP 32953] ref YP_069245.1 putative transposase [Yersinia pseudotuberculosis IP 32953] ref YP_068733.1 putative transposase for IS285 insertion element [Yersinia pseudotuberculosis IP 32953] ref NP_994772.1 transposase for the IS285 insertion element [Yersinia pestis biovar Medievalis str. 91001] ref NP_994258.1 transposase for the IS285 insertion element [Yersinia pestis biovar Medievalis str. 91001] ref NP_994158.1 transposase for the IS285 insertion element [Yersinia pestis biovar Medievalis str. 91001] ref NP_994064.1 transposase for the IS285 insertion element [Yersinia pestis biovar Medievalis str. 91001] ref NP_993887.1 transposase for the IS285 insertion element [Yersinia pestis biovar Medievalis str. 91001] ref NP_993762.1 transposase for the IS285 insertion element [Yersinia pestis biovar Medievalis str. 91001] ref NP	3.6.1.-			
24231, 24232	52788138	66	1.00E-123	Yersinia pestis	COG4679: Phage-related protein [Cytophaga hutchinsonii] O6-methylguanine-DNA methyltransferase [Bacillus cereus G9241] gb EAL14768.1 O6-methylguanine-DNA methyltransferase [Bacillus cereus G9241]				2.1.1.63
24233, 24234	48856841	38	1.00E-07	Cytophaga hutchinsonii					
24235, 24236	47566806	51	1.00E-41	Bacillus cereus G9241					

24237, 24238	53711669	29	2.00E-13	Bacteroides fragilis YCH46	putative TonB-dependent receptor [Bacteroides fragilis YCH46] dbj BAD47127.1 putative TonB-dependent receptor [Bacteroides fragilis YCH46]			
24239, 24240	55377565	27	4.00E-15	Haloarcula marismortui ATCC 43049	universal stress protein [Haloarcula marismortui ATCC 43049] gb AAV45709.1 universal stress protein [Haloarcula marismortui ATCC 43049]			
24241, 24242	34398043	29	2.00E-18	Porphyromonas gingivalis W83	LysM domain protein [Porphyromonas gingivalis W83] ref NP_906204.1 LysM domain protein [Porphyromonas gingivalis W83]			3.2.1.-
24245, 24246	48856971	61	7.00E-66	Cytophaga hutchinsonii	COG0138: AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Afcu) [Cytophaga hutchinsonii] hypothetical protein TTHA1017 [Thermus thermophilus HB8] dbj BAD70840.1 conserved hypothetical protein [Thermus thermophilus HB8]			2.1.2.3
24247, 24248	55980986	23	8.00E-11	Thermus thermophilus HB8				
24249, 24250	31195967	79	3.00E-41	Anopheles gambiae	ENSANGP00000016322 [Anopheles gambiae]			1.6.4.5
2425, 2426	48856035	40	2.00E-20	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]			2.-.-.-
24251, 24252	51246763	36	1.00E-41	Desulfotalea psychrophila LSV54	hypothetical protein DP2911 [Desulfotalea psychrophila LSV54] emb CAC37640.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]			
24253, 24254	56965073	55	1.00E-31	Bacillus clausii KSM-K16	hydrolase, HAD superfamily [Bacillus clausii KSM-K16] dbj BAD65844.1 hydrolase, HAD superfamily [Bacillus clausii KSM-K16]			
24255, 24256	53712488	56	5.00E-55	Bacteroides fragilis YCH46	peptidyl-L-tyrosine hydrolase [Bacteroides fragilis YCH46] dbj BAD47946.1 peptidyl-L-tyrosine hydrolase [Bacteroides fragilis YCH46]			3.1.1.29
24257, 24258	48856955	53	7.00E-68	Cytophaga hutchinsonii	COG0134: Indole-3-glycerol phosphate synthase [Cytophaga hutchinsonii]			4.1.1.48
24259, 24260	48854173	24	5.00E-08	Cytophaga hutchinsonii	hypothetical protein Chut02002840 [Cytophaga hutchinsonii]			
24261, 24262	48853326	47	5.00E-46	Cytophaga hutchinsonii	COG1485: Predicted ATPase [Cytophaga hutchinsonii]			
24263, 24264	27367774	61	1.00E-100	Vibrio vulnificus CMCP6	Phosphoglycerol transferase [Vibrio vulnificus CMCP6] gb AAO08291.1 Phosphoglycerol transferase [Vibrio vulnificus CMCP6]			2.7.8.20
24267, 24268	32476849	42	4.00E-20	Rhodopirella SH 1	hypothetical protein RB11207 [Rhodopirella SH 1] emb CAD78986.1 conserved hypothetical protein [Pirella sp.]			
2427, 2428	48856079	51	7.00E-67	Cytophaga hutchinsonii	COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii]			1.8.-.-
24271, 24272	53712075	25	7.00E-18	Bacteroides fragilis YCH46	hypothetical protein BF0782 [Bacteroides fragilis YCH46] dbj BAD47533.1 hypothetical protein [Bacteroides fragilis YCH46]			

24273, 24274	17936192	31	3.00E-33	Agrobacterium tumefaciens str. C58	xanthine dehydrogenase [Agrobacterium tumefaciens str. C58] gb AAL43298.1 xanthine dehydrogenase [Agrobacterium tumefaciens str. C58] gb AAK88052.1 AGR_C_4202p [Agrobacterium tumefaciens str. C58] pir AD2860 xanthine dehydrogenase xdhA [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir C97637 xanthine dehydrogenase (PA1524) [imported] - Agrobacterium tumefaciens (strain C58, Cereon) ref NP_355267.1 hypothetical protein AGR_C_4202 [Agrobacterium tumefaciens str. C58]	1.1.1.20 4
24275, 24276	53713423	29	1.00E-12	Bacteroides fragilis YCH46	hypothetical protein BF2134 [Bacteroides fragilis YCH46] dbj BAD48881.1 conserved hypothetical protein [Bacteroides fragilis YCH46]	
24277, 24278	29347250	67	2.00E-68	Bacteroides thetaiotaomicron VPI-5482	histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76947.1 histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI- 5482] sp Q8A6N7 SYH_BACTN Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HisRS)	6.1.1.21
24279, 24280	48855464	40	2.00E-28	Cytophaga hutchinsonii	COG1999: Uncharacterized protein SCO1/SenC/PrC, involved in biogenesis of respiratory and photosynthetic systems [Cytophaga hutchinsonii]	
24281, 24282	48859534	69	1.00E-100	Clostridium thermocellum ATCC 27405	COG0804: Urea amidohydrolase (urease) alpha subunit [Clostridium thermocellum ATCC 27405]	89 1.00E-17 3.5.1.5
24283, 24284	52841315	57	7.00E-88	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	reverse transcriptase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27167.1 reverse transcriptase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]	2.7.7.49
24285, 24286	17230079	21	9.00E-15	Nostoc sp. PCC 7120	transcriptional regulator [Nostoc sp. PCC 7120] dbj BAB74286.1 transcriptional regulator [Nostoc sp. PCC 7120] pir AD2129 transcription regulator alr2587 [imported] - Nostoc sp. (strain PCC 7120)	
24287, 24288	15893983	44	2.00E-67	Clostridium acetobutylicum ATCC 824	Altronate oxidoreductase [Clostridium acetobutylicum ATCC 824] gb AAK78672.1 Altronate oxidoreductase [Clostridium acetobutylicum ATCC 824] pir E96985 altronate oxidoreductase CAC0695 [imported] - Clostridium acetobutylicum sp Q97L67 UXAB_CLOAB Altronate oxidoreductase (Tagaturonate reductase) (Tagaturonate dehydrogenase)	1.1.1.58
24289, 24290	48855692	68	1.00E-117	Cytophaga hutchinsonii	COG1080: Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes [Cytophaga hutchinsonii]	2.8.1.6

2429, 2430	18310267	26	2.00E-14	Clostridium perfringens str. 13	hypothetical protein CPE1285 [Clostridium perfringens str. 13] dbj BAB80991.1 hypothetical protein [Clostridium perfringens str. 13]				
24291, 24292	48855692	61	4.00E-85	Cytophaga hutchinsonii	COG1060: Thiamine biosynthesis enzyme ThiH and related uncharacterized enzymes [Cytophaga hutchinsonii]				2.8.1.6
24293, 24294	48854815	44	2.00E-57	Cytophaga hutchinsonii	COG0719: ABC-type transport system involved in Fe-S cluster assembly, permease component [Cytophaga hutchinsonii]				
24295, 24296	48855375	42	1.00E-18	Cytophaga hutchinsonii	COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii]				2.7.3.-
24301, 24302	48853518	39	6.00E-37	Cytophaga hutchinsonii	COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii]				
24305, 24306	47526988	25	5.00E-16	Bacillus anthracis str. 'Ames' Ancestor'	tpg/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] ref YP_027843.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne] ref NP_844138.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAP25624.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAT30812.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] gb AAT53894.1 TPR/glycosyl transferase domain protein [Bacillus anthracis str. Sterne]				
24307, 24308	48854601	44	4.00E-37	Cytophaga hutchinsonii	COG4485: Predicted membrane protein [Cytophaga hutchinsonii]				
24309, 24310	15612709	61	5.00E-61	Bacillus halodurans C-125	50S ribosomal protein L5 [Bacillus halodurans C-125] dbj BAB03865.1 50S ribosomal protein L5 [Bacillus halodurans C-125] pir T44395 ribosomal protein L5 (BL6) rplE [imported] - Bacillus halodurans (strain C-125) sp Q9Z9K2 RL5_BACHD 50S ribosomal protein L5 dbj BAA75283.1 rplE homologue (identity of 88% to B. subtilis) [Bacillus halodurans]	Spiroplasma kunkelii strain CR2- 3x partial genome sequence	92	5.00E-19	
24311, 24312	31195605	70	1.00E-104	Anopheles gambiae	ENSANGP00000013686 [Anopheles gambiae] hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229887.1 hypothetical protein VC0230 [Vibrio cholerae O1 biovar eltor str. N16961] pir H82348 hypothetical protein VC0230 [imported] - Vibrio cholerae (strain N16961 serogroup O1)	Desc:Staphylococcus aureus DNA for cellular proliferation protein #1366. Org:Staphylococcus aureus	85	1.00E-26	
24313, 24314	9654638	51	3.00E-40	Vibrio cholerae O1 biovar eltor str. N16961					

24315,	49484433	29	6.00E-12	Staphylococcus aureus subsp. aureus MRSA252	putative tRNA pseudouridine synthase [Staphylococcus aureus subsp. aureus MRSA252] emb[CAG41283.1] putative tRNA pseudouridine synthase [Staphylococcus aureus subsp. aureus MRSA252] sp Q6GEL6 TRUA_STAAR tRNA pseudouridine synthase A (Pseudouridylate synthase I) (Pseudouridine synthase I) (Uracil hydrolyase)				4.2.1.70
24319,	31195671	53	3.00E-10	Anopheles gambiae	ENSANGP00000000352 [Anopheles gambiae]				
24320,	48782075	30	4.00E-20	Burkholderia fungorum LB400	COG0463: Glycosyltransferases involved in cell wall biogenesis [Burkholderia fungorum LB400]				2.---
24323,				Bacillus cereus ATCC 10987	uroporphyrinogen-III synthase [Bacillus cereus ATCC 10987]				
24324	42783600	31	2.00E-09	Anopheles gambiae	ENSANGP000000015562 [Anopheles gambiae]				2.7.6.5
24325,				Bdellovibrio bacteriovorus HD100	ATP-dependent protease LA [Bdellovibrio bacteriovorus HD100] emb[CAE8111.1] ATP-dependent protease LA [Bdellovibrio bacteriovorus HD100]				3.4.21.5
24326	42525077	78	1.00E-108	Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase/response regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482]			82 2.00E-103	
24329,				Bacteroides fragilis YCH46	C-terminal part of two-component system sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46]				2.7.3.-
24330	29347164	43	8.00E-47	Magnetococcus sp. MC-1	COG3176: Putative hemolysin [Magnetococcus sp. MC-1]				
24331,				Cytophaga hutchinsonii	COG2932: Predicted transcriptional regulator [Cytophaga hutchinsonii]				
24332	53711679	33	2.00E-38	Acinetobacter sp. ADP1	putative ATP-dependent DNA helicase (PcrA) [Acinetobacter sp. ADP1] emb[CAG67422.1] putative ATP-dependent DNA helicase (PcrA) [Acinetobacter sp. ADP1]				3.6.1.-
24333,	48833909	41	7.00E-53	uncultured proteobacterium QS1	conserved hypothetical protein [uncultured proteobacterium QS1]				
24334	48856470	35	9.00E-40	Anopheles gambiae	ENSANGP00000000334 [Anopheles gambiae]				
24335,									
24336	50083734	41	1.00E-69						
24337,									
24338	50956565	25	7.00E-22						
24339,									
24340	31194161	66	2.00E-31						
24341,									
24342									
24343,									
24344									
24345,									
24346									
24347,									
24348									
24349,									
24350									

24351, 24352, 24353, 24354, 24357, 24358, 24359, 24360, 24361, 24362, 24363, 24364, 24365, 24366, 24371, 24372, 24373, 24374, 24377, 24378	53712250 18642520 48855539 53714581 29347413 48853591 48853783 46140632 48856043 53691678	54 37 64 35 32 60 42 36 28 32	7.00E-26 1.00E-36 3.00E-90 1.00E-08 2.00E-17 3.00E-27 3.00E-40 2.00E-37 3.00E-09 3.00E-24	Bacteroides fragilis YCH46 Tolypothrix sp. PCC 7601 Cytophaga hutchinsonii Bacteroides fragilis YCH46 Bacteroides thetataoiaomicron VPI-5482 Cytophaga hutchinsonii Cytophaga hutchinsonii Desulfotomomas aromatica RCB Cytophaga hutchinsonii Desulfotomobrio desulfuricans G20	DNA replication and repair protein RecF [Bacteroides fragilis YCH46] dbj BAD47708.1 DNA replication and repair protein RecF [Bacteroides fragilis YCH46] phytochrome-like protein [Tolypothrix sp. PCC 7601] COG0142: Geranylgeranyl pyrophosphate synthase [Cytophaga hutchinsonii] alpha-amylase [Bacteroides fragilis YCH46] dbj BAD50039.1 alpha-amylase [Bacteroides fragilis YCH46] putative membrane peptidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77110.1 putative membrane peptidase [Bacteroides thetaiotaomicron VPI-5482] COG1021: Peptide arylation enzymes [Cytophaga hutchinsonii] COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii] COG0419: ATPase involved in DNA repair [Dechloromonas aromatica RCB] COG1556: Uncharacterized conserved protein [Cytophaga hutchinsonii] COG0739: Membrane proteins related to metalloendopeptidases [Desulfotomobrio desulfuricans G20]			3.1.11.- 2.7.3.- 2.5.1.- 2.7.7.7 3.1.11.-
24379, 24380, 24383, 24384, 24385, 24386, 24387, 24388	48853531 53715862 29348530	54 66 55	2.00E-74 3.00E-81 2.00E-75	Cytophaga hutchinsonii Bacteroides fragilis YCH46 Bacteroides thetataoiaomicron VPI-5482 Geobacter sulfurreducens PCA	COG0020: Undecaprenyl pyrophosphate synthase [Cytophaga hutchinsonii] DNA mismatch repair protein mutS [Bacteroides fragilis YCH46] dbj BAD51320.1 DNA mismatch repair protein mutS [Bacteroides fragilis YCH46] DNA mismatch repair protein mutS [Bacteroides thetaiotaomicron VPI-5482] gb AAO78227.1 DNA mismatch repair protein mutS [Bacteroides thetaiotaomicron VPI-5482] sp Q8A334 MUTS_BACTN DNA mismatch repair protein mutS DNA mismatch repair protein mutS [Bacteroides thetaiotaomicron VPI-5482] gb AAO78227.1 DNA mismatch repair protein mutS [Bacteroides thetaiotaomicron VPI-5482] sp Q8A334 MUTS_BACTN DNA mismatch repair protein mutS sensory box histidine kinase [Geobacter sulfurreducens PCA] gb AAR36209.1 sensory box histidine kinase [Geobacter sulfurreducens PCA]	86	7.00E-13 2.5.1.31	

24389, 24390 24391, 24392 24395, 24396 24397, 24398	30024199 46316555 29348695	27 29 44	1.00E-09 5.00E-16 9.00E-19	Bacteriophage P2- EC53 Burkholderia cepacia R18194 Bacteroides thetaiotaomicron VPI-5482	putative lysogenic conversion protein [Bacteriophage P2-EC53] COG1289: Predicted membrane protein [Burkholderia cepacia R18194] hypothetical protein BT3286 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78392.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]	Vibrio vulnificus CMCP6 chromosome II section 2 of 6 of the complete sequence 89	2.00E-13	
24399, 24400 24401, 24402	48854339 48855592	65 26	1.00E-68 7.00E-15	Cytophaga hutchinsonii Cytophaga hutchinsonii	COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii] COG1305: Transglutaminase-like enzymes, putative cysteine proteases [Cytophaga hutchinsonii]	Desc:Restriction enzyme AccIII gene. Org:Acinetobacter calcoaceticus	87	1.00E-07 3.4.21.-
24405, 24406 24407, 24408 24409, 24410	53714606 37222107 31790570	63 49 38	1.00E-109 5.00E-11 1.00E-30	Bacteroides fragilis YCH46 uncultured bacterium marine bacterium P99-3	excinuclease ABC subunit A [Bacteroides fragilis YCH46] db BAD50064.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46] Uvs017 [uncultured bacterium] lycopene beta-monocyclase [marine bacterium P99-3] sulfur oxidation protein SoxB [Aquifex aeolicus VF5] gb AAC07634.1 sulfur oxidation protein SoxB [Aquifex aeolicus VF5] pir E70455 sulfur oxidation protein SoxB - Aquifex aeolicus			3.1.3.5
24411, 24412	15606857 31195649	30 34	7.00E-11 1.00E-28	Aquifex aeolicus VF5 Anopheles gambiae	ENSANGP00000000282 [Anopheles gambiae] hydroxymethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase [Porphyromonas gingivalis W83] ref NP_906169.1 hydroxymethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase [Porphyromonas gingivalis W83] COG0351: Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase [Cytophaga hutchinsonii] hypothetical protein BCZK0824 [Bacillus cereus ZK] gb AAU19419.1 conserved hypothetical protein [Bacillus cereus ZK]			
24413, 24414 24415, 24416 24417, 24418	34398008 48855689 52144400	29 40 37	7.00E-17 2.00E-10 3.00E-48	Porphyromonas gingivalis W83 Cytophaga hutchinsonii Bacillus cereus ZK				

24419,	53797765	25	4.00E-11	Chloroflexus aurantiacus	hypothetical protein Chlo02001813 [Chloroflexus aurantiacus]			
24420				Cytophaga hutchinsonii	COG2207: AraC-type DNA-binding domain-containing proteins [Cytophaga hutchinsonii]			
24421,	48854071	54	3.00E-54	Wolinella succinogenes DSM 1740	hypothetical protein WS1135 [Wolinella succinogenes DSM 1740]			
24422					emb CAE10224.1 hypothetical protein [Wolinella succinogenes]			
24423,	34557509	44	2.00E-28	Clostridium acetobutylicum ATCC 824	Translation IF2, GTPase [Clostridium acetobutylicum ATCC 824]			
24424					gb AAK79767.1 Translation IF2, GTPase [Clostridium acetobutylicum ATCC 824] pir D97122 translation IF2, GTPase [imported] - Clostridium acetobutylicum sp Q97151 IF2_CLOAB Translation Initiation factor IF-2			
24425,	15895078	64	6.00E-38	Thermosynechococcus elongatus BP-1	hypothetical protein tir1343 [Thermosynechococcus elongatus BP-1]			
24426					db BAC08895.1 tir1343 [Thermosynechococcus elongatus BP-1]			
24431,	22298886	62	5.00E-37	Cytophaga hutchinsonii	COG3279: Response regulator of the LysR/AlgR family [Cytophaga hutchinsonii]			
24432,	48855702	37	2.00E-34	Cytophaga hutchinsonii	COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii]			
24433,				Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3008 [Bacteroides thetaiotaomicron VPI-5482]			
24434					gb AAO78114.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
24437,	48853433	42	1.00E-61		RNA polymerase ECF(extracytoplasmic function)-type sigma factor (sigma-Z) [Bacillus subtilis subsp. subtilis str. 168] emb CAB14625.1 RNA polymerase ECF(extracytoplasmic function)-type sigma factor (sigma-Z) [Bacillus subtilis subsp. subtilis str. 168] gb AAB80887.1 RNA polymerase sigma factor SigZ [Bacillus subtilis] pir C69707 RNA polymerase ECF-type sigma factor sigZ - Bacillus subtilis sp O05409 SIGZ_BACSU RNA polymerase sigma factor sigZ			
24441,	16079737	32	3.00E-10	Cytophaga hutchinsonii	COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii]			4.1.3.-
24442					argininosuccinate lyase [Bacteroides thetaiotaomicron VPI-5482]			
24443,	48856398	55	1.00E-44	Bacteroides thetaiotaomicron VPI-5482	gb AAO78838.1 argininosuccinate lyase [Bacteroides thetaiotaomicron VPI-5482]			4.3.2.1
24444					hypothetical protein LIC10662 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_713715.1 hypothetical protein LA3535 [Leptospira interrogans serovar Lai str. 56601] gb AAN50733.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601]			
24445,	29349141	59	2.00E-99	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	gb AAS69283.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			
24446					COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]			
24447,	45656560	33	3.00E-22	Cytophaga hutchinsonii				
24448								
2445,	48855183	45	2.00E-66					
2446								

24451,	15899699	31	2.00E-22	Sulfolobus solfataricus P2	Diphosphomevalonate decarboxylase, putative [Sulfolobus solfataricus P2] gb AAK43094.1 Diphosphomevalonate decarboxylase, putative [Sulfolobus solfataricus P2] pir G90479 diphosphomevalonate decarboxylase, probable [Imported] - Sulfolobus solfataricus	4.1.1.33
24452,	10880727	50	3.00E-75	Borrelia coriaceae	glycerophosphodiester phosphodiesterase GlpQ [Borrelia coriaceae] hypothetical protein Jhp1070 [Helicobacter pylori J99] gb AAD06650.1	3.1.4.46
24453,				Helicobacter pylori	putative [Helicobacter pylori J99] pir D71853 hypothetical protein Jhp1070 - Helicobacter pylori (strain J99)	
24455,	15612135	45	3.00E-58	Bacteroides thetaiotaomicron	hypothetical protein BT1057 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76164.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]	
24456,	29346467	33	7.00E-40	Bacillus methanolicus	putative replication initiator protein [Bacillus methanolicus] gb AAR39408.1 putative replication initiator protein [Bacillus methanolicus]	
24457,	41057059	28	4.00E-26	Geobacillus stearothermophilus	methylase fusion protein [Geobacillus stearothermophilus]	2.1.1.73
24460,	34451616	34	1.00E-20	Ornithobacterium rhinotracheale	MbpB [Ornithobacterium rhinotracheale]	
24463,	47059349	25	1.00E-07	Psychrobacter sp.	Desc:Psychrobacter gingivalis protein PG83. Org:Psychrobacter gingivalis	
24464,	AAV3442	32	3.00E-23	Cytophaga hutchinsonii	COG0500: SAM-dependent methyltransferases [Psychrobacter sp. 273-4]	
24465,	1			Geobacter metallireducens GS-15	COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii]	
24466,	46141287	46	9.00E-44	Listeria innocua	COG0057: Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Geobacter metallireducens GS-15]	
24467,	48856125	42	2.00E-33	Cytophaga hutchinsonii	hypothetical protein In0833 [Listeria innocua Clip11262] emb CAC96065.1	
24473,	48846053	33	8.00E-08	Geobacter	hypothetical protein In0833 [Listeria innocua] pir A1536 hypothetical protein In0833 [Imported] - Listeria innocua (strain Clip11262)	
24474,	16799907	47	8.00E-48	Geobacter	COG1071: Pyruvate/2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, eukaryotic type, alpha subunit [Cytophaga hutchinsonii]	1.2.4.1
24475,	48856576	46	7.00E-38	Geobacter	mannose-6-phosphate isomerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75480.1 mannose-6-phosphate isomerase [Bacteroides thetaiotaomicron VPI-5482]	5.3.1.8
24476,				Geobacter	ENSANGP00000000282 [Anopheles gambiae]	2.7.1.37
24477,				Geobacter		
24478,				Geobacter		
24481,				Geobacter		
24482,				Geobacter		
24483,				Geobacter		
24484,				Geobacter		
24485,				Geobacter		
24486,				Geobacter		

24487,	48854985	60	9.00E-49	Cytophaga hutchinsonii	hypothetical protein Chut02002044 [Cytophaga hutchinsonii]				
24488	ABB8477				Desc:DNA polymerase III holoenzyme delta subunit related protein SEQ ID:144. Org: Cytophaga hutchinsonii				2.7.7.7
24490	1	51	1.00E-63						
2449,				Silicibacter sp.					2.7.3.-
2450	52011036	37	6.00E-26	TM1040	COG0642: Signal transduction histidine kinase [Silicibacter sp. TM1040]				
24491,				Pseudoalteromonas		Pseudoalteromonas			
24492	46193747	88	3.00E-46	s haloplanktis	DsbA protein [Pseudoalteromonas haloplanktis]	haloplanktis dsbA	99	0	
24493,				Bifidobacterium	possible alpha beta hydrolase [Bifidobacterium longum NCC2705]				
24494	23465361	44	2.00E-18	longum NCC2705	gb AAN24600.1 possible alpha beta hydrolase [Bifidobacterium longum NCC2705]				3.8.1.2
24497,				Methanosarcina	hypothetical protein MM1155 [Methanosarcina mazel Go1] gb AAM30851.1 conserved protein [Methanosarcina mazel Go1]				
24498	21227257	27	3.00E-08	mazel Go1	ARA1 [Mycoplasma gallisepticum R] ref NP_853218.1 ARA1 [Mycoplasma gallisepticum R]				1.1.1.-
24499,	31541486	48	2.00E-76	Mycoplasma gallisepticum R					
24500				Cytophaga					
245,				Cytophaga					
246	48856118	49	1.00E-46	hutchinsonii	COG0242: N-formylmethionyl-tRNA deformylase [Cytophaga hutchinsonii]				3.5.1.88
24501,				Bacteroides	putative phosphoribosylformylglycinamide cyclo-ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79316.1 putative phosphoribosylformylglycinamide cyclo-ligase [Bacteroides thetaiotaomicron VPI-5482]	Bacteroides fragilis YCH46 DNA, complete genome	88	7.00E-07	6.3.3.1
24502	29349619	80	1.00E-120	VPI-5482					
24505,	55540763	56	1.00E-107	Flavobacterium columnare	MrcA [Flavobacterium columnare]				2.4.2.-
24506				Shewanella	conserved hypothetical protein [Shewanella violacea]				
24507,	32562918	31	1.00E-07	violacea					
24508				Cytophaga					
24509,	48856384	28	2.00E-17	hutchinsonii	hypothetical protein Chut02000101 [Cytophaga hutchinsonii]				
24510					hypothetical protein air1565 [Nostoc sp. PCC 7120] dbj BAB77931.1 air1565 [Nostoc sp. PCC 7120] pir AG2001 hypothetical protein air1565 [Imported] - Nostoc sp. (strain PCC 7120)				
2451,				Nostoc sp. PCC 7120					
2452	17229057	36	5.00E-21		glycerol-3-phosphate dehydrogenase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77230.1 glycerol-3-phosphate dehydrogenase [Bacteroides thetaiotaomicron VPI-5482]				1.1.1.94
24511,				Bacteroides thetaiotaomicron	COG0323: DNA mismatch repair enzyme (predicted ATPase) [Cytophaga hutchinsonii]				
24512	29347533	63	3.00E-37	VPI-5482	tyrosine-protein kinase [Bacteroides fragilis YCH46] dbj BAD49519.1 tyrosine-protein kinase [Bacteroides fragilis YCH46]				
24515,	48854181	36	7.00E-45	Cytophaga hutchinsonii	adenine specific DNA methylase MOD [Azoarcus sp. EbN1]				
24516				Bacteroides fragilis					
24517,				YCH46					
24518	53714061	32	3.00E-19						
24519,									
24520	56476791	53	2.00E-68	Azoarcus sp. EbN1					2.1.1.72

24521, 24522	52008518	42	2.00E-16	Thiobacillus denitrificans ATCC 25259	COG2189: Adenine specific DNA methylase Mod [Thiobacillus denitrificans ATCC 25259]			
24523, 24524	54294349	30	2.00E-19	Legionella pneumophila str. Lens	hypothetical protein lp1417 [Legionella pneumophila str. Lens] emb CAH15657.1 hypothetical protein [Legionella pneumophila str. Lens]			
24527, 24528	48856556	38	9.00E-32	Cytophaga hutchinsonii	hypothetical protein Chut02000288 [Cytophaga hutchinsonii]			
24529, 24530	19704557	62	1.00E-39	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	hypothetical protein FN1222 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95418.1 Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			
2453, 2454	28212149	48	1.00E-23	Clostridium tetani E88	tRNA pseudouridine synthase A [Clostridium tetani E88] gb AAO37030.1 tRNA pseudouridine synthase A [Clostridium tetani E88] sp Q890R5 TRA2_CLOTE tRNA pseudouridine synthase A 2 (Pseudouridylate synthase 1 2) (Pseudouridine synthase 1 2) (Uracil hydrolyase 2)			4.2.1.70
24531, 24532	28210031	32	2.00E-10	Clostridium tetani E88	mannosyltransferase [Clostridium tetani E88] gb AAO34912.1 mannosyltransferase [Clostridium tetani E88]			2.4.1.-
24535, 24536	29349772	39	7.00E-27	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT4364 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79469.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
24537, 24538	48854863	23	9.00E-12	Cytophaga hutchinsonii	COG0358: DNA primase (bacterial type) [Cytophaga hutchinsonii]			
24539, 24540	23502244	29	5.00E-11	Brucella suis 1330	hypothetical protein BR1372 [Brucella suis 1330] ref NP_539548.1 hypothetical protein BMEI0631 [Brucella melitensis 16M] gb AAN30286.1 conserved hypothetical protein [Brucella suis 1330] gb AAL51812.1 hypothetical protein [Brucella melitensis 16M] pir A13330 hypothetical protein BMEI0631 [imported] - Brucella melitensis (strain 16M)			
24541, 24542	20092248	31	1.00E-15	Methanosarcina acetivorans C2A	hypothetical protein MA3436 [Methanosarcina acetivorans C2A] gb AAM06803.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A]			
24543, 24544	53711898	49	1.00E-48	Bacteroides fragilis YCH46	L-asparaginase I [Bacteroides fragilis YCH46] db BAD47356.1 L- asparaginase I [Bacteroides fragilis YCH46]			3.5.1.1
24545, 24546	16272405	47	2.00E-25	Haemophilus influenzae Rd KW20	hypothetical protein HI0457 [Haemophilus influenzae Rd KW20] gb AAC22115.1 conserved hypothetical protein [Haemophilus influenzae Rd KW20] pir E64069 yceG protein homolog HI0457 - Haemophilus influenzae (strain Rd KW20) sp P44720 YCEG_HAEIN Hypothetical protein HI0457			4.---

24547, 24548	53797765	26	3.00E-27	Chloroflexus aurantiacus	hypothetical protein Chio02001813 [Chloroflexus aurantiacus]				
24549, 24550	53685671	27	6.00E-16	Desulfotobacterium hafniense DCB-2	COG2207: AraC-type DNA-binding domain-containing proteins [Desulfotobacterium hafniense DCB-2]				
24551, 24552	54308659	32	2.00E-07	Photobacterium profundum SS9	putative methyl-accepting chemotaxis protein [Photobacterium profundum SS9] emb[CAG19877.1] putative methyl-accepting chemotaxis protein [Photobacterium profundum]				
24553, 24554	52549449	33	2.00E-21	uncultured archaeon GZfos27E6	carboxylesterase [uncultured archaeon GZfos27E6]				3.1.1.1
24555, 24556	27364673	29	5.00E-09	Vibrio vulnificus CMCP6	Transcriptional regulator [Vibrio vulnificus CMCP6] ref NP_935886.1 transcriptional regulator [Vibrio vulnificus YJ016] gb AAO09728.1 Transcriptional regulator [Vibrio vulnificus CMCP6] dbj BAC95857.1 transcriptional regulator [Vibrio vulnificus YJ016]				
24559, 24560	48855208	36	1.00E-25	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit; sigma24 homolog [Cytophaga hutchinsonii]				
24567, 24568	32473966	29	2.00E-10	Rhodopirellula baltica SH 1	serine/threonine protein phosphatase [Rhodopirellula baltica SH 1] emb CAD74502.1 serine/threonine protein phosphatase [Pirellula sp.]				3.1.3.16
24569, 24570	29348712	43	1.00E-45	Bacteroides thetaiotaomicron VPI-5482	ATP-dependent RNA helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78409.1 ATP-dependent RNA helicase [Bacteroides thetaiotaomicron VPI-5482]	Desc:Bacillus anthracis variable region DNA sequence SEQ ID NO 85. Org:Bacillus anthracis	97	5.00E-07	2.7.7.-
2457, 2458	53797741	33	8.00E-32	Chloroflexus aurantiacus	COG0438: Glycosyltransferase [Chloroflexus aurantiacus]				2.4.1.-
24571, 24572	14531032	52	5.00E-82	Flavobacterium johnsoniae	Flo14 [Flavobacterium johnsoniae]				
24579, 24580	23120384	27	7.00E-10	Desulfotobacterium hafniense DCB-2	COG0823: Periplasmic component of the Tol biopolymer transport system [Desulfotobacterium hafniense DCB-2]				
24583, 24584	34397168	47	8.00E-29	Porphyromonas gingivalis W83	ATP:cob(I)alamin adenosyltransferase, putative [Porphyromonas gingivalis W83] ref NP_905333.1 ATP:cob(I)alamin adenosyltransferase, putative [Porphyromonas gingivalis W83]				4.2.1.28
24587, 24588	53714518	22	1.00E-13	Bacteroides fragilis YCH46	DNA polymerase III subunit gamma/tau [Bacteroides fragilis YCH46] dbj BAD49976.1 DNA polymerase III subunit gamma/tau [Bacteroides fragilis YCH46]				

24589,	53712040	39	2.00E-31	Bacteroides fragilis YCH46	putative methyltransferase [Bacteroides fragilis YCH46] dbj BAD47498.1			2.1.1.-
24590					putative methyltransferase [Bacteroides fragilis YCH46]			
2459,	48856618	55	1.00E-86	Cytophaga hutchinsonii	COG1562: Phytoene/squalene synthetase [Cytophaga hutchinsonii]			2.5.1.32
2460								
24591,	5360168	53	8.00E-55	Flavobacterium johnsoniae	GldB [Flavobacterium johnsoniae]			
24592								
24593,	5360169	60	5.00E-35	Flavobacterium johnsoniae	GldC [Flavobacterium johnsoniae]			
24594								
24595,	52853314	27	4.00E-07	Psychrobacter sp. 273-4	COG2755: Lysophospholipase L1 and related esterases [Psychrobacter sp. 273-4]			
24596								
24597,	52006884	33	3.00E-10	Thiobacillus denitrificans ATCC 25259	COG0543: 2-polyphenylphenol hydroxylase and related flavodoxin oxidoreductases [Thiobacillus denitrificans ATCC 25259]			
24598								
24599,	52082356	45	3.00E-13	Bacillus licheniformis ATCC 14580	YwaF [Bacillus licheniformis ATCC 14580] gb AAU25509.1 YwaF [Bacillus licheniformis ATCC 14580] ref YP_093574.1 YwaF [Bacillus licheniformis ATCC 14580] gb AAU42881.1 YwaF [Bacillus licheniformis DSM 13]			
24600								
24601,	53714270	66	3.00E-45	Bacteroides fragilis YCH46	DNA polymerase III epsilon chain [Bacteroides fragilis YCH46] dbj BAD49728.1 DNA polymerase III epsilon chain [Bacteroides fragilis YCH46]			2.7.7.7
24602								
24605,	22958439	33	9.00E-08	Rhodobacter sphaeroides 2.4.1	COG1393: Arsenate reductase and related proteins, glutaredoxin family [Rhodobacter sphaeroides 2.4.1]			
24606								
					hypothetical protein MA4225 [Methanosarcina acetivorans C2A] ref NP_618394.1 hypothetical protein MA3511 [Methanosarcina acetivorans C2A] ref NP_618264.1 hypothetical protein MA3375 [Methanosarcina acetivorans C2A] ref NP_617683.1 hypothetical protein MA2785 [Methanosarcina acetivorans C2A] gb AAM07570.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] gb AAM06874.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] gb AAM06744.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A] gb AAM06163.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A]			
24609,	20093015	47	4.00E-15	Methanosarcina acetivorans C2A	COG0504: CTP synthase (UTP-ammonia lyase) [Cytophaga hutchinsonii]			6.3.4.2
24610								
2461,	48856944	59	1.00E-69	Cytophaga hutchinsonii	putative ribosomal large chain pseudouridine synthase A [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61405.1 putative ribosomal large chain pseudouridine synthase A [Vibrio parahaemolyticus]			4.2.1.70
2462								
24617,	28899917	57	1.00E-90	Vibrio parahaemolyticus RIMD 2210633	COG0441: Threonyl-tRNA synthetase [Cytophaga hutchinsonii]			6.1.1.3
24618								
24619,	48853747	50	3.00E-32	Cytophaga hutchinsonii				
24620								

24621,	48853518	48	1.00E-36	Cytophaga hutchinsonii	COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii]	Desc: Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:2072	95	3.00E-07	
24622				Mesorhizobium loti	hypothetical protein ml5269 [Mesorhizobium loti MAFF303099]	Org: Staphylococcus epidermidis			
24625,	13474394	47	6.00E-16	MAFF303099	dbj BAB51748.1 ml5269 [Mesorhizobium loti MAFF303099]				
24626				Flavobacterium johnsoniae	gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding				
24629,	2281663	66	3.00E-43	johnsoniae	motility protein [imported] - Flavobacterium johnsoniae			1.8.-	
2463,				Mus musculus	Thimet oligopeptidase 1 [Mus musculus]			3.4.24.1	
2464	21619359	43	3.00E-57	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough				5	
24631,					DNA-binding response regulator [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94742.1 DNA-binding response regulator				
24632	46578675	56	2.00E-32	Hildenborough	[Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]				2.7.3.-
24633,				Bacteroides fragilis YCH46	two-component system sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46] dbj BAD51228.1 two-component system				
24634	53715770	38	1.00E-28	YCH46	sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46]				
24635,				Clostridium perfringens str. 13	probable transcriptional regulator [Clostridium perfringens str. 13]				
24636	18311521	33	2.00E-19	perfringens str. 13	dbj BAB82245.1 probable transcriptional regulator [Clostridium perfringens str. 13]				
24637,				Oceanobacillus theyensis HTE831	malate:quinone oxidoreductase [Oceanobacillus theyensis HTE831]				
24638	23098401	46	3.00E-65	theyensis HTE831	sp Q8CV11 MQO_OCEIH Probable malate:quinone oxidoreductase (Malate dehydrogenase [acceptor]) (MQO) dbj BAC12902.1 malate:quinone oxidoreductase [Oceanobacillus theyensis HTE831]			1.1.99.1	6
24641,				Coxiella burnetii RSA 493	nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493]				
24642	29654347	58	2.00E-42	RSA 493	gb AAO90553.1 nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493]			2.4.2.11	
24643,				Bdellovibrio bacteriovorus HD100	hypothetical protein Bd0852 [Bdellovibrio bacteriovorus HD100]				
24644	42522424	27	6.00E-07	HD100	emb CAE78797.1 lepB [Bdellovibrio bacteriovorus HD100]				
24645,				Photobacterium profundum SS9	hypothetical protein PBPRB1077 [Photobacterium profundum SS9]				
24646	54302756	38	2.00E-12	profundum SS9	emb CAG22949.1 conserved hypothetical protein [Photobacterium profundum]				

24647,							glucosamine-fructose-6-phosphate aminotransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75661.1 glucosamine-fructose-6-phosphate aminotransferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8AAB1 GLMS_BACTN Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase)				2.6.1.16
24648	29345964	60	1.00E-73	Bacteroides thetaiotaomicron VPI-5482			ENSANGP00000000454 [Anopheles gambiae]				4.2.1.22
24649,	31195963	58	1.00E-93	Anopheles gambiae			COG0210: Superfamily I DNA and RNA helicases [Chloroflexus aurantiacus]				3.6.1.-
24650	53796853	49	3.00E-68	Chloroflexus aurantiacus			COG1770: Protease II [Anabaena variabilis ATCC 29413]				3.4.21.8 3
24651,	53764144	43	1.00E-54	Anabaena variabilis ATCC 29413			2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Porphyromonas gingivalis W83] ref NP_905665.1 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase [Porphyromonas gingivalis W83]				4.1.1.71
24653,	34397502	29	5.00E-21	Porphyromonas gingivalis W83			Inorganic pyrophosphatase [Methanosarcina mazei Go1] gb AAM31137.1				3.6.1.1
24654	21227543	46	2.00E-21	Methanosarcina mazei Go1			Inorganic pyrophosphatase [Methanosarcina mazei Go1] site-specific recombinase, phage integrase family [Methylococcus capsulatus str. Bath] ref YP_113189.1 site-specific recombinase, phage integrase family [Methylococcus capsulatus str. Bath]				
24655,	53758908	36	2.00E-32	Methylococcus capsulatus str. Bath			ENSANGP00000016322 [Anopheles gambiae str. PEST] ref XP_561003.1				1.8.4.5
24663,	55246919	64	1.00E-68	Anopheles gambiae str. PEST			ENSANGP00000016322 [Anopheles gambiae str. PEST] COG0367: Asparagine synthase (glutamine-hydrolyzing) [Enterococcus faecium]				6.3.5.4
24664	48824812	54	1.00E-36	Enterococcus faecium			glycosyltransferase [Methanosarcina mazei Go1] gb AAM30834.1				2.4.1.-
24665,	21227240	35	2.00E-11	Methanosarcina mazei Go1			glycosyltransferase [Methanosarcina mazei Go1] hypothetical protein NE0847 [Nitrosomonas europaea ATCC 19718] emb CAD84758.1 conserved hypothetical protein [Nitrosomonas europaea ATCC 19718]				
24667,	30248851	30	5.00E-07	Nitrosomonas europaea ATCC 19718			outer membrane efflux protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO75667.1 outer membrane efflux protein [Bacteroides thetaiotaomicron VPI-5482]				
24668	29345970	29	3.00E-26	Bacteroides thetaiotaomicron VPI-5482							
24669,											
24670											
24671,											
24672											

24673, 24674	53712087	37	2.00E-54	Bacteroides fragilis YCH46	putative transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD47545.1 putative transcriptional regulator [Bacteroides fragilis YCH46]				
24677, 24678	53715627	36	4.00E-27	Bacteroides fragilis YCH46	putative haloacid dehalogenase-like hydrolase [Bacteroides fragilis YCH46] dbj BAD51085.1 putative haloacid dehalogenase-like hydrolase [Bacteroides fragilis YCH46]				3.3.2.3
24679, 24680	53713311	45	2.00E-44	Bacteroides fragilis YCH46	hypothetical protein BF2022 [Bacteroides fragilis YCH46] dbj BAD48769.1 conserved hypothetical protein [Bacteroides fragilis YCH46]	Anopheles gambiae ENSANGP000000000 3278 (ENSANGG00000000 02643) mRNA, partial cds	93	5.00E-07	3.4.13.9
24681, 24682	29345572	51	8.00E-80	Bacteroides thetaiotaomicron VPI-5482	penicillin-binding protein 1C (PBP-1c) [Bacteroides thetaiotaomicron VPI- 5482] gbl AAO75269.1 penicillin-binding protein 1C (PBP-1c) [Bacteroides thetaiotaomicron VPI-5482]				2.4.2.-
24683, 24684	48855337	54	1.00E-71	Cytophaga hutchinsonii	COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii]				
24685, 24686	55977207	37	7.00E-37	Comamonas sp. JS46	replicase [Comamonas sp. JS46]				
24687, 24688	50083970	52	3.00E-37	Acinetobacter sp. ADP1	putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1] emb CAG67658.1 putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1]				4.1.99.4
2469, 2470	34397012	47	4.00E-63	Porphyrromonas gingivalis W83	ABC transporter, ATP-binding protein [Porphyrromonas gingivalis W83] ref NP_905177.1 ABC transporter, ATP-binding protein [Porphyrromonas gingivalis W83]				1.8.-
24691, 24692	53713904	72	1.00E-120	Bacteroides fragilis YCH46	exonuclease ABC subunit A [Bacteroides fragilis YCH46] dbj BAD49362.1 exonuclease ABC subunit A [Bacteroides fragilis YCH46]	Staphylococcus epidermidis ATCC 12228, section 2 of 9 of the complete genome	87	2.00E-07	
24699, 24700	53712212	45	1.00E-34	Bacteroides fragilis YCH46	phosphate starvation-inducible protein PhoH [Bacteroides fragilis YCH46] dbj BAD47670.1 phosphate starvation-inducible protein PhoH [Bacteroides fragilis YCH46]				
24701, 24702	48854288	38	7.00E-35	Cytophaga hutchinsonii	COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii]				
24703, 24704	48855384	42	2.00E-39	Cytophaga hutchinsonii	COG0601: ABC-type dipeptide/oligopeptide/nickel transport systems, permease components [Cytophaga hutchinsonii]				
24705, 24706	48856104	42	4.00E-30	Cytophaga hutchinsonii	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii]				

24707, 24708	34397475	25	3.00E-13	Porphyrionas gingivalis W83	hypothetical protein PG1492 [Porphyrionas gingivalis W83] ref NP_905638.1 hypothetical protein PG1492 [Porphyrionas gingivalis W83]				
24709, 24710	29347584	38	8.00E-11	Bacteroides thetaiotaomicron VPI-5482	ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO77281.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482]				
2471, 2472	53715428	55	1.00E-92	Bacteroides fragilis YCH46	histidine ammonia-lyase [Bacteroides fragilis YCH46] dbj BAD50886.1 histidine ammonia-lyase [Bacteroides fragilis YCH46]				4.3.1.3
24711, 24712	45658399	46	2.00E-20	Leptospira interrogans serovar Copenhagen str. Flocruz L1-130	hypothetical protein LIC12558 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS71122.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				
24713, 24714	48853960	32	3.00E-20	Cytophaga hutchinsonii	COG0764: 3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratases [Cytophaga hutchinsonii]				
24715, 24716	57506055	41	4.00E-21	Campylobacter upsaliensis RM3195	RibF, putative [Campylobacter upsaliensis RM3195] gb EAL52454.1 RibF, putative [Campylobacter upsaliensis RM3195]				
24717, 24718	48854571	63	1.00E-61	Cytophaga hutchinsonii	COG0707: UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase [Cytophaga hutchinsonii]				2.4.1.-
24719, 24720	52853382	77	2.00E-27	Psychrobacter sp. 273-4	hypothetical protein Psyc03002036 [Psychrobacter sp. 273-4]				
24723, 24724	48853807	36	2.00E-56	Cytophaga hutchinsonii	COG0793: Periplasmic protease [Cytophaga hutchinsonii]				3.4.21.-
24725, 24726	48855800	63	2.00E-60	Cytophaga hutchinsonii	COG0688: Phosphatidylserine decarboxylase [Cytophaga hutchinsonii]				4.1.1.65
24727, 24728	53711474	37	1.00E-46	Bacteroides fragilis YCH46	hypothetical protein BF0183 [Bacteroides fragilis YCH46] dbj BAD46932.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
2473, 2474	42523724	44	4.00E-18	Bdellovibrio bacteriovorus HD100	putative potassium/proton antiporter [Bdellovibrio bacteriovorus HD100] emb CAE80097.1 putative potassium/proton antiporter [Bdellovibrio bacteriovorus HD100]				
24735, 24736	30248520	31	3.00E-23	Nitrosomonas europaea ATCC 19718	ribD; ribosomal large subunit pseudouridine synthase D [Nitrosomonas europaea ATCC 19718] sp Q82WZ5 RLUD_NITEU Ribosomal large subunit pseudouridine synthase D (Pseudouridylylase synthase) (Uracil hydrolyase)				4.2.1.70
24737, 24738	29346053	58	2.00E-94	Bacteroides thetaiotaomicron VPI-5482	RNA methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75750.1 RNA methyltransferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8AA22 Y643_BACTN Hypothetical RNA methyltransferase BT0643				2.1.1.-

24739, 24740	23103296	33	2.00E-35	Azotobacter vinelandii	COG2194: Predicted membrane-associated, metal-dependent hydrolase [Azotobacter vinelandii]				
24741, 24742	29346131	33	5.00E-44	Bacteroides thetaiotaomicron VPI-5482	DNA repair and recombination protein, putative helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75828.1 DNA repair and recombination protein, putative helicase [Bacteroides thetaiotaomicron VPI-5482]				
24743, 24744	48863475	44	3.00E-63	Microbulbifer degradans 2-40	hypothetical protein Mdeg02001566 [Microbulbifer degradans 2-40]				
24745, 24746	48856334	22	2.00E-07	Cytophaga hutchinsonii	hypothetical protein Chut02000046 [Cytophaga hutchinsonii]				
24747, 24748	AAW9778	35	6.00E-09		Desc:Bacillus subtilis serine protease SP1 (YUXL). Org:Bacillus subtilis imidazole glycerol phosphate synthase subunit hisH [Bacteroides fragilis YCH46] dbj BAD49801.1 imidazole glycerol phosphate synthase subunit hisH [Bacteroides fragilis YCH46]			3.4.21.-	
24749, 24750	53714343	55	5.00E-47	Bacteroides fragilis YCH46	peroxiredoxin [Rhodopirella batlica SH 1] emb CAD77542.1 peroxiredoxin [Pirella sp.]				2.4.2.-
24751, 24752	32477471	38	4.00E-13	Ralstonia metallidurans	COG0463: Glycosyltransferases involved in cell wall biogenesis [Ralstonia metallidurans CH34]				2.4.-.-
24753, 24754	48771048	37	6.00E-29	CH34	COG0463: Glycosyltransferases involved in cell wall biogenesis [Haemophilus somnus 2336]				2.4.1.-
24757, 24758	53728512	43	9.00E-38	Haemophilus sornus 2336	hypothetical maturase [Photobacterium profundum SS9] emb CAG22679.1 hypothetical maturase [Photobacterium profundum]	Photobacterium profundum SS9 chromosome 2; segment 3/7	83	2.00E-16	2.7.7.49
24759, 24760	54302486	72	3.00E-99	Photobacterium profundum SS9	hypothetical protein BT9727_2788 [Bacillus thuringiensis serovar konkukian str. 97-27] gb AA160154.1 conserved hypothetical protein [Bacillus thuringiensis serovar konkukian str. 97-27]				
24761, 24762	49477952	26	1.00E-22	Bacillus thuringiensis serovar konkukian str. 97-27	GTP-binding protein Era [Porphyromonas gingivalis W83] ref NP_906196.1 GTP-binding protein Era [Porphyromonas gingivalis W83]				
24765, 24766	34398035	43	6.00E-39	Porphyromonas gingivalis W83	hypothetical protein BT1057 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76164.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
24767, 24768	29346467	31	3.00E-16	Bacteroides thetaiotaomicron VPI-5482	putative DNA mismatch repair protein [Bacteroides fragilis YCH46] dbj BAD50625.1 putative DNA mismatch repair protein [Bacteroides fragilis YCH46]				
24769, 24770	53715167	37	4.00E-16	Bacteroides fragilis YCH46	hypothetical protein BF3279 [Bacteroides fragilis YCH46] dbj BAD50023.1 hypothetical protein [Bacteroides fragilis YCH46]				

2477,	28377430	55	5.00E-37	Lactobacillus	hypoxanthine-guanine phosphoribosyltransferase [Lactobacillus plantarum WCFS1] emb CAD63163.1 hypoxanthine-guanine				2.4.2.8
2478				plantarum WCFS1	phosphoribosyltransferase [Lactobacillus plantarum WCFS1]				
24771,	48839913	31	7.00E-17	Methanosarcina	COG2120: Uncharacterized proteins, LmbE homologs [Methanosarcina barkeri str. fusaro]				
24772				barkeri str. fusaro					
24773,	21228215	42	1.00E-34	Methanosarcina	hypothetical protein MM2113 [Methanosarcina mazei Go1] gb AAM31809.1				
24774				mazei Go1	hypothetical protein [Methanosarcina mazei Go1]				
24775,					phosphoglycolate phosphatase (putative) [Lactobacillus plantarum WCFS1]				
24776	28379855	27	9.00E-07	Lactobacillus	emb CAD65825.1 phosphoglycolate phosphatase (putative) [Lactobacillus plantarum WCFS1]				
24779,				plantarum WCFS1					
24780	48855589	35	2.00E-34	Cytophaga	COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii]				3.1.-.-
				hutchinsonii					
24781,					probable late competence protein [Clostridium perfringens str. 13]				
24782	18310639	38	2.00E-40	Clostridium	dbj BAB81363.1 probable late competence protein [Clostridium perfringens str. 13]				
24785,				perfringens str. 13					2.4.1.18
24786	48855019	44	1.00E-16	Cytophaga	COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii]				2
24787,				hutchinsonii					
24788	48854120	50	1.00E-81	Cytophaga	COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii]				6.2.1.3
				hutchinsonii					
24789,					hypothetical protein mlr2180 [Mesorhizobium loti MAFF303099]				
24790	13472020	33	5.00E-11	Mesorhizobium loti	dbj BAB49373.1 mlr2180 [Mesorhizobium loti MAFF303099]				
				MAFF303099					
				Photorhabdus					
2479,				luminescens	hypothetical protein plu2609 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE14983.1 unnamed protein product [Photorhabdus				
2480	37526500	52	2.00E-34	subsp. laumondii	luminescens subsp. laumondii TTO1]				
				TTO1					
24793,									
24794	48856297	55	2.00E-40	Cytophaga	COG0735: Fe2+/Zn2+ uptake regulation proteins [Cytophaga hutchinsonii]				
				hutchinsonii	oxygen-independent coproporphyrinogen III oxidase, putative [Pseudomonas				
24795,					putida KT2440] gb AAN70666.1 oxygen-independent coproporphyrinogen III				
24796	26991777	35	6.00E-12	Pseudomonas	oxidase, putative [Pseudomonas putida KT2440]				1.-.-.-
				putida KT2440					
24797,					hypothetical protein PG1493 [Porphyromonas gingivalis W83]				
24798	34397476	33	4.00E-30	Porphyromonas	ref NP_905638.1 hypothetical protein PG1493 [Porphyromonas gingivalis				
				gingivalis W83]	W83]				
24803,					hypothetical protein MA2102 [Methanosarcina acetivorans C2A]				
24804	20090946	35	3.00E-24	Methanosarcina	gb AAM05501.1 hypothetical protein (multi-domain) [Methanosarcina				2.7.7.49
				acetivorans C2A]	acetivorans str. C2A]				
					hypothetical protein AF1548 [Archaeoglobus fulgidus DSM 4304]				
24805,					gb AAB89701.1 A. fulgidus predicted coding region AF1548 [Archaeoglobus				
24806	11499143	31	2.00E-20	Archaeoglobus	fulgidus DSM 4304] pir C69443 hypothetical protein AF1548 -				
				Archaeoglobus	Archaeoglobus fulgidus sp O28724 YF48_ARCFU Hypothetical protein				
				fulgidus DSM 4304	AF1548				

24809, 24810	48853591	59	1.00E-102	Cytophaga hutchinsonii	COG1021: Peptide arylation enzymes [Cytophaga hutchinsonii]				
2481, 2482	29377430	55	5.00E-37	Lactobacillus plantarum WCFS1	hypoxanthine-guanine phosphoribosyltransferase [Lactobacillus plantarum WCFS1] emb CAD63163.1 hypoxanthine-guanine phosphoribosyltransferase [Lactobacillus plantarum WCFS1]				2.4.2.8
24811, 24812	10717100	38	2.00E-37	Streptococcus thermophilus	putative HsdS [Streptococcus thermophilus]				3.1.21.3
24813, 24814	48855375	37	4.00E-21	Cytophaga hutchinsonii	COG0784: FOG: CheY-like receiver [Cytophaga hutchinsonii]				2.7.3.-
24815, 24816	29349055	50	3.00E-31	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3647 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78752.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
24817, 24818	48856944	56	2.00E-26	Cytophaga hutchinsonii	COG0504: CTP synthase (UTP-ammonia lyase) [Cytophaga hutchinsonii]				6.3.4.2
24827, 24828	46120271	47	2.00E-59	Crocospaera watsonii WH 8501	hypothetical protein Cwat03000671 [Crocospaera watsonii WH 8501] penicillin-binding protein AmpH, putative [Caulobacter crescentus CB15] gb AAK25451.1 penicillin-binding protein AmpH, putative [Caulobacter crescentus CB15] pir G87681 penicillin-binding protein AmpH, probable [imported] - Caulobacter crescentus				
2483, 2484	16127719	30	1.00E-27	Caulobacter crescentus CB15	COG0286: Type I restriction-modification system methyltransferase subunit [Burkholderia cepacia R1808]				
24835, 24836	46320397	30	3.00E-08	Burkholderia cepacia R1808	COG0286: Type I restriction-modification system methyltransferase subunit [Burkholderia cepacia R1808]				
24837, 24838	46320397	27	3.00E-15	Burkholderia cepacia R1808	COG0286: Type I restriction-modification system methyltransferase subunit [Burkholderia cepacia R1808]				
24839, 24840	48891775	43	7.00E-10	Trichodesmium erythraeum IMS101	COG1112: Superfamily I DNA and RNA helicases and helicase subunits [Trichodesmium erythraeum IMS101]				3.6.1.-
24841, 24842	16766038	25	7.00E-09	Phage Fels-2	hypothetical protein STM2726 [Phage Fels-2] gb AAL21612.1 Fels-2 prophage protein [Salmonella typhimurium LT2]				
24843, 24844	56480140	34	2.00E-07	Shigella flexneri 2a str. 301	hypothetical protein SF2623 [Shigella flexneri 2a str. 301] gb AAN44120.2 orf, conserved hypothetical protein [Shigella flexneri 2a str. 301] ref NP_838134.1 hypothetical protein S2796 [Shigella flexneri 2a str. 2457T] gb AAP17944.1 hypothetical protein S2796 [Shigella flexneri 2a str. 2457T]				
24845, 24846	34396493	44	1.00E-30	Porphyromonas gingivalis W83	ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83] ref NP_904560.1 ATP-dependent DNA helicase RecG [Porphyromonas gingivalis W83]				3.6.1.-
24847, 24848	29611044	51	2.00E-44	NiFe	putative [NiFe] hydrogenase expression/formation protein [Streptomyces avermitilis MA-4680] ref NP_828553.1 putative [NiFe] hydrogenase expression/formation protein [Streptomyces avermitilis MA-4680]				

24849,	37527577	26	3.00E-07	TT01	Photorhabdus luminescens subsp. laumondii	hypothetical protein plu3714 [Photorhabdus luminescens subsp. laumondii TT01] emb CAE16086.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TT01]				
24850	42761500	41	3.00E-20	dictyostelium	Dictyostelium discoideum	hypothetical protein [Dictyostelium discoideum]				
24857,	42761500	41	3.00E-20	Aeromonas hydrophila	Aeromonas hydrophila	putative ADP-heptose-LPS [Aeromonas hydrophila]				2.4.1.-
24858	39545768	34	2.00E-18	Legionella pneumophila subsp. Philadelphia 1	Legionella pneumophila subsp. Philadelphia 1	sulfate transporter [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU28258.1 sulfate transporter [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]				
24861,	52842406	42	2.00E-25	Legionella pneumophila str. Paris	Legionella pneumophila str. Paris	hypothetical protein lpp3007 [Legionella pneumophila str. Paris] emb CAH14160.1 hypothetical protein [Legionella pneumophila str. Paris]				
24862	54298940	40	1.00E-37	Legionella pneumophila str. Lens	Legionella pneumophila str. Lens	hypothetical protein lpl2876 [Legionella pneumophila str. Lens] emb CAH17120.1 hypothetical protein [Legionella pneumophila str. Lens]				
24863,	54295786	35	3.00E-39	Thermotoga maritima MSB8	Thermotoga maritima MSB8	hypothetical protein TM0445 [Thermotoga maritima MSB8] gb AAD35530.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir H72377				
24864	15643211	41	1.00E-34	Psychrobacter sp. 273-4	Psychrobacter sp. 273-4	conserved hypothetical protein - Thermotoga maritima (strain MSB8) COG2801: Transposase and inactivated derivatives [Psychrobacter sp. 273-4] ref ZP_00146915.2 COG2801: Transposase and inactivated derivatives [Psychrobacter sp. 273-4]				
24865,	52853435	89	1.00E-85	Bacteroides fragilis YCH46	Bacteroides fragilis YCH46	hypothetical protein BF3882 [Bacteroides fragilis YCH46] db BAD50624.1				
24866	53715166	30	4.00E-08	Bacteroides thetaiotaomicron VPI-5482	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein [Bacteroides fragilis YCH46]				
24871,	29347590	50	7.00E-59	Cytophaga hutchinsonii	Cytophaga hutchinsonii	hypothetical protein BT2180 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77287.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
24872	48853745	29	1.00E-09	Porphyrromonas gingivalis W83	Porphyrromonas gingivalis W83	hypothetical protein Chut02003380 [Cytophaga hutchinsonii]				
24875,	48853745	29	1.00E-09	Bacteroides thetaiotaomicron VPI-5482	Bacteroides thetaiotaomicron VPI-5482	capsular polysaccharide transport protein, putative [Porphyrromonas gingivalis W83] ref NP_904737.1 capsular polysaccharide transport protein, putative [Porphyrromonas gingivalis W83]				
24876	34396570	26	2.00E-17	Bacteroides thetaiotaomicron VPI-5482	Bacteroides thetaiotaomicron VPI-5482	putative transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO75703.1 putative transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482]				
24877,	29346006	29	7.00E-12	Clostridium tetani E88	Clostridium tetani E88	hypothetical protein CTC00414 [Clostridium tetani E88] gb AAO35048.1 conserved protein [Clostridium tetani E88]				
24878	28210167	57	3.00E-35							

24895, 24896	29606128	38	2.00E-15	Streptomyces avermittilis MA-4680	hypothetical protein [Streptomyces avermittilis MA-4680] ref NP_823656.1 hypothetical protein SAV2480 [Streptomyces avermittilis MA-4680]			
24897, 24898	48854298	43	7.00E-22	Cytophaga hutchinsonii	COG4867: Uncharacterized protein with a von Willebrand factor type A (vWA) domain [Cytophaga hutchinsonii]			
24899, 24900	48856451	50	6.00E-21	Cytophaga hutchinsonii	COG0040: ATP phosphoribosyltransferase [Cytophaga hutchinsonii]			2.4.2.17
24903, 24904	34397714	63	1.00E-113	Porphyrromonas gingivalis W83	transcription-repair coupling factor [Porphyrromonas gingivalis W83] ref NP_905876.1 transcription-repair coupling factor [Porphyrromonas gingivalis W83]	Streptococcus mutans UA159 section 1 of 185 of the complete genome	85	5.00E-113 3.6.1.-
24905, 24906	48853984	44	2.00E-30	Cytophaga hutchinsonii	COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii]			
24907, 24908	31194223	57	1.00E-72	Anopheles gambiae	ENSANGP00000015562 [Anopheles gambiae]			2.7.6.5
24909, 24910	56480140	41	7.00E-08	Shigella flexneri 2a str. 301	hypothetical protein SF2623 [Shigella flexneri 2a str. 301] gb AA044120.2 orf, conserved hypothetical protein [Shigella flexneri 2a str. 301] ref NP_838134.1 hypothetical protein S2796 [Shigella flexneri 2a str. 2457T] gb AAP17944.1 hypothetical protein S2796 [Shigella flexneri 2a str. 2457T] two-component sensor histidine kinase [Nostoc sp. PCC 7120] pit AH2051 two-component sensor histidine kinase air1966 [imported] - Nostoc sp. (strain PCC 7120) db BAB73665.1 two-component sensor histidine kinase [Nostoc sp. PCC 7120]			2.7.3.-
24911, 24912	17229458	24	8.00E-19	Bdellovibrio bacteriovorus HD100	glutamate synthase [Bdellovibrio bacteriovorus HD100] emb CAE80072.1 glutamate synthase [Bdellovibrio bacteriovorus HD100]			1.4.1.13
24919, 24920	42523699	48	8.00E-29	Shewanella oneidensis MR-1	GGDEF domain protein [Shewanella oneidensis MR-1] gb AA055538.1 GGDEF domain protein [Shewanella oneidensis MR-1]			
24921, 24922	24374051	48	2.00E-46	Anabaena variabilis ATCC 29413	COG2021: Homoserine acetyltransferase [Anabaena variabilis ATCC 29413] COG1674: DNA segregation ATPase FtsK/SpoIIIE and related proteins [Cytophaga hutchinsonii]			2.3.1.31
24923, 24924	48854535	40	1.00E-43	Cytophaga hutchinsonii	COG1674: DNA segregation ATPase FtsK/SpoIIIE and related proteins [Cytophaga hutchinsonii]			
24925, 24926	48854535	42	2.00E-51	Cytophaga hutchinsonii	COG1674: DNA segregation ATPase FtsK/SpoIIIE and related proteins [Cytophaga hutchinsonii]			
24929, 24930	46908547	31	2.00E-21	Listeria monocytogenes str. 4b F2365	hypothetical protein LMO2365_2347 [Listeria monocytogenes str. 4b F2365] gb AA05113.1 conserved domain protein [Listeria monocytogenes str. 4b F2365]			

2493, 2494	48838849	81	8.00E-89	Methanosarcina barkeri str. fusaro	COG4742: Predicted transcriptional regulator [Methanosarcina barkeri str. fusaro]	Methanosarcina acetivorans str. C2A, section 22 of 534 of the complete genome	81	2.00E-27	
24931, 24932	46908547	29	1.00E-24	Listeria monocytogenes str. 4b F2365	hypothetical protein LMO2365_2347 [Listeria monocytogenes str. 4b F2365] gb AAU05113.1 conserved domain protein [Listeria monocytogenes str. 4b F2365]				
24933, 24934	55980986	25	7.00E-13	Thermus thermophilus HB8	hypothetical protein TTHA1017 [Thermus thermophilus HB8] dbj BAD70840.1 conserved hypothetical protein [Thermus thermophilus HB8]				3.6.1.-
24935, 24936	48868352	49	3.00E-48	Haemophilus influenzae 86- 028NP	COG0732: Restriction endonuclease S subunits [Haemophilus influenzae 86- 028NP]				3.1.21.3
24937, 24938	48868352	55	3.00E-68	Haemophilus influenzae 86- 028NP	COG0732: Restriction endonuclease S subunits [Haemophilus influenzae 86- 028NP]				3.1.21.3
24939, 24940	52080497	40	1.00E-14	Bacillus licheniformis ATCC 14580	hypothetical protein BL01869 [Bacillus licheniformis ATCC 14580] gb AAU23650.1 conserved hypothetical protein [Bacillus licheniformis ATCC 14580] ref YP_091706.1 Ydel [Bacillus licheniformis ATCC 14580] gb AAU41013.1 Ydel [Bacillus licheniformis DSM 13]				
24941, 24942	ABB4832 4	40	6.00E-25		Desc:Listeria monocytogenes protein #1028. Org:Listeria monocytogenes Predicted nucleotide-binding protein related to universal stress protein UspA [Methanopyrus kandleri AV19] gb AAM01736.1 Predicted nucleotide-binding protein related to universal stress protein UspA [Methanopyrus kandleri AV19]				
24943, 24944	20093959	30	9.00E-11	Methanopyrus kandleri AV19	Predicted nucleotide-binding protein related to universal stress protein UspA [Methanopyrus kandleri AV19] gb AAM01736.1 Predicted nucleotide-binding protein related to universal stress protein UspA [Methanopyrus kandleri AV19]				
24945, 24946	20093959	30	9.00E-11	Methanopyrus kandleri AV19					
24947, 24948	38145972	30	1.00E-13	Haemophilus influenzae	HIO869 [Haemophilus influenzae]				
2495, 2496	21674173	33	2.00E-28	Chlorobium tepidum TLS	ABC transporter efflux protein [Chlorobium tepidum TLS] gb AAM72580.1 ABC transporter efflux protein [Chlorobium tepidum TLS]				
24951, 24952	48853325	36	3.00E-11	Cytophaga hutchinsonii	hypothetical protein Chut02003941 [Cytophaga hutchinsonii]				
24953, 24954	48853326	44	3.00E-22	Cytophaga hutchinsonii	COG1485: Predicted ATPase [Cytophaga hutchinsonii]				

24955,	48853325	30	2.00E-13	Cytophaga	hypothetical protein Chuf0200394.1 [Cytophaga hutchinsonii]				
24956	ABP7812			hutchinsonii	Desc.N. gonorrhoeae amino acid sequence SEQ ID 2786. Org:Neisseria gonorrhoeae				
24957,	8	28	3.00E-18						
24958									
24959,									
24960	34396448	57	7.00E-81	Porphyrromonas gingivalis W83	phosphoribosylformylglycinamide synthase, putative [Porphyrromonas gingivalis W83] refNP_904615.1 phosphoribosylformylglycinamide synthase, putative [Porphyrromonas gingivalis W83]	Bacteroides thetaiotaomicron VPI-5482, section 8 of 21 of the complete genome	92	9.00E-09	6.3.5.3
24961,									
24962	50083943	29	2.00E-08	Acinetobacter sp. ADP1	hypothetical protein ACIAD0721 [Acinetobacter sp. ADP1] embjCAG67631.1 conserved hypothetical protein [Acinetobacter sp. ADP1]				
24963,									
24964	48854312	39	3.00E-47	Cytophaga hutchinsonii	COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii]				
24969,									
24970	21673117	45	8.00E-32	Chlorobium tepidum TLS	RNA polymerase sigma-70 factor, ECF subfamily [Chlorobium tepidum TLS] gb AAAM71524.1 RNA polymerase sigma-70 factor, ECF subfamily [Chlorobium tepidum TLS]				
2497,									
2498	14521885	37	2.00E-21	Pyrococcus abyssi GE5	hypothetical protein PAB1106 [Pyrococcus abyssi GE5] emb[CAB50591.1] Hypothetical protein [Pyrococcus abyssi] pir A75019 hypothetical protein PAB1106 - Pyrococcus abyssi (strain Orsay) splQ9UY21 YG87_PYRAB Hypothetical UPF0218 protein PYRAB16870				
24971,									
24972	21673117	45	2.00E-34	Chlorobium tepidum TLS	RNA polymerase sigma-70 factor, ECF subfamily [Chlorobium tepidum TLS] gb AAAM71524.1 RNA polymerase sigma-70 factor, ECF subfamily [Chlorobium tepidum TLS]				
24973,									
24974	48861126	35	5.00E-24	Microbulifer degradans 2-40	COG2303: Choline dehydrogenase and related flavoproteins [Microbulifer degradans 2-40]				1.-.-
24975,									
24976	46140301	47	5.00E-61	Dechloromonas aromatica RCB	COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Dechloromonas aromatica RCB]				2.7.3.-
24977,									
24978	48845156	43	2.00E-62	Geobacter metallireducens GS-15	COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Geobacter metallireducens GS-15]				2.7.3.-
24983,									
24984	29345890	30	8.00E-28	Bacteroides thetaiotaomicron VPI-5482	glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75587.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.7.8.6
24985,									
24986	46142542	36	3.00E-19	Methanococcoides burtonii DSM 6242	COG0367: Asparagine synthase (glutamine-hydrolyzing) [Methanococcoides burtonii DSM 6242]				6.3.5.4
24987,									
24988	29346171	32	1.00E-47	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0761 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75868.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				

24989, 24990, 24991, 24992, 24993, 24994, 24995, 24996, 24997, 24998, 24999, 25000, 25001, 25002, 25003, 25004, 25007, 25008, 25009, 25010, 25011, 25012, 25015, 25016	29346171 46401879 24373032 24373032 24373032 24373032 48854243 29347752 48855252 48831933 53713593 48853586 21226130 47779387 48853770	30 34 40 40 36 34 26 54 31 29 59 46 34 41 71	3.00E-31 2.00E-11 1.00E-45 1.00E-52 2.00E-10 2.00E-09 2.00E-72 2.00E-14 1.00E-16 6.00E-85 1.00E-10 1.00E-20 1.00E-50 2.00E-88	Bacteroides thetaiotaomicron VPI-5482 Bacteriophage T5 Shewanella oneidensis MR-1 Shewanella oneidensis MR-1 Cytophaga hutchinsonii Bacteroides thetaiotaomicron VPI-5482 Geobacter metallireducens GS 15 Bdellovibrio bacteriovorus HD100 Cytophaga hutchinsonii Magnetococcus sp. MC-1 Bacteroides fragilis YCH46 Cytophaga hutchinsonii Methanosarcina mazel Go1 uncultured gamma proteobacterium eBACHOT4E07 Cytophaga hutchinsonii	hypothetical protein BT0761 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75868.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482] putative prohead protease [Bacteriophage T5] type I restriction-modification system, M subunit, putative [Shewanella oneidensis MR-1] gb AAN54519.1 type I restriction-modification system, M subunit, putative [Shewanella oneidensis MR-1] type I restriction-modification system, M subunit, putative [Shewanella oneidensis MR-1] gb AAN54519.1 type I restriction-modification system, M subunit, putative [Shewanella oneidensis MR-1] COG2207: AraC-type DNA-binding domain-containing proteins [Cytophaga hutchinsonii] transcription regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO77449.1 transcription regulator [Bacteroides thetaiotaomicron VPI- 5482] COG3604: Transcriptional regulator containing GAF, AAA-type ATPase, and DNA binding domains [Geobacter metallireducens GS-15] hypothetical protein Bd1537 [Bdellovibrio bacteriovorus HD100] emb CAE79417.1 hypothetical protein predicted by Glimmer/Critica [Bdellovibrio bacteriovorus HD100] COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] ATP-dependent protease [Bacteroides fragilis YCH46] db BAD49051.1 ATP dependent protease [Bacteroides fragilis YCH46] COG0466: ATP-dependent Lon protease, bacterial type [Cytophaga hutchinsonii] Superfamily I DNA and RNA helicase [Methanosarcina mazel Go1] gb AAM29724.1 Superfamily I DNA and RNA helicase [Methanosarcina mazel Go1] predicted HsdR [uncultured gamma proteobacterium eBACHOT4E07] COG0046: Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Cytophaga hutchinsonii]	2.1.1.72 2.1.1.72 3.1.21.3 3.4.21.5 3.4.21.5 3.6.1.- 3.1.21.3 6.3.5.3
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25017,	34398448	61	1.00E-106	Porphyromonas gingivalis W83	phosphoribosylformylglycinamide synthase, putative [Porphyromonas gingivalis W83] ref NP_904815.1 phosphoribosylformylglycinamide synthase, putative [Porphyromonas gingivalis W83]	Bacteroides thetaiotaomicron VPI-5482, section 8 of 21 of the complete genome	92	1.00E-08	6.3.5.3
25018	48853326	47	7.00E-21	Cytophaga hutchinsonii	COG1485: Predicted ATPase [Cytophaga hutchinsonii]				
25019,				Bdellovibrio bacteriovorus	oxaloductase [Bdellovibrio bacteriovorus HD100] emb CAE79695.1				
25020	42523322	24	1.00E-11	Bdellovibrio bacteriovorus HD100	oxaloductase [Bdellovibrio bacteriovorus HD100]				
25023,				Bdellovibrio bacteriovorus	oxaloductase [Bdellovibrio bacteriovorus HD100] emb CAE79695.1				
25024	42523322	29	1.00E-11	Bdellovibrio bacteriovorus HD100	oxaloductase [Bdellovibrio bacteriovorus HD100]				
25025,				Bacteroides fragilis	putative DNA mismatch repair protein [Bacteroides fragilis YCH46]				
25026	53715167	37	4.00E-16	Bacteroides fragilis YCH46	putative DNA mismatch repair protein [Bacteroides fragilis YCH46]				
25027,				Bacteroides fragilis	putative DNA mismatch repair protein [Bacteroides fragilis YCH46]				
25028	53715167	37	4.00E-16	Bacteroides fragilis YCH46	putative DNA mismatch repair protein [Bacteroides fragilis YCH46]				
25029,				Nostoc sp. PCC 7120	hypothetical protein alr7052 [Nostoc sp. PCC 7120] dbj BAB78136.1				
25030	53715167	37	4.00E-16	Nostoc sp. PCC 7120	hypothetical protein alr7052 [Nostoc sp. PCC 7120] pir AD2484 hypothetical protein alr7052 [Imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha				
25031,	17233068	28	4.00E-07	uncultured cyanobacterium	putative transposase [uncultured cyanobacterium] pir S16892 probable transposase (insertion sequence IS702) - Calothrix sp. (PCC 7601)				
25032	581004	43	3.00E-24	uncultured cyanobacterium	sp Q00462 T702_FREDI Probable transposase for insertion sequence element IS702				
25033,				uncultured cyanobacterium	putative transposase [uncultured cyanobacterium] pir S16892 probable transposase (insertion sequence IS702) - Calothrix sp. (PCC 7601)				
25034	581004	43	3.00E-24	uncultured cyanobacterium	sp Q00462 T702_FREDI Probable transposase for insertion sequence element IS702				
25037,				Cytophaga hutchinsonii	COG1196: Chromosome segregation ATPases [Cytophaga hutchinsonii]				
25038	48854028	38	5.00E-36	Burkholderia cepacia R18194	hypothetical protein Bcep03007254 [Burkholderia cepacia R18194]				
25045,	46310883	36	4.00E-26	Bacteroides thetaiotaomicron VPI-5482	putative flagellar motor protein MotB [Bacteroides thetaiotaomicron VPI-5482] gb AA078235.1 putative flagellar motor protein MotB [Bacteroides thetaiotaomicron VPI-5482]				
25047,				Microbulbifer degradans 2-40	COG0784: FOG: CheY-like receiver [Microbulbifer degradans 2-40]				2.7.3.-
25048	29348538	30	6.00E-34	Microbulbifer degradans 2-40					
25049,									
25050	48864200	27	9.00E-31						

25053,	15896323	40	2.00E-40	Clostridium acetobutylicum ATCC 824	Mannose-1-phosphate guanylyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK81012.1 Mannose-1-phosphate guanylyltransferase [Clostridium acetobutylicum ATCC 824] pir J97278 mannose-1-phosphate guanylyltransferase [imported] - Clostridium acetobutylicum			2.7.7.22
25054	48838445	51	2.00E-59	Methanosarcina barkeri str. fusaro	COG0696: Phosphoglyceromutase [Methanosarcina barkeri str. fusaro]			5.4.2.1
25055,	48855722	33	1.00E-09	Cytophaga hutchinsonii	hypothetical protein Chut02000926 [Cytophaga hutchinsonii]			
25056	17229681	39	2.00E-28	Nostoc sp. PCC 7120	regulatory protein [Nostoc sp. PCC 7120] dbj BAB73888.1 regulatory protein [Nostoc sp. PCC 7120] pir JAG2079 regulatory protein at2189 [imported] - Nostoc sp. (strain PCC 7120)			
25057,	18310182	43	1.00E-53	Clostridium perfringens str. 13	hypothetical protein CPE1200 [Clostridium perfringens str. 13] dbj BAB80906.1 hypothetical protein [Clostridium perfringens str. 13]			
25058	48838061	86	1.00E-127	Methanosarcina barkeri str. fusaro	COG3385: FOG: Transposase and inactivated derivatives [Methanosarcina barkeri str. fusaro]			
25059,	48854139	58	2.00E-51	Cytophaga hutchinsonii	COG1066: Predicted ATP-dependent serine protease [Cytophaga hutchinsonii]		89	0
2507,	20091497	60	1.00E-49	Methanosarcina acetivorans C2A	inorganic pyrophosphatase [Methanosarcina acetivorans C2A] gb AAM06052.1 inorganic pyrophosphatase [Methanosarcina acetivorans str. C2A] sp Q8TMI3 PYR_METAC inorganic pyrophosphatase			3.6.1.1
25074	53712258	53	1.00E-57	Bacteroides fragilis YCH46	(Pyrophosphate phospho-hydrolase) (PPase) peptidyl-dipeptidase [Bacteroides fragilis YCH46] dbj BAD47716.1 peptidyl-dipeptidase [Bacteroides fragilis YCH46]			3.4.15.5
25075,	53712055	34	2.00E-15	Bacteroides fragilis YCH46	putative peptidase [Bacteroides fragilis YCH46] dbj BAD47513.1 putative peptidase [Bacteroides fragilis YCH46]			
25076	48854967	54	4.00E-24	Cytophaga hutchinsonii	COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii]			
25077,	13476784	32	1.00E-09	Mesorhizobium loti MAFF303099	transcriptional regulator [Mesorhizobium loti MAFF303099] dbj BAB53814.1 transcriptional regulator [Mesorhizobium loti MAFF303099]			
25078	30019270	31	2.00E-33	Bacillus cereus ATCC 14579	Transcriptional regulator, AraC family [Bacillus cereus ATCC 14579] gb AAP08102.1 Transcriptional regulator, AraC family [Bacillus cereus ATCC 14579]			2.1.1.63
25079,	28974569	52	5.00E-60	Pseudomonas sp. Y2	putative ring-oxidation complex protein 5 [Pseudomonas sp. Y2]			1.6.99.7
25080	48853628	49	4.00E-34	Cytophaga hutchinsonii	COG0006: Xaa-Pro aminopeptidase [Cytophaga hutchinsonii]			3.4.11.9

25093, 25094	48854571	63	2.00E-59	Cytophaga hutchinsonii	COG0707: UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase [Cytophaga hutchinsonii]			2.4.1.-
25095, 25096	22094897	48	1.00E-41	Flavobacterium johnsoniae	MurF [Flavobacterium johnsoniae]			6.3.2.15
25097, 25098	48856302	54	1.00E-12	Cytophaga hutchinsonii	COG1396: Predicted transcriptional regulators [Cytophaga hutchinsonii]			
25099, 25100	29349623	46	2.00E-28	Bacteroides thetataoamicon VPI-5482	shikimate 5-dehydrogenase [Bacteroides thetataoamicon VPI-5482] gb AAO79320.1 shikimate 5-dehydrogenase [Bacteroides thetataoamicon VPI-5482]			1.1.1.25
251, 252	53712013	50	7.00E-29	Bacteroides fragilis YCH46	putative ATP/GTP hydrolase [Bacteroides fragilis YCH46] dbj BAD47471.1 putative ATP/GTP hydrolase [Bacteroides fragilis YCH46]			
25101, 25102	53711995	48	1.00E-25	Bacteroides fragilis YCH46	hypothetical protein BF0706 [Bacteroides fragilis YCH46] dbj BAD47453.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			3.1.-
25103, 25104	48853536	45	4.00E-24	Cytophaga hutchinsonii	COG1619: Uncharacterized proteins, homologs of microcin C7 resistance protein MccF [Cytophaga hutchinsonii]			3.4.17.1 3
25105, 25106	53711995	48	1.00E-25	Bacteroides fragilis YCH46	hypothetical protein BF0706 [Bacteroides fragilis YCH46] dbj BAD47453.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			3.1.-
25107, 25108	23508812	36	2.00E-07	Plasmodium falci-parum 3D7	hypothetical protein PFL0575w [Plasmodium falci-parum 3D7] gb AAN36204.1 hypothetical protein PFL0575w [Plasmodium falci-parum 3D7]			
25109, 25110	23508812	36	2.00E-07	Plasmodium falci-parum 3D7	hypothetical protein PFL0575w [Plasmodium falci-parum 3D7] gb AAN36204.1 hypothetical protein PFL0575w [Plasmodium falci-parum 3D7]			
2511, 2512	53712708	40	1.00E-60	Bacteroides fragilis YCH46	hypothetical protein BF1415 [Bacteroides fragilis YCH46] dbj BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
25111, 25112	48853940	53	5.00E-62	Cytophaga hutchinsonii	COG0036: Pentose-5-phosphate-3-epimerase [Cytophaga hutchinsonii]			5.1.3.1
25113, 25114	57471283	91	1.00E-101	Flavobacterium johnsoniae	RpoD [Flavobacterium johnsoniae]	Treponema denticola ATCC 35405, section 4 of 10 of the complete genome	94 3.00E-11	
25117, 25118	53728512	35	2.00E-39	Haemophilus sommus 2336	COG0463: Glycosyltransferases involved in cell wall biogenesis [Haemophilus sommus 2336]			2.4.1.-
25119, 25120	53712106	45	5.00E-11	Bacteroides fragilis YCH46	probable glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD47564.1 probable glycosyltransferase [Bacteroides fragilis YCH46]			

25123, 25124	15895588	40	2.00E-07	Clostridium acetobutylicum ATCC 824	Predicted glycosyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK80277.1 Predicted glycosyltransferase [Clostridium acetobutylicum ATCC 824] pir B97186 probable glycosyltransferase CAC2321 [imported] - Clostridium acetobutylicum				
25127, 25128	53711566	22	7.00E-07	Bacteroides fragilis YCH46	RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD47024.1 RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46]				
2513, 2514	46317628	28	2.00E-12	Burkholderia cepacia R18194	COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Burkholderia cepacia R18194]				
25131, 25132	53732951	27	1.00E-18	Haemophilus influenzae R2846	COG0642: Signal transduction histidine kinase [Haemophilus influenzae R2846]				
25133, 25134	41690757	97	2.00E-34	Psychrobacter sp. 273-4	COG2975: Uncharacterized protein conserved in bacteria [Psychrobacter sp. 273-4]				
25135, 25136	41690757	97	2.00E-34	Psychrobacter sp. 273-4	COG2975: Uncharacterized protein conserved in bacteria [Psychrobacter sp. 273-4]				
25137, 25138	54302404	31	4.00E-21	Photobacterium profundum SS9	hypothetical protein PBPRB0725 [Photobacterium profundum SS9] emb CAG22597.1 hypothetical protein [Photobacterium profundum]				
25139, 25140	45656536	28	3.00E-14	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	hypothetical protein LIC10638 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS69259.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				
25145, 25146	23097681	30	6.00E-16	Oceanobacillus ihayensis HTE831	mevalonate diphosphate decarboxylase [Oceanobacillus ihayensis HTE831] dbj BAC12182.1 mevalonate diphosphate decarboxylase [Oceanobacillus ihayensis HTE831]				4.1.1.33
25147, 25148	45357986	29	2.00E-14	Methanococcus maripaludis S2	hypothetical protein MMP0423 [Methanococcus maripaludis S2] emb CAF29979.1 hypothetical [Methanococcus maripaludis S2]				
25149, 25150	46100870	37	5.00E-08	Ustilago maydis 521	hypothetical protein UM05700.1 [Ustilago maydis 521] ref XP_403315.1 hypothetical protein UM05700.1 [Ustilago maydis 521]				
25151, 25152	29345677	37	2.00E-40	Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase/response regulator, hybrid (one component system) [Bacteroides thetaiotaomicron VPI-5482] gb AAO75374.1 two-component system sensor histidine kinase/response regulator, hybrid (one component system) [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-

25153, 25154	15902916	33	1.00E-24	Streptococcus pneumoniae R6	Formamidopyrimidine-DNA glycosylase [Streptococcus pneumoniae R6] gb AAK99676.1 Formamidopyrimidine-DNA glycosylase [Streptococcus pneumoniae R6] sp Q8DQ33 FPG_STRR6 Formamidopyrimidine-DNA glycosylase (Fapy-DNA glycosylase) (DNA-(apurinic or apyrimidinic site) lyase mutM) (AP lyase mutM) pir H97980 DNA-formamidopyrimidine glycosylase (EC 3.2.2.23) [imported] - Streptococcus pneumoniae (strain R6)				3.2.2.23
25155, 25156	15902916	34	3.00E-20	Streptococcus pneumoniae R6	Formamidopyrimidine-DNA glycosylase [Streptococcus pneumoniae R6] gb AAK99676.1 Formamidopyrimidine-DNA glycosylase [Streptococcus pneumoniae R6] sp Q8DQ33 FPG_STRR6 Formamidopyrimidine-DNA glycosylase (Fapy-DNA glycosylase) (DNA-(apurinic or apyrimidinic site) lyase mutM) (AP lyase mutM) pir H97980 DNA-formamidopyrimidine glycosylase (EC 3.2.2.23) [imported] - Streptococcus pneumoniae (strain R6)				3.2.2.23
25157, 25158 25161, 25162	15894287 48855355	34 31	2.00E-19 8.00E-42	Clostridium acetobutylicum ATCC 824 Cytophaga hutchinsonii	Uncharacterized protein, homolog of yhfF B. subtilis [Clostridium acetobutylicum ATCC 824] gb AAK78976.1 Uncharacterized protein, homolog of yhfF B. subtilis [Clostridium acetobutylicum ATCC 824] pir E97023 uncharacterized protein, homolog of yhfF B. subtilis [imported] - Clostridium acetobutylicum COG4796: Type II secretory pathway, component HofQ [Cytophaga hutchinsonii]				
25163, 25164	56459804	34	3.00E-26	Idiomarina loihensis L2TR	Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihensis L2TR] gb AAV81536.1 Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihensis L2TR]				
25165, 25166	56459804	33	2.00E-23	Idiomarina loihensis L2TR	Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihensis L2TR] gb AAV81536.1 Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihensis L2TR]				
25167, 25168	49478685	37	3.00E-30	Bacillus thuringiensis serovar konkukian str. 97-27	pseudouridylylase synthase [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAAT60887.1 pseudouridylylase synthase [Bacillus thuringiensis serovar konkukian str. 97-27]				4.2.1.70
25173, 25174	53715188	39	1.00E-08	Bacteroides fragilis YCH46	putative chloride channel protein [Bacteroides fragilis YCH46] dbj BAD50646.1 putative chloride channel protein [Bacteroides fragilis YCH46]				
25175, 25176 25177, 25178	48892234 48856952	58 44	1.00E-29 2.00E-36	Trichodesmium erythraeum IMS101 Cytophaga hutchinsonii	COG1132: ABC-type multidrug transport system, ATPase and permease components [Trichodesmium erythraeum IMS101] COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii]				3.4.21.- 4.1.3.27

25179, 25180	56460975	36	5.00E-26	Idiomarina loihensis L2TR	hypothetical protein IL1875 [Idiomarina loihensis L2TR] gb AAV82707.1 Uncharacterized conserved protein [Idiomarina loihensis L2TR]				
25187, 25188	53715101	31	2.00E-19	Bacteroides fragilis YCH46	hypothetical protein BF3817 [Bacteroides fragilis YCH46] dbj BAD50559.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
25191, 25192	53711382	55	3.00E-73	Bacteroides fragilis YCH46	DNA polymerase I [Bacteroides fragilis YCH46] dbj BAD46840.1 DNA polymerase I [Bacteroides fragilis YCH46]				2.7.7.7
25193, 25194	53711382	42	2.00E-67	Bacteroides fragilis YCH46	DNA polymerase I [Bacteroides fragilis YCH46] dbj BAD46840.1 DNA polymerase I [Bacteroides fragilis YCH46]				2.7.7.7
25199, 25200	48855224	36	4.00E-12	Cytophaga hutchinsonii	COG0010: Arginase/agmatinase/formimionoglutamate hydrolase, arginase family [Cytophaga hutchinsonii]				
25201, 25202	29606128	39	2.00E-16	Streptomyces avermitilis MA-4680	hypothetical protein [Streptomyces avermitilis MA-4680] ref NP_823656.1 hypothetical protein SAV2480 [Streptomyces avermitilis MA-4680]				
25203, 25204	28900996	65	8.00E-40	Vibrio parahaemolyticus RIMD 2210633	gamma-carboxymuconolactone decarboxylase [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62484.1 gamma-carboxymuconolactone decarboxylase [Vibrio parahaemolyticus]				4.1.1.44
25207, 25208	53714372	49	2.00E-27	Bacteroides fragilis YCH46	hypothetical protein BF3085 [Bacteroides fragilis YCH46] dbj BAD49830.1 hypothetical protein [Bacteroides fragilis YCH46]				
25209, 25210	53714371	63	1.00E-67	Bacteroides fragilis YCH46	putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] dbj BAD49829.1 putative ATPase involved in DNA repair [Bacteroides fragilis YCH46]				
25211, 25212	48854073	44	2.00E-58	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii] putative transcriptional regulator [Bacteroides fragilis YCH46]				2.7.3.-
25213, 25214	53715260	52	2.00E-33	Bacteroides fragilis YCH46	dbj BAD50718.1 putative transcriptional regulator [Bacteroides fragilis YCH46]				
25215, 25216	38195402	48	8.00E-25	Flavobacterium johnsoniae	GidI [Flavobacterium johnsoniae]				
25219, 25220	48853532	31	1.00E-16	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]				
25227, 25228	48855336	71	9.00E-57	Cytophaga hutchinsonii		Desc:Haemophilus influenzae complete genome sequence. Org:Haemophilus influenzae	86	3.00E-07	6.1.1.22
25229, 25230	29348988	47	3.00E-56	Bacteroides thetalaotomicron VPI-5482	COG0017: Aspartyl/asparaglyl-tRNA synthetases [Cytophaga hutchinsonii] topoisomerase IV subunit A [Bacteroides thetalaotomicron VPI-5482] gb AAO78685.1 topoisomerase IV subunit A [Bacteroides thetalaotomicron VPI-5482]				

2523, 2524	34396289	39	9.00E-19	Porphyromonas gingivalis W83	conserved domain protein [Porphyromonas gingivalis W83] ref NP_904457.1 hypothetical protein PG0113 [Porphyromonas gingivalis W83]			
25231, 25232	53714264	61	8.00E-65	Bacteroides fragilis YCH46	folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 folypolyglutamate synthase [Bacteroides fragilis YCH46]			6.3.2.17
25233, 25234	53711292	62	2.00E-52	Bacteroides fragilis YCH46	tRNA/rRNA methyltransferase [Bacteroides fragilis YCH46] dbj BAD48750.1 tRNA/rRNA methyltransferase [Bacteroides fragilis YCH46]			2.1.1.-
25235, 25236	29348700	29	2.00E-21	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3291 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78397.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482]			
25237, 25238	46156085	27	1.00E-10	Haemophilus sommus 2336	COG3298: Predicted 3'-5' exonuclease related to the exonuclease domain of PolB [Haemophilus somnus 2336]			
25239, 25240	48854571	58	4.00E-51	Cytophaga hutchinsonii	COG0707: UDP-N-acetylglucosamine:LPS N-acetylglucosamine transferase [Cytophaga hutchinsonii]			2.4.1.-
25241, 25242	34397452	22	8.00E-12	Porphyromonas gingivalis W83	type I restriction-modification system, M subunit, putative [Porphyromonas gingivalis W83] ref NP_905615.1 type I restriction-modification system, M subunit, putative [Porphyromonas gingivalis W83]			
25243, 25244	54302903	60	6.00E-45	Photobacterium profundum SS9	putative transcriptional regulator [Photobacterium profundum SS9] emb CAG23096.1 putative transcriptional regulator [Photobacterium profundum]			
25245, 25246	46446568	43	1.00E-42	Parachlamydia sp. UWE25	hypothetical protein pc0934 [Parachlamydia sp. UWE25] emb CAF23658.1 conserved hypothetical protein [Parachlamydia sp. UWE25]			5.4.2.6
25247, 25248	48862250	68	4.00E-35	Microbulbifer degradans 2-40	COG0386: Glutathione peroxidase [Microbulbifer degradans 2-40]			1.11.1.9
25251, 25252	50364936	41	1.00E-10	Mesoplasma florum L1	deoxyribose-phosphate aldolase [Mesoplasma florum L1] gb AAT75477.1 deoxyribose-phosphate aldolase [Mesoplasma florum L1]			4.1.2.4
25255, 25256	15608643	47	9.00E-50	Mycobacterium tuberculosis H37Rv	hypothetical protein Rv1505c [Mycobacterium tuberculosis H37Rv] ref NP_855195.1 hypothetical protein Mb1543c [Mycobacterium bovis AF2122/97] pir D70713 hypothetical protein Rv1505c - Mycobacterium tuberculosis (strain H37Rv) emb CAB02019.1 CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv] emb CAD96210.1 CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium bovis AF2122/97]			2.3.1.11 7
25257, 25258	53715360	40	2.00E-27	Bacteroides fragilis YCH46	ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] dbj BAD50818.1 ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46]			3.6.1.-

25259,	48854804	51	1.00E-70	Cytophaga hutchinsonii	COG0661: Predicted unusual protein kinase [Cytophaga hutchinsonii]				
25260					hypothetical protein DP0077 [Desulfotalea psychrophila LSV54]				
25261,				Desulfotalea	embjCAG34806.1 conserved hypothetical protein [Desulfotalea				
25262	51243929	56	3.00E-65	psychrophila LSV54	psychrophila LSV54]				
					c-di-GMP phosphodiesterase A-related protein [Vibrio cholerae O1 biovar				
25263,				Vibrio cholerae O1	eltor str. N16961] ref NP_230302.1 c-di-GMP phosphodiesterase A-related				
25264	9655090	43	4.00E-19	N16961	protein [Vibrio cholerae O1 biovar eltor str. N16961] pir H82296 c-di-GMP				
25265,					phosphodiesterase A-related protein VC0653 [imported] - Vibrio cholerae				
25266	48856860	40	5.00E-23	Cytophaga hutchinsonii	(strain N16961 serogroup O1)				
25267,				uncultured	COG0781: Transcription termination factor [Cytophaga hutchinsonii]				
25268	40062908	40	9.00E-42	bacterium 442	metallo-beta-lactamase family protein [uncultured bacterium 442]			3.---	
25269,				Bacillus					
25270	13027221	33	9.00E-32	thermoamyloliquefa	alpha-glucosidase III [Bacillus thermoamyloliquefaciens]			3.2.1.20	
2527,									
2528	48854564	53	5.00E-67	Cytophaga hutchinsonii	COG0745: Response regulators consisting of a CheY-like receiver domain			2.7.3.-	
25271,					and a winged-helix DNA-binding domain [Cytophaga hutchinsonii]				
25272	48856559	37	9.00E-25	Cytophaga hutchinsonii	COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga				
25273,				Methanosarcina	hutchinsonii]				
25274	21227229	29	8.00E-08	mazei Go1	glycosyltransferase [Methanosarcina mazei Go1] gb AAM30823.1				
					glycosyltransferase [Methanosarcina mazei Goe1]				
25281,				Chromobacterium	conserved hypothetical protein [Chromobacterium violaceum ATCC 12472]				
25282	34101691	41	2.00E-20	violaceum ATCC 12472	ref NP_900051.1 hypothetical protein CV0381 [Chromobacterium violaceum				
					ATCC 12472]				
25285,				Clostridium					
25286	48860369	30	9.00E-24	thermoocellum	COG4585: Signal transduction histidine kinase [Clostridium thermoocellum			2.7.3.-	
25289,				ATCC 27405	ATCC 27405]				
25290	29335925	32	2.00E-35	Bacteroides	TraG-like [Bacteroides thetaiotaomicron] ref NP_818964.1 TraG-like protein				
				thetaitaomicron	[Bacteroides thetaiotaomicron]				
25293,									
25294	53713685	52	8.00E-37	Bacteroides fragilis	hypothetical protein BF2394 [Bacteroides fragilis YCH46] dbj BAD49143.1				
25295,				YCH46	conserved hypothetical protein [Bacteroides fragilis YCH46]				
25296	48855491	40	2.00E-17	Cytophaga hutchinsonii	hypothetical protein Chut02001830 [Cytophaga hutchinsonii]				

25297, 25298, 25299, 25300	29349770 48855551	66 37	4.00E-92 3.00E-21	Bacteroides thetaiotaomicron VPI-5482 Cytophaga hutchinsonii	preprotein translocase SecA subunit [Bacteroides thetaiotaomicron VPI-5482] gb AAO79467.1 preprotein translocase SecA subunit [Bacteroides thetaiotaomicron VPI-5482]	Bacteroides thetaiotaomicron VPI-5482, section 20 of 21 of the complete genome	83	1.00E-11	
25301, 25302	48855551 30249356	37 40	3.00E-21 4.00E-09	Nitrosomonas europaea ATCC 19718	COG3569: Topoisomerase IB [Cytophaga hutchinsonii] hypothetical protein NE1380 [Nitrosomonas europaea ATCC 19718] emb CAD85291.1 hypothetical protein [Nitrosomonas europaea ATCC 19718]				
25307, 25308	29349757	31	2.00E-10	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT4349 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79454.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
25309, 25310	48855938	40	4.00E-49	Cytophaga hutchinsonii	COG1132: ABC-type multidrug transport system, ATPase and permease components [Cytophaga hutchinsonii]				
25311, 25312	48855711	34	6.00E-22	Cytophaga hutchinsonii	hypothetical protein Chut02000915 [Cytophaga hutchinsonii]				
25317, 25318	27367623	42	3.00E-22	Vibrio vulnificus CMCP6	Predicted membrane protein [Vibrio vulnificus CMCP6] gb AAO08140.1 Predicted membrane protein [Vibrio vulnificus CMCP6]				
25321, 25322	57092777	35	3.00E-08	Canis familiaris	PREDICTED: similar to 3-mercaptopyruvate sulfurtransferase [Canis familiaris]			2.8.1.2	
25323, 25324	21673251	46	4.00E-40	Chlorobium tepidum TLS	iron(III) ABC transporter, ATP-binding protein, putative [Chlorobium tepidum TLS] gb AAM71658.1 iron(III) ABC transporter, ATP-binding protein, putative [Chlorobium tepidum TLS]			1.8.-.-	
25325, 25326, 25327, 25328	19879252 48854116	65 55	5.00E-89 1.00E-65	Flavobacterium johnsoniae Cytophaga hutchinsonii	hypothetical pseudouridine synthase [Flavobacterium johnsoniae] COG1250: 3-hydroxyacyl-CoA dehydrogenase [Cytophaga hutchinsonii]	Flavobacterium johnsoniae beta- lactamase JOHN-1 (blaJOHN-1), hypothetical primosomal replication factor Y, hypothetical pseudouridine synthase, and hypothetical transcription regulator protein genes, complete cds	84	1.00E-07	4.2.1.70 1.1.1.35

25329,	45656852	38	4.00E-25	Leptospira interrogans serovar Copenhagen str. Flocruz L1-130	TonB-dependent outer membrane hemin receptor [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130]				
25330					outer membrane hemin receptor [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130]				
25331,	48853539	33	5.00E-33	Cytophaga hutchinsonii	COG3021: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
25332									
25333,				Erwinia carotovora subsp. atroseptica	dTDP-4-dehydrohamnose reductase [Erwinia carotovora subsp. atroseptica SCR1043]				1.1.1.13
25334	50120379	46	9.00E-50	SCR1043	[Erwinia carotovora subsp. atroseptica SCR1043]				3
25335,				Clostridium perfringens str. 13	hypothetical protein CPE1460 [Clostridium perfringens str. 13]				
25336	18310442	32	3.00E-20	perfringens str. 13	dbj BAB81166.1 hypothetical protein [Clostridium perfringens str. 13]				
25337,				Bacteroides thetaiotaomicron	FKBP-type peptidyl-prolyl cis-trans isomerase (trigger factor) [Bacteroides thetaiotaomicron VPI-5482]				
25338	29349249	41	2.00E-29	VPI-5482	transisomerase (trigger factor) [Bacteroides thetaiotaomicron VPI-5482]				
25339,				Symbiobacterium thermophilum IAM 14863	hypothetical protein STH2170 [Symbiobacterium thermophilum IAM 14863]				
25340	51893308	26	4.00E-16	thermophilum IAM 14863	dbj BAD41155.1 conserved hypothetical protein [Symbiobacterium thermophilum IAM 14863]				
25341,				Porphyromonas gingivalis W83	DNA-binding response regulator RprY [Porphyromonas gingivalis W83]				2.7.3.-
25342	34397138	51	5.00E-47	gingivalis W83	ref NP_905303.1 DNA-binding response regulator RprY [Porphyromonas gingivalis W83]				
25343,				Bacteroides thetaiotaomicron	hypothetical protein BT3618 [Bacteroides thetaiotaomicron VPI-5482]				
25344	29349026	40	2.00E-10	VPI-5482	gb AAO78723.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
25345,				Anabaena variabilis	hypothetical protein Avar03004767 [Anabaena variabilis ATCC 29413]				
25346	53763669	27	8.00E-07	ATCC 29413	RNA methyltransferase [Bacteroides fragilis YCH46]				2.1.1.-
25347,				Bacteroides fragilis	methyltransferase [Bacteroides fragilis YCH46]				
25348	53713830	66	9.00E-83	YCH46					
25349,				Escherichia coli	putative GlcNAc transferase [Escherichia coli]				
25350	2586167	29	3.00E-14	Escherichia coli					
25351,				Cytophaga hutchinsonii	COG0438: Glycosyltransferase [Cytophaga hutchinsonii]				2.4.1.-
25352	48856222	22	4.00E-07	hutchinsonii					
25353,				Novosphingobium aromaticivorans	hypothetical protein Saro02003107 [Novosphingobium aromaticivorans DSM 12444]				
25354	48848300	35	9.00E-11	DSM 12444	putative thioredoxin family protein [Bacteroides thetaiotaomicron VPI-5482]				
25355,				Bacteroides thetaiotaomicron	putative thioredoxin family protein [Bacteroides thetaiotaomicron VPI-5482]				
25356	29348731	36	2.00E-08	VPI-5482	thetaiotaomicron VPI-5482				

25357, 25358	48854257	34	2.00E-22	Cytophaga hutchinsonii	hypothetical protein Chut02002927 [Cytophaga hutchinsonii]				
25363, 25364	54024369	44	6.00E-22	Nocardia farcinica [FM 10152]	putative acetyltransferase [Nocardia farcinica [FM 10152] dbj BAD57247.1]				
25365, 25366	29346516	66	1.00E-49	Bacteroides thetaiotaomicron VPI-5482	putative acetyltransferase [Nocardia farcinica [FM 10152]] fructose-bisphosphate aldolase class I [Bacteroides thetaiotaomicron VPI-5482] gb AAO76213.1 fructose-bisphosphate aldolase class I [Bacteroides thetaiotaomicron VPI-5482]				4.1.2.13
2537, 2538	21673456	34	2.00E-17	Chlorobium tepidum TLS	transcriptional regulator, NusG/RfaH family [Chlorobium tepidum TLS] gb AAM71863.1 transcriptional regulator, NusG/RfaH family [Chlorobium tepidum TLS]				
25379, 25380	45658436	26	2.00E-17	Leptospira interrogans serovar Copenhagen str. Flocruz L1-130	alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhagen] str. Flocruz L1-130 ref NP_711250.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar Lai str. 56601] gb AA48268.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar lai str. 56601] gb AAS71159.1 alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhagen] str. Flocruz L1-130]				
25381, 25382	48854545	47	1.00E-19	Cytophaga hutchinsonii	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Cytophaga hutchinsonii]				2.1.1.-
25383, 25384	56461428	39	2.00E-56	Idiomarina loihlensis L2TR	Dipeptidyl aminopeptidase [Idiomarina loihlensis L2TR] gb AAV83160.1 Dipeptidyl aminopeptidase [Idiomarina loihlensis L2TR]				3.4.14.-
25387, 25388	48854949	28	4.00E-18	Cytophaga hutchinsonii	COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii]				
25389, 25390	48853612	38	4.00E-19	Cytophaga hutchinsonii	COG1452: Organic solvent tolerance protein OstA [Cytophaga hutchinsonii]				
25397, 25398	46141605	62	2.00E-45	Psychrobacter sp. 273-4	hypothetical protein Pyc03000593 [Psychrobacter sp. 273-4]				
25399, 25400	46141620	59	3.00E-28	Psychrobacter sp. 273-4	COG3335: Transposase and inactivated derivatives [Psychrobacter sp. 273-4]				
25401, 25402	56461359	68	7.00E-82	Idiomarina loihlensis L2TR	ABC-type multidrug transport system, ATPase component [Idiomarina loihlensis L2TR] gb AAV83091.1 ABC-type multidrug transport system, ATPase component [Idiomarina loihlensis L2TR]			86	2.00E-22 1.8.-
25403, 25404	1944167	35	7.00E-28	Actinobacillus actinomycetemcomitans	unnamed protein product [Actinobacillus actinomycetemcomitans]				

25409, 25410	48854730	49	5.00E-26	Cytophaga hutchinsonii	COG2207: AraC-type DNA-binding domain-containing proteins [Cytophaga hutchinsonii]					
2541, 2542	29425233	37	1.00E-09	Mycobacteriophage Che9d	gp109 [Mycobacteriophage Che9d] ref NP_818074.1 gp109 [Mycobacteriophage Che9d]					
25411, 25412	17229681	30	5.00E-20	Nostoc sp. PCC 7120	regulatory protein [Nostoc sp. PCC 7120] dbj BAB73888.1 regulatory protein [Nostoc sp. PCC 7120] pir AG2079 regulatory protein alr2189 [imported] - Nostoc sp. (strain PCC 7120)				2.1.1.63	
25413, 25414	47525436	42	5.00E-31	Bacillus anthracis str. 'Ames Ancestor'	alcohol dehydrogenase, zinc-containing [Bacillus anthracis str. 'Ames Ancestor'] ref YP_026463.1 alcohol dehydrogenase, zinc-containing [Bacillus anthracis str. Sterne] ref NP_842740.1 alcohol dehydrogenase, zinc-containing [Bacillus anthracis str. Ames] gb AAP24226.1 alcohol dehydrogenase, zinc-containing [Bacillus anthracis str. Ames] gb AAT29260.1 alcohol dehydrogenase, zinc-containing [Bacillus anthracis str. 'Ames Ancestor'] gb AAT52514.1 alcohol dehydrogenase, zinc- containing [Bacillus anthracis str. Sterne]	Moraxella sp. O245 insertion sequence IS1599, isolate O245	96	0	1.1.1.1	
25415, 25416	28611027	95	1.00E-125	Moraxella sp. O245	transposase [Moraxella sp. O245]					2.4.2.-
25417, 25418	48855155	39	2.00E-16	Cytophaga hutchinsonii	COG5009: Membrane carboxypeptidase/penicillin-binding protein [Cytophaga hutchinsonii]					
25419, 25420	48853613	37	2.00E-09	Cytophaga hutchinsonii	COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cytophaga hutchinsonii]					
25421, 25422	16767739	28	2.00E-22	Salmonella typhimurium LT2	putative type II restriction enzyme methylase subunit [Salmonella typhimurium LT2] gb AAL23313.1 putative type II restriction enzyme, methylase subunit [Salmonella typhimurium LT2]					3.1.21.4
25423, 25424	52007969	46	2.00E-13	Thiobacillus denitrificans ATCC 25259	COG0796: Glutamate racemase [Thiobacillus denitrificans ATCC 25259] hypothetical protein BT2838 [Bacteroides thetaiotaomicron VPI-5482] gb AAO77944.1 conserved hypothetical protein [Bacteroides thetaitotaomicron VPI-5482]					5.1.1.3
25425, 25426	29348247	29	2.00E-34	Bacteroides thetaitotaomicron VPI-5482	probable aminopeptidase [Rhodopirellula baetica SH 1] emb CAD78184.1 probable aminopeptidase [Pirellula sp.]					3.4.11.-
25427, 25428	32473409	38	8.00E-43	Rhodopirellula baetica SH 1	two-component response regulator [Bradyrhizobium japonicum USDA 110] dbj BAC48129.1 two-component response regulator [Bradyrhizobium japonicum USDA 110]					4.6.1.1
25429, 25430	27377975	37	3.00E-32	Bradyrhizobium japonicum USDA 110	conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_904597.1 hypothetical protein PG0276 [Porphyromonas gingivalis W83]					
25433, 25434	34396430	37	2.00E-27	Porphyromonas gingivalis W83						

25435, 25436	15669547	34	6.00E-42	Methanocaldococcus jannaschii DSM 2661	potassium channel protein, putative [Methanocaldococcus jannaschii DSM 2661] gb AAB99365.1 potassium channel protein, putative [Methanocaldococcus jannaschii DSM 2661] sp Q58752 MJUK2_METJA			
25437, 25438	53713469	64	2.00E-46	Bacteroides fragilis YCH46	Probable potassium channel protein 2 (MjK2) p I D64469 potassium channel homolog - Methanocaldococcus jannaschii			
25439, 25440	9950580	36	9.00E-21	Pseudomonas aeruginosa PAO1	putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1 putative helicase [Bacteroides fragilis YCH46]			3.1.11.5
25441, 25442	48858490	41	2.00E-18	Clostridium thermocellum ATCC 27405	conserved hypothetical protein [Pseudomonas aeruginosa PAO1] ref ZP_00137838.2 COG3124: Uncharacterized protein conserved in bacteria [Pseudomonas aeruginosa UC8PP-PA14] p I A83102 conserved hypothetical protein PA4353 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_253043.1 hypothetical protein PA4353 [Pseudomonas aeruginosa PAO1]			
25443, 25444	34397809	65	1.00E-84	Porphyromonas gingivalis W83	COG3867: Arabinogalactan endo-1,4-beta-galactosidase [Clostridium thermocellum ATCC 27405]			
25445, 25446	52078781	32	3.00E-41	Bacillus licheniformis ATCC 14580	GTP-binding protein HflX [Porphyromonas gingivalis W83] ref NP_905971.1 GTP-binding protein HflX [Porphyromonas gingivalis W83]			
25449, 25450	53712371	31	1.00E-22	Bacteroides fragilis YCH46	penicillin-binding protein [Bacillus licheniformis ATCC 14580] gb AAU21934.1 penicillin-binding protein [Bacillus licheniformis ATCC 14580] ref YP_089980.1 hypothetical protein BLI00328 [Bacillus licheniformis ATCC 14580] gb AAU39287.1 putative protein [Bacillus licheniformis DSM 13]			
2545, 2546	50119383	39	9.00E-13	Erwinia carotovora subsp. atroseptica SCR11043	hypothetical protein BF1079 [Bacteroides fragilis YCH46] dbj BAD47829.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
25451, 25452	48854288	55	9.00E-21	Cytophaga hutchinsonii	hypothetical protein ECA0432 [Erwinia carotovora subsp. atroseptica SCR11043] emb CAG73347.1 conserved hypothetical protein [Erwinia carotovora subsp. atroseptica SCR11043]			
25453, 25454	48845905	54	1.00E-72	Geobacter metallireducens GS-15	COG0419: ATPase involved in DNA repair [Cytophaga hutchinsonii]			
25465, 25466	41689416	78	3.00E-54	Psychrobacter sp. 273-4	COG1640: 4-alpha-glucanotransferase [Geobacter metallireducens GS-15]			2.4.1.25
25467, 25468	53711359	72	2.00E-72	Bacteroides fragilis YCH46	COG1393: Arsenate reductase and related proteins, glutaredoxin family [Psychrobacter sp. 273-4]			1.---
					tyrosyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD46817.1 tyrosyl-tRNA synthetase [Bacteroides fragilis YCH46]			6.1.1.1

25471, 25472	41408154	37	8.00E-19	Mycobacterium avium subsp. paratuberculosis str. k10	hypothetical protein MAP2056c [Mycobacterium avium subsp. paratuberculosis str. k10] gb AA04373.1 hypothetical protein MAP2056c [Mycobacterium avium subsp. paratuberculosis str. k10]				
25473, 25474	41408154	37	8.00E-19	Mycobacterium avium subsp. paratuberculosis str. k10	hypothetical protein MAP2056c [Mycobacterium avium subsp. paratuberculosis str. k10] gb AA04373.1 hypothetical protein MAP2056c [Mycobacterium avium subsp. paratuberculosis str. k10]				
25475, 25476	48856725	56	3.00E-72	Cytophaga hutchinsonii	COG0159: Tryptophan synthase alpha chain [Cytophaga hutchinsonii]				
25477, 25478	48770125	37	3.00E-24	Ralstonia metallidurans CH34	COG0642: Signal transduction histidine kinase [Ralstonia metallidurans CH34]				2.7.3.-
25479, 25480	48787591	36	4.00E-24	Burkholderia fungorum LB400	COG0210: Superfamily I DNA and RNA helicases [Burkholderia fungorum LB400]				3.6.1.-
25483, 25484	AAO2094 8	41	6.00E-45		Desc:Protein of the Bpm1 M1 methylase gene (Bpm1M1). Org: Bacillus pumilus				
25485, 25486	45157173	52	4.00E-76	Escherichia coli	endonuclease [Escherichia coli] sp P25239 T257_ECOLI Type IIS restriction enzyme Eco57I (Endonuclease Eco57I) [Includes: Adenine-specific methyltransferase activity Eco57IA (M.Eco57IA)]				2.1.1.72
25487, 25488	AAB6907 4	56	3.00E-84		Desc:Aquifex aeolicus VF5 1,4-alpha-glucan branching enzyme SEQ ID NO:1. Org:Aquifex aeolicus				2.4.1.18
25489, 25490	48854720	41	1.00E-45	Cytophaga hutchinsonii	COG1559: Predicted periplasmic solute-binding protein [Cytophaga hutchinsonii]				4.-.-.-
2549, 2550	53714487	56	9.00E-44	Bacteroides fragilis YCH46	SsrA-binding protein [Bacteroides fragilis YCH46] dbj BAD49945.1 SsrA- binding protein [Bacteroides fragilis YCH46]				
25491, 25492	34332880	56	2.00E-29	Chromobacterium violaceum ATCC 12472	probable transmembrane protein [Chromobacterium violaceum ATCC 12472] ref NP_903091.1 probable transmembrane protein [Chromobacterium violaceum ATCC 12472]				
25493, 25494	48863063	45	3.00E-29	Microbulbifer degradans 2-40	hypothetical protein Mdeg02001127 [Microbulbifer degradans 2-40]				
25495, 25496	48854920	36	6.00E-35	Cytophaga hutchinsonii	COG0389: Nucleotidyltransferase/DNA polymerase involved in DNA repair [Cytophaga hutchinsonii]				3.4.21.-
255, 256	29346772	47	5.00E-18	Bacteroides thetaiotaomicron VPI-5482	flavoprotein [Bacteroides thetaiotaomicron VPI-5482] gb AA076489.1 flavoprotein [Bacteroides thetaiotaomicron VPI-5482]				6.3.2.5
25505, 25506	29654347	55	6.00E-27	Coxiella burnetii RSA 493	nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493] gb AA090553.1 nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493]				

25507, 25508	29654347	58	3.00E-43	Coxiella burnetii RSA 493	nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493] gb AAO90553.1 nicotinate phosphoribosyltransferase, putative [Coxiella burnetii RSA 493]				2.4.2.11
25509, 25510	23099137	42	3.00E-10	Oceanobacillus ihayensis HTE831	cytochrome c biogenesis [Oceanobacillus ihayensis HTE831] dbj BAC13638.1 cytochrome c biogenesis (thiol:disulfide interchange protein) [Oceanobacillus ihayensis HTE831]				
2551, 2552	29349611	49	1.00E-22	Bacteroides thetaitaomicron VPI-5482	tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides thetaitaomicron VPI-5482] gb AAO79308.1 tRNA delta(2)- isopentenylpyrophosphate transferase [Bacteroides thetaiotaomicron VPI- 5482] sp Q8A018 MAA_BACTN tRNA delta(2)-isopentenylpyrophosphate transferase (IPP transferase) (isopentenyl-diphosphate:tRNA isopentenyltransferase) (IPTase) (IPT)			2.5.1.8	
25511, 25512	23099137	42	3.00E-10	Oceanobacillus ihayensis HTE831	cytochrome c biogenesis [Oceanobacillus ihayensis HTE831] dbj BAC13638.1 cytochrome c biogenesis (thiol:disulfide interchange protein) [Oceanobacillus ihayensis HTE831]				
25513, 25514	48859742	31	3.00E-14	Clostridium thermocellum ATCC 27405	hypothetical protein Chte02000885 [Clostridium thermocellum ATCC 27405]				
25515, 25516	48859742	31	5.00E-28	Clostridium thermocellum ATCC 27405	hypothetical protein Chte02000885 [Clostridium thermocellum ATCC 27405]				
25517, 25518	48856112	40	2.00E-52	Cytophaga hutchinsonii	COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
25519, 25520	48854446	42	2.00E-12	Cytophaga hutchinsonii	COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii]				
25521, 25522	56461337	27	2.00E-11	Idiomarina lohiensis L2TR	Peptidase, M23/M37 family [Idiomarina lohiensis L2TR] gb AAV83069.1 Peptidase, M23/M37 family [Idiomarina lohiensis L2TR]				
25523, 25524	37528207	57	1.00E-102	Photorhabdus luminescens subsp. laumondii TTO1	glucose-6-phosphate isomerase (GPI) (phosphoglucoseisomerase) (PGI) (phosphohexose isomerase) (PHI) [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16751.1 glucose-6-phosphate isomerase (GPI) (phosphoglucoseisomerase) (PGI) (phosphohexose isomerase) (PHI) [Photorhabdus luminescens subsp. laumondii TTO1]			5.3.1.9	
25525, 25526	29349609	29	4.00E-26	Bacteroides thetaitaomicron VPI-5482	hypothetical protein BT4201 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79306.1 conserved hypothetical protein [Bacteroides thetaitaomicron VPI-5482]				
25527, 25528	48855337	54	2.00E-76	Cytophaga hutchinsonii	COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii]				
2553, 2554	34396896	61	4.00E-48	Porphyrromonas gingivalis W83	polyA polymerase family protein [Porphyrromonas gingivalis W83] ref NP_905062.1 polyA polymerase family protein [Porphyrromonas gingivalis W83]				2.7.7.19

25535, 25536	48854286	32	3.00E-30	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]			
25539, 25540	29347849	42	2.00E-34	Bacteroides thetaiotaomicron VPI-5482	beta-N-acetylglucosaminidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77546.1 beta-N-acetylglucosaminidase [Bacteroides thetaiotaomicron VPI-5482]			
25541, 25542	29347849	42	6.00E-39	Bacteroides thetaiotaomicron VPI-5482	beta-N-acetylglucosaminidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77546.1 beta-N-acetylglucosaminidase [Bacteroides thetaiotaomicron VPI-5482]			
25543, 25544	48854034	33	3.00E-09	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]			
2555, 2556	53712197	33	9.00E-14	Bacteroides fragilis YCH46	hypothetical protein BF0904 [Bacteroides fragilis YCH46] dbj BAD47655.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
25551, 25552	51598184	66	1.00E-111	Yersinia pseudotuberculosis IP 32953	possible type I restriction enzyme (restriction subunit) [Yersinia pseudotuberculosis IP 32953] emb CAH23117.1 possible type I restriction enzyme (restriction subunit) [Yersinia pseudotuberculosis IP 32953]			3.1.21.3
25555, 25556	52081206	45	2.00E-55	Bacillus licheniformis ATCC 14580	cystathionine gamma-lyase YrHB [Bacillus licheniformis ATCC 14580] gb AAU24359.1 cystathionine gamma-lyase YrHB [Bacillus licheniformis ATCC 14580] ref YP_092416.1 YrHB [Bacillus licheniformis ATCC 14580] gb AAU41723.1 YrHB [Bacillus licheniformis DSM 13]			4.4.1.8
25559, 25560	46141805	94	1.00E-121	Psychrobacter sp. 273-4	COG3328: Transposase and inactivated derivatives [Psychrobacter sp. 273- 4]	Erwinia sp. Ejp 556 plasmid pEJ30, complete sequence	87	1.00E-07
25561, 25562	48855899	58	3.00E-71	Cytophaga hutchinsonii	COG0321: Lipote-protein ligase B [Cytophaga hutchinsonii]			6.---
25565, 25566	48855572	47	4.00E-21	Cytophaga hutchinsonii	COG1733: Predicted transcriptional regulators [Cytophaga hutchinsonii]			
25567, 25568	48853984	38	8.00E-14	Cytophaga hutchinsonii	COG1197: Transcription-repair coupling factor (superfamily II helicase) [Cytophaga hutchinsonii]			
2557, 2558	53795203	31	1.00E-20	Chloroflexus aurantiacus	COG1680: Beta-lactamase class C and other penicillin binding proteins [Chloroflexus aurantiacus]			3.5.2.6
25573, 25574	52627365	47	1.00E-49	Prevotella intermedia	phosphorylase family protein [Prevotella intermedia]			2.4.2.3
25579, 25580	48855702	37	2.00E-40	Cytophaga hutchinsonii	COG3279: Response regulator of the LysR/Agr family [Cytophaga hutchinsonii]			3.1.1.61
25581, 25582	28899875	37	7.00E-10	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VPA0020 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61363.1 conserved hypothetical protein [Vibrio parahaemolyticus]			2.7.3.-

25583, 25584	48855703	30	2.00E-18	Cytophaga hutchinsonii	COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii]			2.7.3.-
25585, 25586	16945755	51	1.00E-20	Photobacterium damselfae subsp. piscicida	hypothetical protein [Photobacterium damselfae subsp. piscicida]			
2559, 2560	52549895	44	4.00E-50	uncultured archaeon GZfos33E1	trehalose-6-phosphate synthase [uncultured archaeon GZfos33E1]			2.4.1.15
25591, 25592	29348143	63	1.00E-93	Bacteroides thetaiotaomicron VPI-5482	DNA-directed RNA polymerase beta chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO77840.1 DNA-directed RNA polymerase beta chain [Bacteroides thetaiotaomicron VPI-5482] sp Q8A469 RPOB_BACTN DNA-directed RNA polymerase beta chain (RNAP beta subunit) (Transcriptase beta chain) (RNA polymerase beta subunit)	Porphyrromonas gingivalis W83 section 2 of 8 of the complete genome	85	3.00E-15
25593, 25594	32475491	42	2.00E-24	Rhodopirellula baltica SH 1	probable oxidoreductase [Rhodopirellula baltica SH 1] emb CAD75862.1 probable oxidoreductase [Pirellula sp.]			1.3.-
25595, 25596	32475491	43	3.00E-26	Rhodopirellula baltica SH 1	probable oxidoreductase [Rhodopirellula baltica SH 1] emb CAD75862.1			1.3.-
25597, 25598	53715737	43	2.00E-54	Bacteroides fragilis YCH46	hypothetical protein BF4458 [Bacteroides fragilis YCH46] dbj BAD51195.1 hypothetical protein [Bacteroides fragilis YCH46]			
25603, 25604	53713063	34	3.00E-25	Bacteroides fragilis YCH46	[S110 family transposase [Bacteroides fragilis YCH46] dbj BAD48521.1 [S110 family transposase [Bacteroides fragilis YCH46]			
25605, 25606	48853783	45	7.00E-25	Cytophaga hutchinsonii	COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii]			2.7.7.7
25607, 25608	48853783	37	3.00E-42	Cytophaga hutchinsonii	COG0847: DNA polymerase III, epsilon subunit and related 3'-5' exonucleases [Cytophaga hutchinsonii]			2.7.7.7
25609, 25610	53730177	47	1.00E-48	Dechloromonas aromatica RCB	COG2308: Uncharacterized conserved protein [Dechloromonas aromatica RCB]			
2561, 2562	48853533	45	2.00E-36	Cytophaga hutchinsonii	COG2825: Outer membrane protein [Cytophaga hutchinsonii]			
25611, 25612	53730177	48	2.00E-50	Dechloromonas aromatica RCB	COG2308: Uncharacterized conserved protein [Dechloromonas aromatica RCB]			
25613, 25614	53715757	35	4.00E-32	Bacteroides fragilis YCH46	hypothetical protein BF4478 [Bacteroides fragilis YCH46] dbj BAD51215.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
25615, 25616	30023424	36	1.00E-31	Bacillus cereus ATCC 14579	Potassium channel protein [Bacillus cereus ATCC 14579] gb AAP12556.1 Potassium channel protein [Bacillus cereus ATCC 14579]			
25617, 25618	25809040	55	9.00E-63	Gram-negative bacterium 0471	hypothetical protein [Gram-negative bacterium 0471]			3.1.21.3

25619, 25620	28897799	60	9.00E-32	Vibrio parahaemolyticus RIMD 2210633	putative beta-ketoadipate enol-lactone hydrolase [Vibrio parahaemolyticus RIMD 2210633] dbj BAC59288.1 putative beta-ketoadipate enol-lactone hydrolase [Vibrio parahaemolyticus]			3.1.1.1
25625, 25626	24376152	65	7.00E-37	Shewanella oneidensis MR-1	hypothetical protein SO4680 [Shewanella oneidensis MR-1] gb AA57639.1 conserved hypothetical protein [Shewanella oneidensis MR-1]			
25627, 25628	51246929	46	3.00E-59	Desulfotalea psychrophila LSv54	probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSv54] emb CAG37806.1 probable periplasmic tail-specific proteinase [Desulfotalea psychrophila LSv54]			3.4.21.-
25629, 25630	29347578	38	4.00E-17	Bacteroides thetaiotaomicron VPI-5482	coproporphyrinogen III oxidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77275.1 coproporphyrinogen III oxidase [Bacteroides thetaiotaomicron VPI-5482]			
2563, 2564	48855581	61	3.00E-36	Cytophaga hutchinsonii	COG0112: Glycine/serine hydroxymethyltransferase [Cytophaga hutchinsonii]			2.1.2.1
25631, 25632	29347578	41	6.00E-23	Bacteroides thetaiotaomicron VPI-5482	coproporphyrinogen III oxidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77275.1 coproporphyrinogen III oxidase [Bacteroides thetaiotaomicron VPI-5482]			1.-.-.-
25633, 25634	53712075	26	2.00E-12	Bacteroides fragilis YCH46	hypothetical protein BF0782 [Bacteroides fragilis YCH46] dbj BAD47533.1 hypothetical protein [Bacteroides fragilis YCH46]			
25635, 25636	32474967	48	5.00E-63	Rhodopirellula baltica SH 1	hypothetical protein RB7682 [Rhodopirellula baltica SH 1] emb CAD75508.1 hypothetical protein [Pirellula sp.]			
25637, 25638	41725421	44	2.00E-24	Dechloromonas aromatica RCB	hypothetical protein Daro03000355 [Dechloromonas aromatica RCB] COG0551: Zn-finger domain associated with topoisomerase type I			
25639, 25640	52853389	66	1.00E-103	Psychrobacter sp. 273-4	[Psychrobacter sp. 273-4]			
25641, 25642	32475496	42	2.00E-32	Rhodopirellula baltica SH 1	chloromuconate cycloisomerase YkfB1 [Rhodopirellula baltica SH 1] emb CAD75867.1 chloromuconate cycloisomerase YkfB1 [Pirellula sp.]			5.5.-.-
25643, 25644	48854032	53	4.00E-22	Cytophaga hutchinsonii	COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii] COG1778: Low specificity phosphatase (HAD superfamily) [Cytophaga hutchinsonii]			
25645, 25646	48856974	54	6.00E-46	Cytophaga hutchinsonii	hypothetical protein MS129 [Microscilla sp. PRE1] gb AAK62851.1 MS129, hypothetical protein [Microscilla sp. PRE1]			3.1.3.29
25649, 25650	14518334	37	4.00E-21	Microscilla sp. PRE1	hydroxymethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase [Porphyromonas gingivalis W83] ref NP_906169.1 hydroxymethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase [Porphyromonas gingivalis W83]			
25655, 25656	34398008	29	7.00E-17	Porphyromonas gingivalis W83	COG0352: Thiamine monophosphate synthase [Cytophaga hutchinsonii]			2.5.1.3
25657, 25658	48855690	49	1.00E-32	Cytophaga hutchinsonii				

25659, 25660	48855689	38	2.00E-13	Cytophaga hutchinsonii	COG0351: Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase [Cytophaga hutchinsonii]		
25661,				Bacteroides			
25662	37962667	52	3.00E-58	uniformis	Tn10-like transposase [Bacteroides uniformis]		
25665,							
25666	37927544	47	3.00E-14	Escherichia coli	unknown [Escherichia coli]		
25667,				Zymomonas	conserved hypothetical protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_162420.1 hypothetical protein ZMO0685 [Zymomonas mobilis subsp. mobilis ZM4]		
25668	56543155	33	1.00E-14	mobilis subsp. mobilis ZM4			
25669,				Cytophaga			
25670	48856049	51	2.00E-45	hutchinsonii	hypothetical protein Chut02001282 [Cytophaga hutchinsonii]		
2567,				Cytophaga	COG3021: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]		
2568	48853539	40	5.00E-23	hutchinsonii			
				Vibrio			
25673,				parahaemolyticus	hypothetical protein VPA1269 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC62612.1 hypothetical protein [Vibrio parahaemolyticus]		
25674	28901124	45	3.00E-48	RIMD 2210633	probable oxidoreductase [Rhodopirellula baltica SH 1] emb CAD75862.1		1.3.3.4
25677,				Rhodopirellula			
25678	32475491	43	1.00E-47	baltica SH 1	probable oxidoreductase [Pirellula sp.]		
25679,				Cytophaga	COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases [Cytophaga hutchinsonii]		6.2.1.1
25680	48856843	57	9.00E-71	hutchinsonii			
25681,				Cytophaga			
25682	48854812	42	1.00E-19	hutchinsonii	COG1522: Transcriptional regulators [Cytophaga hutchinsonii]		
					related to isochorismate synthase (MenF) [Desulfotalea psychrophila LSV54] emb CAG34983.1 related to isochorismate synthase (MenF) [Desulfotalea psychrophila LSV54]		5.4.99.6
25683,				Desulfotalea			
25684	51244106	43	3.00E-22	psychrophila LSV54	2-oxoglutarate decarboxylase and 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Bacteroides thetaiotaomicron VPI-5482] gbl AAO79806.1 2-oxoglutarate decarboxylase and 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase [Bacteroides thetaiotaomicron VPI-5482]		
25685,				Bacteroides			
25686	29350109	34	7.00E-11	thetaiotaomicron VPI-5482			
25687,				Cytophaga	COG0436: Aspartate/tyrosine/aromatic aminotransferase [Cytophaga hutchinsonii]		2.6.1.17
25688	48856186	49	3.00E-67	hutchinsonii			
				Ralstonia			
25689,				solanacearum	hypothetical protein RS03686 [Ralstonia solanacearum GMI1000] emb CAD17429.1 HYPOTHETICAL PROTEIN [Ralstonia solanacearum]		
25690	17548499	46	1.00E-13	GMI1000			
2569,				Lactobacillus			
2570	23003059	33	1.00E-23	gasserii	COG0266: Formamidopyrimidine-DNA glycosylase [Lactobacillus gasserii] putative Ni,Fe-hydrogenase I cytochrome b subunit [Bdellovibrio bacteriovorus HD100] emb CAE79300.1 putative Ni,Fe-hydrogenase I cytochrome b subunit [Bdellovibrio bacteriovorus HD100]		3.2.2.23
25691,				Bdellovibrio			
25692	42522927	28	6.00E-10	HD100			

25693, 25694	53715357	26	6.00E-18	Bacteroides fragilis YCH46	hypothetical protein BF4073 [Bacteroides fragilis YCH46] dbj BAD50815.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
25695, 25696	53764561	28	4.00E-23	Anabaena variabilis ATCC 29413	COG2021: Homoserine acetyltransferase [Anabaena variabilis ATCC 29413]				2.3.1.31
25697, 25698	53797271	27	3.00E-16	Chloroflexus aurantiacus	COG0249: Mismatch repair ATPase (MutS family) [Chloroflexus aurantiacus]				
25701, 25702	48854285	39	1.00E-46	Cytophaga hutchinsonii	COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
25703, 25704	15610037	42	7.00E-47	Mycobacterium tuberculosis H37Rv	POSSIBLE FORMATE DEHYDROGENASE H FDHF (FORMATE-HYDROGEN-LYASE-LINKED, SELENOCYSTEINE-CONTAINING POLYPEPTIDE) (FORMATE DEHYDROGENASE-H ALPHA SUBUNIT) (FDH-H) [Mycobacterium tuberculosis H37Rv] ref NP_856569.1 POSSIBLE FORMATE DEHYDROGENASE H FDHF (FORMATE-HYDROGEN-LYASE-LINKED, SELENOCYSTEINE-CONTAINING POLYPEPTIDE) (FORMATE DEHYDROGENASE-H ALPHA SUBUNIT) (FDH-H) [Mycobacterium bovis AF2122/97] ref NP_337480.1 formate dehydrogenase, alpha subunit, putative [Mycobacterium tuberculosis CDC1551] gb AAK47294.1 formate dehydrogenase, alpha subunit, putative [Mycobacterium tuberculosis CDC1551] sp P65409 YT24_MYCBO Hypothetical protein Mb2924c sp P65408 YT00_MYCTU Hypothetical protein Rv2900c/MT2968 pir G70926 probable fdhF protein - Mycobacterium tuberculosis (strain H37Rv) emb CAA98338.1 POSSIBLE FORMATE DEHYDROGENASE H FDHF (FORMATE-HYDROGEN-LYASE-LINKED, SELENOCYSTEINE-CONTAINING POLYPEPTIDE) (FORMATE DEHYDROGENASE-H ALPHA SUBUNIT) (FDH-H) [Mycobacterium tuberculosis H37Rv] emb CAD96611.1 POSSIBLE FORMATE DEHYDROGENASE H FDHF (FORMATE-HYDROGEN-LYASE-LINKED, SELENOCYSTEINE-CONTAINING POLYPEP			1.2.1.2	
25709, 25710	37521791	33	2.00E-11	Gloeobacter violaceus PCC 7421	L-2,4-diaminobutyrate decarboxylase [Gloeobacter violaceus PCC 7421] dbj BAC90163.1 L-2,4-diaminobutyrate decarboxylase [Gloeobacter violaceus PCC 7421]				4.1.1.-
2571, 2572	17547014	26	7.00E-16	Ralstonia solanacearum GMI1000	HYPOTHETICAL SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum GMI1000] emb CAD16002.1 HYPOTHETICAL SIGNAL PEPTIDE PROTEIN [Ralstonia solanacearum]				
25713, 25714	AAG9091 0	47	2.00E-10		Desc:C glutamicum protein fragment SEQ ID NO: 4664. Org:Corynebacterium glutamicum				
25715, 25716	28210167	56	3.00E-36	Clostridium tetani E88	hypothetical protein CTC00414 [Clostridium tetani E88] gb AAO35048.1 conserved protein [Clostridium tetani E88]				

25719, 25720	24375159	50	8.00E-64	Shewanella oneidensis MR-1	sigma-54 dependent transcriptional regulator/sensory box protein [Shewanella oneidensis MR-1] gb AAN56646.1 sigma-54 dependent transcriptional regulator/sensory box protein [Shewanella oneidensis MR-1]				
25723, 25724	29347290	36	1.00E-15	Bacteroides thetaiotaomicron VPI-5482	tetraacyldisaccharide 4'-kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76987.1 tetraacyldisaccharide 4'-kinase [Bacteroides thetaiotaomicron VPI-5482]				2.7.1.13 0
25725, 25726	53759291	42	3.00E-19	Methylobacillus flagellatus KT	COG2895: GTPases - Sulfate adenylylate transferase subunit 1 [Methylobacillus flagellatus KT]				2.7.7.4
25731, 25732	21244950	36	4.00E-10	Xanthomonas axonopodis pv. citri str. 306	bleomycin resistance protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM390088.1 bleomycin resistance protein [Xanthomonas axonopodis pv. citri str. 306]				
25733, 25734	48853549	55	5.00E-27	Cytophaga hutchinsonii	COG0277: FAD/FMN-containing dehydrogenases [Cytophaga hutchinsonii] hypothetical protein BT4201 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79306.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				1.1.3.15
25737, 25738	29349609	30	4.00E-07	Bacteroides thetaiotaomicron VPI-5482	D-amino acid dehydrogenase [Bdellovibrio bacteriovorus HD100] emb CAE77978.1 D-amino acid dehydrogenase [Bdellovibrio bacteriovorus HD100]				1.4.99.1
25741, 25742	42521944	38	5.00E-25	Bdellovibrio bacteriovorus HD100	dGTP triphosphohydrolase [Bacteroides fragilis YCH46] dbj BAD47072.1 dGTP triphosphohydrolase [Bacteroides fragilis YCH46] COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]				3.1.5.1
25743, 25744	53711614	32	2.00E-10	Bacteroides fragilis YCH46	histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				2.7.3.-
25745, 25746	48855448	27	9.00E-17	Cytophaga hutchinsonii	COG0564: Pseudouridylyl synthases, 23S RNA-specific [Cytophaga hutchinsonii]				4.2.1.70
25749, 25750	45657883	60	5.00E-32	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	hypothetical protein BF3706 [Bacteroides fragilis YCH46] dbj BAD50449.1 conserved hypothetical protein [Bacteroides fragilis YCH46] conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_906110.1 hypothetical protein PG2044 [Porphyromonas gingivalis W83]				
2575, 2576	48854010	49	2.00E-42	Cytophaga hutchinsonii	COG0615: Cytidylyltransferase [Pediococcus pentosaceus ATCC 25745]				2.7.7.39
25751, 25752	53714991	57	4.00E-48	Bacteroides fragilis YCH46					
25757, 25758	34397949	51	1.00E-41	Porphyromonas gingivalis W83					
25759, 25760	48869829	30	3.00E-07	Pediococcus pentosaceus ATCC 25745					

25761,	52853382	78	6.00E-31	Psychrobacter sp. 273-4	hypothetical protein Psc03002036 [Psychrobacter sp. 273-4]				
25762									
25763,				Cytophaga hutchinsonii					
25764	48854536	51	2.00E-65		COG0167: Dihydroorotate dehydrogenase [Cytophaga hutchinsonii]				1.3.3.1
				Bacteroides fragilis YCH46	tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]				
25765,					dbj BAD47405.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]				
25766	53711947	33	6.00E-07						
25767,				Rhodopirellula baltica SH 1	hypothetical protein RB11227 [Rhodopirellula baltica SH 1]				
25768	32476862	48	1.00E-10		emb CAD78999.1 conserved hypothetical protein [Pirellula sp.]				3.1.2.6
					putative restriction modification enzyme S subunit [Escherichia coli O157:H7] ref NP_290962.1 putative restriction modification enzyme S subunit [Escherichia coli O157:H7 EDL933] ref NP_313333.1 type I restriction-modification enzyme S subunit [Escherichia coli O157:H7] dbj BAB38729.1 type I restriction-modification enzyme S subunit [Escherichia coli O157:H7] pir E86133 hypothetical protein Z5946 [imported] - Escherichia coli (strain O157:H7, substrain EDL933) pir B91292 hypothetical protein ECs5306 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) unnamed protein product [Kluyveromyces fragilis] emb CAH02391.1 unnamed protein product [Kluyveromyces fragilis NRRL Y-1140]				
25769,	12519366	68	3.00E-77	Escherichia coli O157:H7		Photobacterium profundum SS9; segment 6/12	88	8.00E-15	3.1.21.3
25770,									
25775,	50304097	31	7.00E-10	Kluyveromyces fragilis					
25776				uncultured archaeon					
25777,					two-component sensor histidine kinase [uncultured archaeon GZfos26B2]				2.7.3.-
25778	52549170	42	2.00E-30	GZfos26B2	conserved hypothetical protein [Porphyromonas gingivalis W83]				
					ref NP_904796.1 hypothetical protein PG0501 [Porphyromonas gingivalis W83]				
25781,				Porphyromonas gingivalis W83					
25782	34396629	37	2.00E-32						
				Bacteroides thetaiotaomicron VPI-5482	putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]				
25789,					gb AAO79669.1 putative glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.4.1.83
25780	29349972	65	1.00E-89	VPI-5482					
					putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD47806.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46]				
25791,				Bacteroides fragilis YCH46					
25792	53712348	33	7.00E-10		COG4704: Uncharacterized protein conserved in bacteria [Geobacter metallireducens GS-15]				
				Geobacter metallireducens GS-15					
25793,									
25794	48847033	32	4.00E-17						
25795,				Bacteroides thetaiotaomicron VPI-5482	two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO76183.1 two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-
25796	29346486	48	2.00E-29	VPI-5482					

25797, 25798	29345596	39	9.00E-17	Bacteroides thetataotomicron VPI-5482	thiol:disulfide interchange protein dsbD precursor [Bacteroides thetataotomicron VPI-5482] gb AAO75293.1 thiol:disulfide interchange protein dsbD precursor [Bacteroides thetataotomicron VPI-5482]			
25799, 25800	56459804	35	4.00E-21	Idiomarina loihlensis L2TR	Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihlensis L2TR] gb AAV81536.1 Secreted protein containing N-terminal Zinc-dependent carboxypeptidase related domain [Idiomarina loihlensis L2TR]			
25801, 25802	56460815	58	4.00E-25	Idiomarina loihlensis L2TR	Anti-anti-sigma regulatory factor [Idiomarina loihlensis L2TR] gb AAV82547.1 Anti-anti-sigma regulatory factor [Idiomarina loihlensis L2TR]	Idiomarina loihlensis L2TR, complete genome	88	1.00E-06
25803, 25804	53712688	25	9.00E-09	Bacteroides fragilis YCH46	hypothetical protein BF1395 [Bacteroides fragilis YCH46] dbj BAD48146.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
25805, 25806	48854662	30	4.00E-16	Cytophaga hutchinsonii	COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Cytophaga hutchinsonii]			
25809, 25810	50084459	34	4.00E-14	Acinetobacter sp. ADP1	hypothetical protein ACIAD1273 [Acinetobacter sp. ADP1] emb CAG68147.1 conserved hypothetical protein [Acinetobacter sp. ADP1]			
2581, 2582	48838849	72	1.00E-103	Methanosarcina barkeri str. fusaro	COG4742: Predicted transcriptional regulator [Methanosarcina barkeri str. fusaro]	Methanosarcina acetivorans str. C2A, section 22 of 534 of the complete genome	81	3.00E-27
25813, 25814	53712512	33	1.00E-26	Bacteroides fragilis YCH46	Iron(III) ABC transporter periplasmic iron-binding protein [Bacteroides fragilis YCH46] dbj BAD47970.1 Iron(III) ABC transporter periplasmic iron-binding protein [Bacteroides fragilis YCH46]			
25817, 25818	17229380	26	7.00E-12	Nostoc sp. PCC 7120	hypothetical protein all1888 [Nostoc sp. PCC 7120] pir AB2042 hypothetical protein all1888 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB73587.1 all1888 [Nostoc sp. PCC 7120]			
25819, 25820	54294157	36	3.00E-13	Legionella pneumophila str. Lens	hypothetical protein lpi1221 [Legionella pneumophila str. Lens] emb CAH15460.1 hypothetical protein [Legionella pneumophila str. Lens]			
25821, 25822	48855642	36	4.00E-12	Cytophaga hutchinsonii	COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii] putative nitrogen utilization substance protein [Bacteroides thetataotomicron VPI-5482] gb AAO79696.1 putative nitrogen utilization substance protein [Bacteroides thetataotomicron VPI-5482]			
25823, 25824	29349999	41	2.00E-41	Bacteroides thetataotomicron VPI-5482	transcriptional regulator, AraC/XylS family [Bacillus clausii KSM-K16] dbj BAD62945.1 transcriptional regulator, AraC/XylS family [Bacillus clausii KSM-K16]			
25825, 25826	56962183	27	2.00E-12	Bacillus clausii KSM-K16				

25829,	48853435	67	3.00E-60	Cytophaga hutchinsonii	COG1088: dTDP-D-glucose 4,6-dehydratase [Cytophaga hutchinsonii]			4.2.1.46
25830				Methylobacillus	COG2010: Cytochrome c, mono- and diheme variants [Methylobacillus flagellatus KT]			1.7.99.3
2583,	53759377	34	7.00E-14	flagellatus KT				
2584				Thiobacillus denitrificans ATCC 25259	COG0189: Glutathione synthase/Ribosomal protein S6 modification enzyme (glutaminyl transferase) [Thiobacillus denitrificans ATCC 25259]			
25835,				Legionella pneumophila subsp.	ribosomal protein S6 modification protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_122785.1 hypothetical protein lpp0446 [Legionella pneumophila str. Paris] gb AAU26476.1 ribosomal protein S6 modification protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH11594.1 hypothetical protein [Legionella pneumophila str. Paris]			
25836	52840624	36	2.00E-11	Philadelphia 1	hypothetical protein, predicted Glutamate--cysteine ligase [Azoarcus sp. Ebn1] emb CAI10097.1 hypothetical protein, predicted Glutamate--cysteine ligase [Azoarcus sp. Ebn1]			
25839,	56479409	48	4.00E-64	Azoarcus sp. Ebn1	putative nucleoside-diphosphate sugar epimerases/dehydratase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75705.1 putative nucleoside-diphosphate sugar epimerases/dehydratase [Bacteroides thetaiotaomicron VPI-5482]	Clostridium tetani E88, section 8 of 10 of the complete genome	84	4.00E-17
25841,				Bacteroides thetaiotaomicron	hypothetical protein Chut02003040 [Cytophaga hutchinsonii]			
25842	29346008	60	2.00E-74	VPI-5482	COG0212: 5-formyltetrahydrofolate cyclo-ligase [Cytophaga hutchinsonii]			6.3.3.2
25843,	48854367	58	2.00E-69	Cytophaga hutchinsonii	COG1459: Type II secretory pathway, component PulF [Cytophaga hutchinsonii]			
25844				Cytophaga hutchinsonii	COG1217: Predicted membrane GTPase involved in stress response [Cytophaga hutchinsonii]			
25845,	48856113	33	1.00E-20	Cytophaga hutchinsonii	COG1408: Predicted phosphohydrolases [Cytophaga hutchinsonii]			
25846				Cytophaga hutchinsonii	hypothetical protein EF0112 [Enterococcus faecalis V583] gb AAO79987.1 conserved domain protein [Enterococcus faecalis V583]			
25849,	48855359	38	2.00E-32	Cytophaga hutchinsonii	hypothetical protein Chut02002154 [Cytophaga hutchinsonii]			
25850				Cytophaga hutchinsonii	putative sun protein [Bdellovibrio bacteriovorus HD100] emb CAE79023.1 putative sun protein [Bdellovibrio bacteriovorus HD100]			2.1.1.-
2585,	48854524	62	2.00E-80	Cytophaga hutchinsonii	COG2374: Predicted extracellular nuclease [Exiguobacterium sp. 255-15]			
2586,				Cytophaga hutchinsonii				
25851,	48856245	53	6.00E-60	Cytophaga hutchinsonii				
25852				Enterococcus faecalis V583				
25855,	29374763	29	8.00E-10	faecalis V583				
25856				Cytophaga hutchinsonii				
25859,	48855090	34	1.00E-27	Cytophaga hutchinsonii				
25860				Bdellovibrio bacteriovorus HD100				
25861,				Bdellovibrio bacteriovorus HD100				
25862	42522650	53	6.00E-43	HD100				
25863,				Exiguobacterium				
25864	46113550	36	5.00E-07	sp. 255-15				

25865, 25866	11279060	44	1.00E-35	Imported	cell wall lipoprotein ewlA [imported] - Erysipelothrix rhusiopathiae gb AAB01156.1 EwIA			
2587, 2588	42523429	72	2.00E-94	Bdellovibrio bacteriovorus HD100	hypothetical protein Bd1952 [Bdellovibrio bacteriovorus HD100] emb CAE79802.1 mp [Bdellovibrio bacteriovorus HD100]			6.3.2.-
25871, 25872	51598164	67	6.00E-87	Yersinia pseudotuberculosis IP 32953	possible type I restriction enzyme (restriction subunit) [Yersinia pseudotuberculosis IP 32953] emb CAH23117.1 possible type I restriction enzyme (restriction subunit) [Yersinia pseudotuberculosis IP 32953]			3.1.21.3
25873, 25874	29348700	29	1.00E-21	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3291 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78397.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482]			
25875, 25876	48855613	34	4.00E-14	Cytophaga hutchinsonii	COG0308: Aminopeptidase N [Cytophaga hutchinsonii]			
25877, 25878	48853831	50	8.00E-68	Cytophaga hutchinsonii	COG0527: Aspartokinases [Cytophaga hutchinsonii]			2.7.2.4
25881, 25882	48855337	51	4.00E-64	Cytophaga hutchinsonii	COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii]			
25883, 25884	31195677	61	2.00E-82	Anopheles gambiae	ENSANGP00000000375 [Anopheles gambiae]			6.1.1.18
25887, 25888	21231990	61	4.00E-58	Xanthomonas campestris pv. campestris str. ATCC 33913	hypothetical protein XCC2559 [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM41831.1 conserved hypothetical protein [Xanthomonas campestris pv. campestris str. ATCC 33913]			3.6.1.13
2589, 2590	28375463	36	5.00E-55	Cytophaga hutchinsonii	SMC protein [Cytophaga hutchinsonii] ref ZP_00308092.1 COG1196: Chromosome segregation ATPases [Cytophaga hutchinsonii]			
25891, 25892	29345486	50	1.00E-57	Bacteroides thetaiotaomicron VPI-5482	transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75183.1 transposase [Bacteroides thetaiotaomicron VPI-5482]			
25893, 25894	48854473	45	3.00E-40	Cytophaga hutchinsonii	COG1648: Siroheme synthase (precorrin-2 oxidase/ferrochelatase domain) [Cytophaga hutchinsonii]			2.1.1.10 7
25899, 25900	48856102	38	4.00E-18	Cytophaga hutchinsonii	COG2353: Uncharacterized conserved protein [Cytophaga hutchinsonii]			
259, 260	32474367	53	2.00E-32	Rhodopirellula baltica SH 1	probable secreted glycosyl hydrolase [Rhodopirellula baltica SH 1] emb CAD74907.1 probable secreted glycosyl hydrolase [Pirellula sp.]			
25901, 25902	57236797	47	2.00E-34	Flavobacterium johnsoniae	SprA [Flavobacterium johnsoniae]			
25903, 25904	31790365	35	2.00E-33	uncultured Acidobacteria bacterium	hypothetical protein [uncultured Acidobacteria bacterium]			

2591,	29349999	25	5.00E-16	Bacteroides thetaiotaomicron	putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79696.1 putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482]			
2592	AAB1851							
25911,	5	41	1.00E-36		Desc:Amino acid sequence of prolyl-tripeptidyl peptidase DPP.			3.4.14.5
25912					Org:Porphyromonas gingivalis			
25913,	55819125	33	4.00E-07	Mimivirus	HNH endonuclease [Mimivirus] gb AAV50519.1 HNH endonuclease			
25914					[Mimivirus]			
25917,					tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]			
25918	53712631	33	7.00E-37	Bacteroides fragilis YCH46	dbj BAD48089.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]			
25919,					COG0286: Type I restriction-modification system methyltransferase subunit			
25920	46320397	32	1.00E-14	Burkholderia cepacia R1808	[Burkholderia cepacia R1808]			
25921,					tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]			
25922	53712631	42	6.00E-52	Bacteroides fragilis YCH46	dbj BAD48089.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]			
25923,								2.4.1.15
25924	48854183	52	4.00E-28	Cytophaga hutchinsonii	COG0438: Glycosyltransferase [Cytophaga hutchinsonii]			1
25927,					COG4277: Predicted DNA-binding protein with the Helix-hairpin-helix motif			
25928	48855675	86	1.00E-84	Cytophaga hutchinsonii	[Cytophaga hutchinsonii]		94	7.00E-12
25929,								
25930	41690267	77	9.00E-29	Psychrobacter sp. 273-4	hypothetical protein Psyc03000442 [Psychrobacter.sp. 273-4]			
2593,					preprotein translocase, YajC subunit [Porphyromonas gingivalis W83]			
25931,	34396613	34	2.00E-13	Porphyromonas gingivalis W83	ref NP_904780.1 preprotein translocase, YajC subunit [Porphyromonas gingivalis W83]			
25932	24374604	32	8.00E-30	Shewanella oneidensis MR-1	sensory box protein [Shewanella oneidensis MR-1] gb AAN56091.1 sensory box protein [Shewanella oneidensis MR-1]			2.7.3.-
25933,					helicase [Shewanella oneidensis MR-1] gb AAN53453.1 helicase			
25934	24371966	48	2.00E-38	Shewanella oneidensis MR-1	[Shewanella oneidensis MR-1]			
25935,					Amidohydrolase family enzyme [Idiomarina loihiensis L2TR] gb AAV82933.1			
25936	56461201	63	2.00E-87	Idiomarina loihiensis L2TR	Amidohydrolase family enzyme [Idiomarina loihiensis L2TR]			
25937,					COG1262: Uncharacterized conserved protein [Azotobacter vinelandii]			
25938	53610376	50	6.00E-36	Azotobacter vinelandii				
25939,								
25940	48854843	42	8.00E-49	Cytophaga hutchinsonii	COG0196: FAD synthase [Cytophaga hutchinsonii]			2.7.1.26
25941,								
25942	48854067	30	1.00E-12	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-

25943, 25944	29346245	70	6.00E-55	Bacteroides thetaiotaomicron VPI-5482	tRNA-guanine transglycosylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75942.1 tRNA-guanine transglycosylase [Bacteroides thetaiotaomicron VPI-5482]	Bacteroides thetaiotaomicron VPI-5482, section 4 of 21 of the complete genome	91	1.00E-09	2.4.2.29
25945, 25946	53711597	53	2.00E-55	Bacteroides fragilis YCH46	UDP-N-acetylglucosamine-N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Bacteroides fragilis YCH46] dbj BAD47055.1 UDP-N-acetylglucosamine-N- acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N- acetylglucosamine transferase [Bacteroides fragilis YCH46]			2.4.1.-	
25947, 25948	22652003	43	2.00E-15	Synechococcus sp. PCC 7002	hypothetical protein [Synechococcus sp. PCC 7002]				
25949, 25950	28898510	63	2.00E-68	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VP1736 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC59999.1 conserved hypothetical protein [Vibrio parahaemolyticus] hypothetical cell division control protein [Sulfolobus tokodaii str. 7] dbj BAB67696.1 700aa long hypothetical cell division control protein [Sulfolobus tokodaii str. 7]			3.1.6.-	
25951, 25952	15922918	36	4.00E-26	Sulfolobus tokodaii str. 7		Photobacterium profundum SS9 chromosome 2; segment 3/7	83	2.00E-16	2.7.1.-
25953, 25954	54302486	70	1.00E-102	Photobacterium profundum SS9	hypothetical maturase [Photobacterium profundum SS9] emb CAG22679.1 hypothetical maturase [Photobacterium profundum] type I site-specific deoxyribonuclease [Methanosarcina acetivorans C2A] gb AAM05520.1 type I site-specific deoxyribonuclease [Methanosarcina acetivorans str. C2A]				3.1.21.3
25955, 25956	20090965	61	9.00E-32	Methanosarcina acetivorans C2A					3.1.21.3
25957, 25958	9789464	41	1.00E-19	Lactococcus lactis subsp. lactis	HsdS [Lactococcus lactis subsp. lactis] ref NP_862616.1 HsdS [Lactococcus lactis subsp. lactis] gb AAF69139.1 HsdS [Lactococcus lactis] type I site-specific deoxyribonuclease [Methanosarcina acetivorans C2A] gb AAM05518.1 type I site-specific deoxyribonuclease [Methanosarcina acetivorans str. C2A]				3.1.21.3
25959, 25960	20090963	56	2.00E-25	Methanosarcina acetivorans C2A					3.1.21.3
25967, 25968	53713424	28	7.00E-11	Bacteroides fragilis YCH46	ATP-dependent helicase [Bacteroides fragilis YCH46] dbj BAD48882.1 ATP- dependent helicase [Bacteroides fragilis YCH46] tyrosine type site-specific recombinase [Bacteroides fragilis YCH46] dbj BAD48089.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]				
25969, 25970	53712631	37	6.00E-30	Bacteroides fragilis YCH46					

2597, 2598	13508374	32	6.00E-09	Mycoplasma pneumoniae M129	hypothetical protein MPN635 [Mycoplasma pneumoniae M129] gb AA895855.1 conserved hypothetical protein [Mycoplasma pneumoniae M129] pir S73533 hypothetical protein E30_orf352 - Mycoplasma pneumoniae (strain ATCC 29342) sp P75162 YG35_MYCPN Hypothetical protein MPN635 (E30_orf352)				
25971, 25972	53713920	49	2.00E-55	Bacteroides fragilis YCH46	putative ABC transporter ATP-binding protein or permease protein [Bacteroides fragilis YCH46] dbj BAD49378.1 putative ABC transporter ATP-binding protein or permease protein [Bacteroides fragilis YCH46]				
25973, 25974	29348441	32	4.00E-36	Bacteroides thetaiotaomicron VPI-5482	conserved hypothetical protein, with a weak acyltransferase domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO78138.1 conserved hypothetical protein, with a weak acyltransferase domain [Bacteroides thetaiotaomicron VPI-5482]				
25977, 25978	29345890	56	4.00E-39	Bacteroides thetaiotaomicron VPI-5482	glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75587.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.---
25983, 25984	48853718	45	5.00E-66	Cytophaga hutchinsonii	COG2120: Uncharacterized proteins, LmbE homologs [Cytophaga hutchinsonii]				
25985, 25986	38174845	36	3.00E-09	Melittangium lichenicola	hypothetical protein [Melittangium lichenicola]				
25987, 25988	53757541	52	1.00E-43	Methylococcus capsulatus str. Bath	type I restriction-modification system, R subunit [Methylococcus capsulatus str. Bath] ref YP_114328.1 type I restriction-modification system, R subunit [Methylococcus capsulatus str. Bath]				3.1.21.3
25989, 25990	34396756	56	3.00E-26	Porphyromonas gingivalis W83	(thiamine monophosphate kinase [Porphyromonas gingivalis W83] ref NP_904922.1 thiamine monophosphate kinase [Porphyromonas gingivalis W83])				2.7.4.16
2599, 2600	53795689	28	1.00E-17	Chloroflexus aurantiacus	COG1205: Distinct helicase family with a unique C-terminal domain including a metal-binding cysteine cluster [Chloroflexus aurantiacus]				
25991, 25992	42630866	35	4.00E-18	Haemophilus influenzae R2866	COG0457: FOG: TPR repeat [Haemophilus influenzae R2866]				
25993, 25994	4184091	23	5.00E-12	Bacteroides fragilis	BfmB [Bacteroides fragilis]				
25995, 25996	34397651	69	8.00E-70	Porphyromonas gingivalis W83	DNA gyrase, B subunit [Porphyromonas gingivalis W83] ref NP_905814.1 DNA gyrase, B subunit [Porphyromonas gingivalis W83]				
25997, 25998	29349537	35	1.00E-08	Bacteroides thetaiotaomicron VPI-5482	outer membrane assembly protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79234.1 outer membrane assembly protein [Bacteroides thetaiotaomicron VPI-5482]			82 2.00E-36 5.99.1.3	

26001,	48855613	36	7.00E-24	Cytophaga hutchinsonii	COG0308: Aminopeptidase N [Cytophaga hutchinsonii]			
26002								
26005,	48855423	28	3.00E-16	Cytophaga hutchinsonii	COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii]			
26006								
26007,								
26008	48855521	26	4.00E-13	Cytophaga hutchinsonii	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii]			
26009,	48861416	71	2.00E-60	Microbulbifer degradans 2-40	COG0177: Predicted EndoIII-related endonuclease [Microbulbifer degradans 2-40]			4.2.99.18
26010								
26011,								
26012	56460382	54	9.00E-61	Idiomarina loihiensis L2TR	Carboxyl-terminal protease, periplasmic [Idiomarina loihiensis L2TR]			3.4.21.-
26017,								
26018	46316058	49	2.00E-32	Burkholderia cepacia R18194	COG3265: Glucanase [Burkholderia cepacia R18194]			2.7.1.12
26019,								
26020	29347800	56	2.00E-65	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT2390 [Bacteroides thetaiotaomicron VPI-5482]			
26021,								
26022	53713020	45	5.00E-32	Bacteroides fragilis YCH46	glb/AAO77497.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
26023,								
26024	48854977	60	1.00E-60	Cytophaga hutchinsonii	siolate O-acetyltransferase [Bacteroides fragilis YCH46]			3.1.1.47
26029,								
26030	19703530	43	2.00E-30	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	siolate O-acetyltransferase [Bacteroides fragilis YCH46]			1.7.99.5
26031,								
26032	57159854	27	1.00E-08	Thermococcus kodakaraensis	COG0685: 5,10-methylenetetrahydrofolate reductase [Cytophaga hutchinsonii]			
26033,								
26034	15669403	28	8.00E-13	Methanocaldococcus jannaschii DSM 2661	hypothetical protein FN0185 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]			
26035,								
26036	48730332	34	1.00E-14	Pseudomonas fluorescens PfO-1	predicted ATP-dependent endonuclease, OLD family [Thermococcus kodakaraensis] ref YP_183808.1 predicted ATP-dependent endonuclease, OLD family [Thermococcus kodakaraensis]			
26041,								
26042	29347623	26	4.00E-13	Bacteroides thetaiotaomicron VPI-5482	type I restriction-modification enzyme 1, S subunit [Methanocaldococcus jannaschii DSM 2661] gb AAB99219.1 type I restriction-modification enzyme 1, S subunit [Methanocaldococcus jannaschii DSM 2661] pir A64452 type I restriction-modification enzyme, S subunit homolog - Methanocaldococcus jannaschii sp Q58615 YC18 METJA Hypothetical protein MJ1218			3.1.21.3
26035,								
26036	48730332	34	1.00E-14	Pseudomonas fluorescens PfO-1	COG1368: Phosphoglycerol transferase and related proteins, alkaline phosphatase superfamily [Pseudomonas fluorescens PfO-1]			
26041,								
26042	29347623	26	4.00E-13	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT2213 [Bacteroides thetaiotaomicron VPI-5482]			

26043,	45857883	37	9.00E-48	Leptospira interrogans serovar Copenhageni str.	histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAST0606.1 histidine kinase sensor protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			2.7.3.-
26044				Flocruz L1-130	hypothetical protein BT0761 [Bacteroides thetaiotaomicron VPI-5482]			
26045,				Bacteroides thetaitotaomicron	gb AAO75868.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
26046	29346171	29	4.00E-28	VPI-5482	hypothetical protein BF2022 [Bacteroides fragilis YCH46] dbj BAD48769.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			3.4.13.9
26051,	53713311	49	6.00E-44	Bacteroides fragilis YCH46	hypothetical protein BB0756 [Borrelia burgdorferi B31] gb AAC67104.1 B. burgdorferi predicted coding region BB0756 [Borrelia burgdorferi B31]			
26053,				Borrelia burgdorferi B31	pir C70194 hypothetical protein BB0756 - Lyme disease spirochete			
26054	15595101	25	1.00E-12		ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76349.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482]			
26055,	29346652	68	2.00E-72	Bacteroides thetaitotaomicron VPI-5482	conserved hypothetical protein [Silicibacter pomeroyi DSS-3] ref YP_168196.1 hypothetical protein SPO2990 [Silicibacter pomeroyi DSS-3]			
26057,				Silicibacter pomeroyi DSS-3	hypothetical protein RB9659 [Rhodopirellula baltica SH 1] emb CAD76391.1 conserved hypothetical protein [Pirellula sp.]			2.4.1.18 2
26058	56679562	32	3.00E-17	Rhodopirellula baltica SH 1	COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii]			
26059,	32476012	55	2.00E-36	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Pseudomonas syringae pv. syringae B728a]			
26063,	48855019	48	2.00E-65	Pseudomonas syringae pv. syringae B728a	putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD50166.1 putative glycosyltransferase [Bacteroides fragilis YCH46]			
26064	23472289	43	7.00E-20	Bacteroides fragilis YCH46	COG3385: FOG; Transposase and inactivated derivatives [Dechloromonas aromatica RCB]			
26067,				Dechloromonas aromatica RCB	possible peptidase [Rhodopseudomonas palustris CGA009]			
26068	53714708	32	5.00E-28	Rhodopseudomonas palustris CGA009	COG3265: Gluconate kinase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]			3.4.21.-
26071,	53730535	57	5.00E-36	Rhodopseudomonas palustris CGA009				
26072								
26077,								
26078	39934964	25	1.00E-08	Actinobacillus pleuropneumoniae serovar 1 str. 4074				2.7.1.12
26085,								
26086								
26087,								
26088	53728938	71	6.00E-35					

26089, 26090, 2609, 2610	15894619 48854018	37 62	5.00E-14 2.00E-85	Clostridium acetobutylicum ATCC 824 Cytophaga hutchinsonii	Transcriptional regulator of the LacI family [Clostridium acetobutylicum ATCC 824] gb AAK79308.1 Transcriptional regulator of the LacI family [Clostridium acetobutylicum ATCC 824] pir A97065 transcription regulator of the LacI family [Imported] - Clostridium acetobutylicum				
26091, 26092	51243929	54	2.00E-64	Desulfotalea psychrophila LSV54	COG0423: Glycyl-tRNA synthetase (class I) [Cytophaga hutchinsonii] hypothetical protein DP0077 [Desulfotalea psychrophila LSV54] emb CAG34806.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]				6.1.1.14
26093, 26094	29349716	47	5.00E-19	Bacteroides thetaiotaomicron VPI-5482	pantoate--beta-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79413.1 pantoate--beta-alanine ligase [Bacteroides thetaiotaomicron VPI-5482]				1.6.5.3
26095, 26096	15895943	49	2.00E-84	Clostridium acetobutylicum ATCC 824	Trehalose/maltose hydrolase (phosphorylase) [Clostridium acetobutylicum ATCC 824] gb AAK80632.1 Trehalose/maltose hydrolase (phosphorylase) [Clostridium acetobutylicum ATCC 824] pir E97230 trehalose/maltose hydrolase (phosphorylase) [Imported] - Clostridium acetobutylicum	Clostridium acetobutylicum ATCC 824 section 254 of 356 of the complete genome	86	5.00E-11	2.4.1.8
261, 262	28852364	66	2.00E-78	Pseudomonas syringae pv. tomato str. DC3000	aminotransferase, DegT/DnrJ/EryC1/StrS family [Pseudomonas syringae pv. tomato str. DC3000] ref NP_791743.1 aminotransferase, DegT/DnrJ/EryC1/StrS family [Pseudomonas syringae pv. tomato str. DC3000]				
26101, 26102	29346728	39	7.00E-28	Bacteroides thetaiotaomicron VPI-5482	signaling protein without kinase domain [Bacteroides thetaiotaomicron VPI- 5482] gb AAO76425.1 signaling protein without kinase domain [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-
26103, 26104	29349375	38	7.00E-19	Bacteroides thetaiotaomicron VPI-5482	putative two-component system sensor protein histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79072.1 putative two-component system sensor protein histidine kinase [Bacteroides thetaiotaomicron VPI- 5482]				
26109, 26110	53712202	56	2.00E-66	Bacteroides fragilis YCH46	orotidine 5'-phosphate decarboxylase [Bacteroides fragilis YCH46] dbj BAD47660.1 orotidine 5'-phosphate decarboxylase [Bacteroides fragilis YCH46]				4.1.1.23
2611, 2612	1208896	37	1.00E-31	Anaerocellum thermophilum	hypothetical protein [Anaerocellum thermophilum]				5.3.1.9
26111, 26112	48848828	70	2.00E-36	Novosphingobium aromaticivorans DSM 12444	COG5394: Uncharacterized protein conserved in bacteria [Novosphingobium aromaticivorans DSM 12444]				
26115, 26116	28898411	25	6.00E-12	Vibrio parahaemolyticus RIMD 2210633	putative GGDEF family protein [Vibrio parahaemolyticus RIMD 2210633] dbj BAC59900.1 putative GGDEF family protein [Vibrio parahaemolyticus]				4.6.1.2
26117, 26118	48853831	43	1.00E-54	Cytophaga hutchinsonii	COG0527: Aspartokinases [Cytophaga hutchinsonii]				2.7.2.4

26119, 26120	53714264	39	1.00E-33	Bacteroides fragilis YCH46	folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 folypolyglutamate synthase [Bacteroides fragilis YCH46]				6.3.2.17
26123, 26124	16124596	32	7.00E-19	Caulobacter crescentus CB15	hypothetical protein CO0341 [Caulobacter crescentus CB15]				
26125, 26126	34396714	37	3.00E-37	Porphyromonas gingivalis W83	glrA protein [Porphyromonas gingivalis W83] ref NP_904880.1 htrA protein [Porphyromonas gingivalis W83]				3.4.21.-
26127, 26128	38195402	42	2.00E-34	Flavobacterium johnsoniae	GldI [Flavobacterium johnsoniae]				5.2.1.8
26129, 26130	48854578	45	2.00E-61	Cytophaga hutchinsonii	COG0768: Cell division protein FtsI/penicillin-binding protein 2 [Cytophaga hutchinsonii]				2.3.2.-
2613, 2614	39997334	62	1.00E-122	Geobacter sulfurreducens PCA	GTP pyrophosphokinase [Geobacter sulfurreducens PCA] gb AAR35612.1 GTP pyrophosphokinase [Geobacter sulfurreducens PCA]				2.7.6.5
26133, 26134	5360188	38	6.00E-32	Flavobacterium johnsoniae	GldB [Flavobacterium johnsoniae]				
26135, 26136	3329480	40	7.00E-21	Trichinella pseudospiralis	unknown [Trichinella pseudospiralis]				
26137, 26138	48855182	33	2.00E-10	Cytophaga hutchinsonii	COG2911: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
26141, 26142	52853569	93	1.00E-100	Psychrobacter sp. 273-4	COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Psychrobacter sp. 273-4]				3.1.21.3
26145, 26146	56477485	35	2.00E-12	Azoarcus sp. EbN1	predicted ABC-type Fe3+-hydroxamate transport system, periplasmic component [Azoarcus sp. EbN1] emb CA08173.1 predicted ABC-type Fe3+-hydroxamate transport system, periplasmic component [Azoarcus sp. EbN1]				
26147, 26148	48854332	60	6.00E-42	Cytophaga hutchinsonii	COG0216: Protein chain release factor A [Cytophaga hutchinsonii]				
2615, 2616	48854899	55	2.00E-35	Cytophaga hutchinsonii	COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii]				2.1.1.-
26153, 26154	53711472	30	1.00E-15	Bacteroides fragilis YCH46	signal peptidase I [Bacteroides fragilis YCH46] dbj BAD46930.1 signal peptidase I [Bacteroides fragilis YCH46]				
26155, 26156	53712193	28	4.00E-15	Bacteroides fragilis YCH46	hypothetical protein BF0900 [Bacteroides fragilis YCH46] dbj BAD47651.1 hypothetical protein [Bacteroides fragilis YCH46]				2.7.3.-
26157, 26158	29349974	33	4.00E-23	Bacteroides thetaiotaomicron VPI-5482	two-component system response regulator protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79671.1 two-component system response regulator protein [Bacteroides thetaiotaomicron VPI-5482]				

26159,	48855208	39	4.00E-22	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]			
26160				Flavobacterium johnsoniae	gliding motility protein GldG [Flavobacterium johnsoniae]			
26161,	14531035	45	8.00E-22					
26162								
26163,				Psychrobacter sp.	COG3328: Transposase and inactivated derivatives [Psychrobacter sp. 273-4] ref ZP_00147021.1 COG3328: Transposase and inactivated derivatives [Psychrobacter sp. 273-4]	Desc:E. coli CFT073 genomic sequence #251.	86	6.00E-07
26164	41688937	92	1.00E-146	Shewanella oneidensis MR-1	hypothetical protein S00366 [Shewanella oneidensis MR-1] gb AA53451.1			
26165,					hypothetical protein [Shewanella oneidensis MR-1]			
26166	24371964	37	4.00E-26	Cytophaga hutchinsonii	COG1587: Uroporphyrinogen-III synthase [Cytophaga hutchinsonii]			
26167,	48855619	27	2.00E-07	Bacteroides fragilis YCH46	DNA primase [Bacteroides fragilis YCH46] dbj BAD50689.1 DNA primase [Bacteroides fragilis YCH46]			2.7.7.-
26168	53715231	36	4.00E-53	Cytophaga hutchinsonii	hypothetical protein Chut02003866 [Cytophaga hutchinsonii]			
2617,								
26177,	48853367	29	6.00E-09	Bacteroides thetaiotaomicron VPI-5482	ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482]	Desc:Streptococcus polynucleotide SEQ ID NO 4279.	90	5.00E-07
26181,								
26182	29349217	56	1.00E-58	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	type I restriction-modification system, M subunit [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]	Xanthomonas campestris pv. campestris str. ATCC 33913, section 312 of 460 of the complete genome	90	3.00E-15
26183,								2.1.1.72
26184	46580119	74	1.00E-114	Cytophaga hutchinsonii	COG3182: Uncharacterized iron-regulated membrane protein [Cytophaga hutchinsonii]			
26185,								
26186	48855705	37	7.00E-17	Cytophaga hutchinsonii	COG3182: Uncharacterized iron-regulated membrane protein [Cytophaga hutchinsonii]			1.8.1.2
26187,								
26188	48855705	45	3.00E-16	Bacteroides fragilis YCH46	hypothetical protein BF1415 [Bacteroides fragilis YCH46] dbj BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
26189,								
26190	53712708	35	3.00E-34	Cytophaga hutchinsonii	COG0210: Superfamily I DNA and RNA helicases [Cytophaga hutchinsonii]			
2619,								
2620	48855421	33	5.00E-17	Cytophaga hutchinsonii	COG0513: Superfamily II DNA and RNA helicases [Cytophaga hutchinsonii]			2.7.7.-
26191,								
26192	48855274	44	6.00E-46					

26193,	29348750	38	6.00E-24	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3341 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78447.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
26194				Trichinella	unknown [Trichinella pseudospiralis]				
26195,	3329480	31	2.00E-10	pseudospiralis	COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii]				
26196				Cytophaga hutchinsonii					
26201,	48855337	59	4.00E-44	Desulfovibrio	COG3004: Na ⁺ /H ⁺ antiporter [Desulfovibrio desulfuricans G20]				3.4.---
26202,	23473914	54	4.00E-42	desulfuricans G20					
26205,				Cytophaga hutchinsonii	hypothetical protein Chut02003091 [Cytophaga hutchinsonii]				
26206	48854003	42	5.00E-29	Cytophaga hutchinsonii					
26207,				Cytophaga hutchinsonii	hypothetical protein Chut02003091 [Cytophaga hutchinsonii]				
26208	48854003	27	6.00E-20	Cytophaga hutchinsonii	COG0685: 5,10-methylenetetrahydrofolate reductase [Cytophaga hutchinsonii]				1.5.1.20
26209,				Cytophaga hutchinsonii					
26210	48854003	27	6.00E-20	Cytophaga hutchinsonii	hypothetical protein BF3300 [Bacteroides fragilis YCH46] db BAD50044.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
26211,	48854977	58	6.00E-44	Bacteroides fragilis YCH46					
26212				Anopheles gambiae	ENSANGP00000000474 [Anopheles gambiae]				
26215,						Desc:Restriction enzyme AccIII gene.			
26216	53714586	39	2.00E-20	Bacteroides fragilis YCH46	excinuclease ABC subunit A [Bacteroides fragilis YCH46] db BAD50064.1 excinuclease ABC subunit A [Bacteroides fragilis YCH46]	Org:Acinetobacter calcoaceticus	97	5.00E-07	3.4.24.5 7
26217,	31195541	61	6.00E-30	Anopheles gambiae					
26218									
26219,				Bacteroides fragilis YCH46	CAMP factor [Riemerella anatipestifer]				
26220	53714606	64	2.00E-68	Riemerella anatipestifer	COG0123: Deacetylases, including yeast histone deacetylase and acetoin utilization protein [Cytophaga hutchinsonii]				
26221,	11692013	66	7.00E-63	Cytophaga hutchinsonii	beta 1,4 glucosyltransferase [Aquifex aeolicus VF5] gb AAC07593.1 beta 1,4 glucosyltransferase - Aquifex aeolicus				
26222	48855767	57	6.00E-37	Cytophaga hutchinsonii	small heat shock protein (hsp20-1) [Archaeoglobus fulgidus DSM 4304] gb AB89949.1 small heat shock protein (hsp20-1) [Archaeoglobus fulgidus DSM 4304] pir G69411 small heat shock protein (hsp20-1) homolog - Archaeoglobus fulgidus				2.---
26225,				Aquifex aeolicus VF5	putative translation factor [Bacteroides fragilis YCH46] db BAD50647.1 putative translation factor [Bacteroides fragilis YCH46]				
26226									
26229,	15606814	37	2.00E-21	Archaeoglobus fulgidus DSM 4304					
26230				Bacteroides fragilis YCH46					
2623,	11498894	48	1.00E-20	Crocospaera watsonii WH 8501	hypothetical protein Cwat03004451 [Crocospaera watsonii WH 8501]				
2624									
26231,	53715189	42	5.00E-24						
26232									
26233,	45525072	46	6.00E-43						
26234									

26235,	29348887	32	5.00E-23	Bacteroides thetaiotaomicron VPI-5482	integrase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78584.1 integrase [Bacteroides thetaiotaomicron VPI-5482]			
26236								
26243,	48855612	34	4.00E-36	Cytophaga hutchinsonii	COG0845: Membrane-fusion protein [Cytophaga hutchinsonii]			
26244,								
26245,	24375180	30	2.00E-10	Shewanella oneidensis MR-1	hypothetical protein SO3682 [Shewanella oneidensis MR-1] gb AAN56667.1 hypothetical protein [Shewanella oneidensis MR-1]			
26246								
26247,								
26248	15842808	23	1.00E-07	Thermotoga maritima MSB8	hypothetical protein TM0033 [Thermotoga maritima MSB8] gb AAD35127.1 hypothetical protein TM0033 [Thermotoga maritima MSB8] pir F72424			
26249,								
26250	42527168	33	2.00E-15	Treponema denticola ATCC 35405	hypothetical protein - Thermotoga maritima (strain MSB8) hypothetical protein TDE1661 [Treponema denticola ATCC 35405] gb AAS12177.1 conserved hypothetical protein [Treponema denticola ATCC 35405]			
2625,								
2626	21244775	38	1.00E-51	Xanthomonas axonopodis pv. citri str. 306	beta-xylosidase [Xanthomonas axonopodis pv. citri str. 306] gb AAM38893.1 beta-xylosidase [Xanthomonas axonopodis pv. citri str. 306]			3.2.1.37
26253,								
26254	33861696	36	2.00E-29	Prochlorococcus marinus subsp. pastoris str. CCMP1986	DNA polymerase I [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19599.1 DNA polymerase I [Prochlorococcus marinus subsp. pastoris str. CCMP1986]			2.7.7.7
26255,								
26256	29346867	34	5.00E-30	Bacteroides thetaiotaomicron VPI-5482	two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO76564.1 two-component system response regulator [Bacteroides thetaiotaomicron VPI-5482]			
26259,								
26260	48853613	41	2.00E-20	Cytophaga hutchinsonii	COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cytophaga hutchinsonii]			
26261,								
26262	29345596	39	2.00E-24	Bacteroides thetaiotaomicron VPI-5482	thiol:disulfide interchange protein dsbD precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO75293.1 thiol:disulfide interchange protein dsbD precursor [Bacteroides thetaiotaomicron VPI-5482]			
26263,								
26264	54302756	39	2.00E-13	Photobacterium profundum SS9	hypothetical protein PBPR81077 [Photobacterium profundum SS9] emb CAG22949.1 conserved hypothetical protein [Photobacterium profundum]			
26267,								
26268	53714565	28	4.00E-19	Bacteroides fragilis YCH46	hypothetical protein BF3279 [Bacteroides fragilis YCH46] dbj BAD50023.1 hypothetical protein [Bacteroides fragilis YCH46]			
26269,								
26270	48855808	43	9.00E-24	Cytophaga hutchinsonii	COG0694: Thioredoxin-like proteins and domains [Cytophaga hutchinsonii]			
26271,								
26272	52841852	49	4.00E-28	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	alpha/beta hydrolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27704.1 alpha/beta hydrolase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			

26273, 26274	41690505	76	4.00E-28	Psychrobacter sp. 273-4	COG1826: Sec-independent protein secretion pathway components [Psychrobacter sp. 273-4]				
26275, 26276	53714594	41	5.00E-17	Bacteroides fragilis YCH46	LacI family transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD50052.1 LacI family transcriptional regulator [Bacteroides fragilis YCH46]				
26277, 26278	53711667	61	6.00E-50	Bacteroides fragilis YCH46	hypothetical protein BF0376 [Bacteroides fragilis YCH46] dbj BAD47125.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
26279, 26280	31790365	43	1.00E-25	uncultured Acidobacteria bacterium	hypothetical protein [uncultured Acidobacteria bacterium]				
26281, 26282	15807914	32	1.00E-24	Deinococcus radiodurans R1	acyl-CoA dehydrogenase, putative [Deinococcus radiodurans R1] gb AAF12388.1 acyl-CoA dehydrogenase, putative [Deinococcus radiodurans] pir C75578 probable acyl-CoA dehydrogenase - Deinococcus radiodurans (strain R1)				1.3.99.2
26283, 26284	53691838	31	8.00E-32	Desulfovibrio desulfuricans G20	COG0642: Signal transduction histidine kinase [Desulfovibrio desulfuricans G20]				2.7.3.-
26285, 26286	54308990	83	1.00E-119	Photobacterium profundum SS9	putative type I restriction enzyme EcoEI Mprotein [Photobacterium profundum SS9] emb CAG20208.1 putative type I restriction enzyme EcoEI Mprotein [Photobacterium profundum]	Escherichia coli EcoE type I restriction- modification enzyme R subunit (hsdR) and EcoE type I restriction modification enzyme M subunit (hsdM) genes, complete cds; and hsdS gene, partial sequence	78	7.00E-16	2.1.1.72
26289, 26290	48855629	42	9.00E-21	Cytophaga hutchinsonii	COG0356: F0F1-type ATP synthase, subunit a [Cytophaga hutchinsonii] hypothetical protein LIC11677 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_712440.1 hypothetical protein LA2259 [Leptospira interrogans serovar Lai str. 56601] gb AA049458.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS70268.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				
26293, 26294	45657545	44	2.00E-29	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	COG2217: Cation transport ATPase [Cytophaga hutchinsonii]				
26295, 26296	48854664	41	1.00E-42	Cytophaga hutchinsonii					3.6.1.-

26333, 26334	32477073	28	1.00E-16	Rhodopirellula baltica SH 1	similar to preprotein translocase SecA chain [Rhodopirellula baltica SH 1 emb]CAD79222.1] similar to preprotein translocase SecA chain [Pirellula sp.]			
26335, 26336	20807328	32	2.00E-09	Thermoanaerobact er tengcongensis MB4	transposase [Thermoanaerobacter tengcongensis MB4] transposase [Thermoanaerobacter tengcongensis MB4]			
26339, 26340	506709	39	1.00E-34	Staphylococcus aureus	type 1 capsule synthesis gene; CapM [Staphylococcus aureus] sp P39862 CAPM_STAAU Capsular polysaccharide biosynthesis glycosyl transferase capM	2.4.1.-		
26347, 26348	57636503	44	1.00E-13	Staphylococcus epidermidis RP62A	rhodanese-like domain protein [Staphylococcus epidermidis RP62A] ref YP_189979.1 rhodanese-like domain protein [Staphylococcus epidermidis RP62A]	1.6.-		
26349, 26350	48855702	40	3.00E-32	Cytophaga hutchinsonii	COG3279: Response regulator of the LysR/AIGR family [Cytophaga hutchinsonii]			
2635, 2636	45250014	34	6.00E-07	Aneurinibacillus thermoaerophilus	putative transposase [Aneurinibacillus thermoaerophilus]			
26351, 26352	29349257	34	8.00E-30	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3849 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78954.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
26353, 26354	29346745	57	1.00E-55	Bacteroides thetaiotaomicron VPI-5482	folypolyglutamate synthase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76442.1 folypolyglutamate synthase [Bacteroides thetaiotaomicron VPI-5482]	6.3.2.17		
26355, 26356	48831629	39	2.00E-29	Magnetococcus sp. MC-1	COG0248: Exopolyphosphatase [Magnetococcus sp. MC-1] polyphosphate kinase [Vibrio parahaemolyticus RIMD 2210633] db BAC58836.1 polyphosphate kinase [Vibrio parahaemolyticus]	3.6.1.11		
26357, 26358	28997347	51	9.00E-72	Vibrio parahaemolyticus RIMD 2210633	sp Q87S51 PPK_VIBPA Polyphosphate kinase (Polyphosphoric acid kinase) (ATP-polyphosphate phosphotransferase)	2.7.4.1		
26359, 26360	16119697	43	4.00E-39	Agrobacterium tumefaciens str. C58	hypothetical protein AGR_pAT_692 [Agrobacterium tumefaciens str. C58] gb AAK90844.1 AGR_pAT_692p [Agrobacterium tumefaciens str. C58] sp Q8UUK7 DP42_AGR15 DNA polymerase IV 2 (Pol IV 2)	2.7.7.7		
26361, 26362	45658436	29	3.00E-13	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_711250.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar Lai str. 56601] gb AAO48268.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar lai str. 56601] gb AAS71159.1 alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			

26297,	29350005	63	2.00E-82	Bacteroides thetataoiaomicon VPI-5482	endopeptidase Cip ATP-binding chain B [Bacteroides thetataoiaomicon VPI-5482] sp Q89Y3 CLPB_BACTN_Chaperone clpB gb AAO79702.1	Desc:Staphylococcus aureus DNA for cellular proliferation protein #1366. Org:Staphylococcus aureus	85	1.00E-32	
26298					endopeptidase Cip ATP-binding chain B [Bacteroides thetataoiaomicon VPI-5482]				
26301,	48854653	60	4.00E-86	Cytophaga hutchinsonii	COG0635: Coproporphyrinogen III oxidase and related Fe-S oxidoreductases [Cytophaga hutchinsonii]				1.00E-32
26302					nitrogen fixation specific regulatory protein NifA [Chlorobium tepidum TLS]				
26303,	21674349	55	1.00E-33	Chlorobium tepidum TLS	gb AAAM72756.1 nitrogen fixation specific regulatory protein NifA [Chlorobium tepidum TLS]				
26304									
26305,	53711685	32	3.00E-09	Bacteroides fragilis YCH46	putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD47143.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46]				
26306									
26307,	9656796	31	9.00E-21	Vibrio cholerae O1 biovar eltor str. N16961	membrane-bound lytic murein transglycosylase D [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_231868.1 membrane-bound lytic murein transglycosylase D [Vibrio cholerae O1 biovar eltor str. N16961] pir B82102				
26308					membrane-bound lytic murein transglycosylase D VC2237 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				3.2.1.-
26309,	28211400	32	3.00E-07	Clostridium tetani E88	molybdopterin biosynthesis protein moeB [Clostridium tetani E88]				
26310					gb AAO36281.1 molybdopterin biosynthesis protein moeB [Clostridium tetani E88]				
2631,	48856332	67	8.00E-38	Cytophaga hutchinsonii	hypothetical protein Chut02000044 [Cytophaga hutchinsonii]				
2632									
26313,	48856112	32	2.00E-17	Cytophaga hutchinsonii	COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
26314									
26319,	46188140	39	1.00E-24	Pseudomonas syringae pv. B728a	COG1946: Acyl-CoA thioesterase [Pseudomonas syringae pv. syringae B728a]				3.1.2.-
26320									
26321,	29346791	50	5.00E-53	Bacteroides thetataoiaomicon VPI-5482	formyltetrahydrofolate deformylase [Bacteroides thetataoiaomicon VPI-5482] gb AAO76488.1 formyltetrahydrofolate deformylase [Bacteroides thetataoiaomicon VPI-5482]				3.5.1.10
26322									
26323,	28897146	43	1.00E-44	Vibrio parahaemolyticus RIMD 2210633	putative hemolysin [Vibrio parahaemolyticus RIMD 2210633] dbj BAC58635.1 putative hemolysin [Vibrio parahaemolyticus]				
26324									
26327,	55540762	49	3.00E-34	Flavobacterium columnare	GldH [Flavobacterium columnare]				
26328									
2633,	48856489	44	2.00E-61	Cytophaga hutchinsonii	COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii]				2.7.3.-
2634									

26363, 26364	48846331	36	7.00E-30	15	Geobacter metallireducens GS	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]			2.7.3.-
26365, 26366	48855464	38	7.00E-24		Cytophaga hutchinsonii	COG1999: Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems [Cytophaga hutchinsonii]			
26367, 26368	48854312	41	1.00E-23		Cytophaga hutchinsonii	COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii]			
						Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930575.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930493.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_930331.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_928792.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_928083.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] ref NP_927821.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16814.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15731.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15484.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15473.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE13790.1 Transposase, IS630 family [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE13033.1 Transposase, IS630			
2637, 2638	37528266	27	6.00E-11		Photorhabdus luminescens subsp. laumondii TTO1	hypothetical protein BF0706 [Bacteroides fragilis YCH46] db BAD47453.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			3.1.-
26371, 26372	53711995	47	2.00E-16		Bacteroides fragilis YCH46	GGDEF domain protein [Shewanella oneidensis MR-1] gb AAN55538.1			
26373, 26374	24374051	45	9.00E-54		Shewanella oneidensis MR-1	GGDEF domain protein [Shewanella oneidensis MR-1]			
26375, 26376	5006988	34	3.00E-31		Klebsiella pneumoniae	putative glycosyltransferase [Klebsiella pneumoniae]			
26377, 26378	23005587	32	2.00E-09		Magnetospirillum magnetotacticum MS-1	COG1112: Superfamily I DNA and RNA helicases and helicase subunits [Magnetospirillum magnetotacticum MS-1]			
26379, 26380	48854362	23	1.00E-17		Cytophaga hutchinsonii	COG1033: Predicted exporters of the RND superfamily [Cytophaga hutchinsonii]			
26381, 26382	48853518	41	1.00E-43		Cytophaga hutchinsonii	COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii]			

26385,						Legionella	hypothetical protein lp2876 [Legionella pneumophila str. Lens]				
26386	54295786	41	4.00E-44			pneumophila str. Lens	emb CAH17120.1 hypothetical protein [Legionella pneumophila str. Lens]				3.4.21.5
26387,						Cytophaga	COG0466: ATP-dependent Lon protease, bacterial type [Cytophaga hutchinsonii]				3
26388	48853586	48	3.00E-55			hutchinsonii					
26389,						Microscilla sp.	putative transposase [Microscilla sp. PRE1] gb AAK62882.1 MS160,				
26390	14518365	42	9.00E-42			PRE1	putative transposase [Microscilla sp. PRE1]				
26391,						Dehalococcoides	radical SAM/B12 binding domain protein [Dehalococcoides ethenogenes				
26392	57233930	43	1.00E-18			ethenogenes 195	195] gb AAW39435.1 radical SAM/B12 binding domain protein				
26393,						Dictyostelium	[Dehalococcoides ethenogenes 195]				
26394	28829330	38	1.00E-26			discoideum	hypothetical protein [Dictyostelium discoideum]				5.2.1.8
26395,							hypothetical protein, predicted Glutamate-cysteine ligase [Azoarcus sp.				
26396	56479409	50	5.00E-48			Azoarcus sp. Ebn1	Ebn1] emb CAI10097.1 hypothetical protein, predicted Glutamate-cysteine				
26397,						Desulfovibrio	ligase [Azoarcus sp. Ebn1]				
26398	53690939	41	4.00E-22			desulfuricans G20	COG0732: Restriction endonuclease S subunits [Desulfovibrio desulfuricans				3.1.21.3
							G20]				
26399,											
26400	48895665	68	6.00E-61			Trichodesmium	COG0286: Type I restriction-modification system methyltransferase subunit				
						erythraeum IMS101	[Trichodesmium erythraeum IMS101]				
26401,							XANTHINE DEHYDROGENASE [Brucella melitensis 16M] gb AAL52756.1				
26402	17987858	37	8.00E-40			Brucella melitensis	XANTHINE DEHYDROGENASE [Brucella melitensis 16M] pir A13448				1.1.1.20
						16M	xanthine dehydrogenase (EC 1.1.1.204) [imported] - Brucella melitensis				4
26403,						Clostridium	(strain 16M)				
26404	48859543	36	3.00E-40			thermocellum	COG0642: Signal transduction histidine kinase [Clostridium thermocellum				2.7.3.-
26405,						ATCC 27405	ATCC 27405]				
26406	37962765	43	5.00E-10			Salmonella	hypothetical protein [Salmonella typhimurium]				
						typhimurium					
26407,											
26408	53712444	31	2.00E-09			Bacteroides fragilis	hypothetical protein BF1152 [Bacteroides fragilis YCH46] db BAD47902.1				
26409,						YCH46	conserved hypothetical protein [Bacteroides fragilis YCH46]				
26410	48854999	46	1.00E-24			Cytophaga	COG1832: Predicted CoA-binding protein [Cytophaga hutchinsonii]				
2641,						hutchinsonii	COG0466: ATP-dependent Lon protease, bacterial type [Cytophaga				3.4.21.5
2642	48853586	55	2.00E-86			Cytophaga	hutchinsonii]				3

26419,	48856761	36	2.00E-38	Cytophaga hutchinsonii	COG0550: Topoisomerase IA [Cytophaga hutchinsonii]				5.99.1.2
26420				Bacteroides fragilis YCH46	putative UDP-glucose-6 dehydrogenase [Bacteroides fragilis YCH46]				
26421,	53712734	53	6.00E-35	Bacteroides fragilis YCH46	dbj BAD48192.1 putative UDP-glucose-6 dehydrogenase [Bacteroides fragilis YCH46]				1.1.1.-
26422				Bacteroides thetaiotaomicron VPI-5482	thiol:disulfide interchange protein [Bacteroides thetaiotaomicron VPI-5482]				
26423,	29346702	36	4.00E-26	Bacteroides thetaiotaomicron VPI-5482	gb AAO76399.1 thiol:disulfide interchange protein [Bacteroides thetaiotaomicron VPI-5482]				
26424				Cytophaga hutchinsonii	COG1459: Type II secretory pathway, component PulF [Cytophaga hutchinsonii]				
26425,	48855359	37	2.00E-57	Bacteroides thetaiotaomicron VPI-5482	Integrase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78584.1				
26426				Bacteroides thetaiotaomicron VPI-5482	Integrase [Bacteroides thetaiotaomicron VPI-5482]				
26427,	29348887	35	1.00E-22	Bacteroides thetaiotaomicron VPI-5482	Desc:Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3480. Org:Staphylococcus epidermidis				1.1.99.1
26428	ABP3863								6
26429,	5	53	2.00E-62	Psychrobacter sp. 273-4	COG0367: Asparagine synthase (glutamine-hydrolyzing) [Psychrobacter sp. 273-4]				6.3.5.4
26430	52853615	48	1.00E-58	Clostridium thermocellum ATCC 27405	COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405]				2.7.3.-
26433,	48859543	41	7.00E-42	Bacteroides fragilis YCH46	putative aminotransferase [Bacteroides fragilis YCH46] dbj BAD47862.1				
26434				Thermoanaerobacter tengcongensis MB4	putative aminotransferase [Bacteroides fragilis YCH46]				
26435,	53712404	55	1.00E-50	Thermoanaerobacter tengcongensis MB4	predicted glycosyltransferases [Thermoanaerobacter tengcongensis MB4]				
26436				Nostoc punctiforme PCC 73102	gb AAM23373.1 predicted glycosyltransferases [Thermoanaerobacter tengcongensis MB4]				
26437,	20806598	38	2.00E-33	Nostoc punctiforme PCC 73102	COG5278: Predicted periplasmic ligand-binding sensor domain [Nostoc punctiforme PCC 73102]				2.7.3.-
26438				Geobacillus kaustophilus HTA426	transcriptional repressor of sporulation and degradative enzymes production [Geobacillus kaustophilus HTA426] dbj BAD75024.1 transcriptional repressor of sporulation and degradative enzymes production [Geobacillus kaustophilus HTA426]				
26439,	23128582	39	2.00E-39	Cytophaga hutchinsonii	COG0451: Nucleoside-diphosphate-sugar epimerases [Cytophaga hutchinsonii]				5.1.3.20
26440				Mesorhizobium sp. BNC1	Desc:Porphorymonas gingivalis protein PG111. Org:Porphorymonas gingivalis				
26445,	56419274	45	5.00E-11	Geobacillus kaustophilus HTA426	COG0419: ATPase involved in DNA repair [Mesorhizobium sp. BNC1]				
26446				Cytophaga hutchinsonii	HrgA protein [Campylobacter jejuni RM1221] gb AAW36198.1 HrgA protein [Campylobacter jejuni RM1221]				
26445,	48855023	61	8.00E-33	Cytophaga hutchinsonii					
26453,	AA3433								
26454	1	39	4.00E-32	Mesorhizobium sp. BNC1					
26455,	45680928	25	1.00E-12	Campylobacter jejuni RM1221					
26456									
26457,	57238615	33	4.00E-25						
26458									

26461, 26462	55378462	38	6.00E-18	Haloarcula marismortui ATCC 43049	sulfatase [Haloarcula marismortui ATCC 43049] gblAAV46606.1] sulfatase [Haloarcula marismortui ATCC 43049]				
26463, 26464				Caulobacter crescentus CB15	hypothetical protein CC0341 [Caulobacter crescentus CB15] gblAAK22328.1] hypothetical protein [Caulobacter crescentus CB15] pif[D87291 hypothetical protein CC0341 [imported] - Caulobacter crescentus				3.2.1.41
26467, 26468	16124596	35	6.00E-35	Cytophaga hutchinsonii	COG2812: DNA polymerase III, gamma/tau subunits [Cytophaga hutchinsonii]				2.7.7.7
26469, 26470	48855923	41	3.00E-41	Riemerella anatipestifer	OmpA [Riemerella anatipestifer]				
2647, 2648	50235077	46	2.00E-51	Silicibacter pomeroi DSS-3	conserved domain protein [Silicibacter pomeroi DSS-3] ref[YP_166471.1] hypothetical protein SPO1224 [Silicibacter pomeroi DSS-3]				
26471, 26472	56677853	36	4.00E-25	Cytophaga hutchinsonii	COG0845: Membrane-fusion protein [Cytophaga hutchinsonii]				
26473, 26474	48854902	36	8.00E-35	Cytophaga hutchinsonii	COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
26475, 26476	48856112	33	3.00E-20	Pseudomonas fluorescens PfO-1	COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Pseudomonas fluorescens PfO-1]				
26477, 26478	48732855	43	5.00E-43	Clostridium thermocellum ATCC 27405	COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405]				2.7.3.-
26485, 26486	48859543	41	6.00E-19	Cytophaga hutchinsonii	COG1363: Cellulase M and related proteins [Cytophaga hutchinsonii]				3.2.1.4
26489, 26490	48855760	64	2.00E-76	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT1085 [Bacteroides thetaiotaomicron VPI-5482] gblAAO76192.1] hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482]				
2649, 2650	29346495	39	1.00E-07	Cytophaga hutchinsonii	hypothetical protein Chut02001282 [Cytophaga hutchinsonii]				
26491, 26492	48856049	44	7.00E-32	Vibrio cholerae O1 biovar eltor str. N16961	transcriptional regulator, LuxR family [Vibrio cholerae O1 biovar eltor str. N16961] ref[NP_233336.1] transcriptional regulator, LuxR family [Vibrio cholerae O1 biovar eltor str. N16961] pif[H82395 transcription regulator LuxR family VCA0952 [imported] - Vibrio cholerae (strain N16961 serogroup O1)]				
26493, 26494	96583390	40	2.00E-07	Xanthomonas axonopodis pv. citri str. 306	hypothetical protein XAC4358 [Xanthomonas axonopodis pv. citri str. 306] gblAAM39188.1] conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306]				2.7.3.-

26495, 26496	16080603	39	1.00E-20	168	Bacillus subtilis subsp. subtilis str.	two-component sensor histidine kinase [Bacillus subtilis subsp. subtilis str. 168] emb[CAB15567.1] two-component sensor histidine kinase [Bacillus subtilis subsp. subtilis str. 168] pir[RGBSDS degradative enzyme regulator / competence regulator degS - Bacillus subtilis gb AAC44937.1] histidine kinase sp P13799 DEGS_BACSU Sensor protein degS gb AAA22734.1] transcriptional activator protein gb AAA22732.1] degS protein				2.7.3.-
265, 266	48862089	50	8.00E-64	degradans 2-40	Microbulbifer	hypothetical protein Mdeg02002723 [Microbulbifer degradans 2-40]				
26501, 26502	24374891	52	2.00E-36	Shewanella oneidensis MR-1		hypothetical protein SO3380 [Shewanella oneidensis MR-1] gb AAN56378.1] conserved hypothetical protein [Shewanella oneidensis MR-1]				
26507, 26508	17227649	43	3.00E-40	7120	Nostoc sp. PCC	penicillin-binding protein [Nostoc sp. PCC 7120] pir A11825 penicillin-binding protein [imported] - Nostoc sp. (strain PCC 7120) dbj BAB77677.1] penicillin-binding protein [Nostoc sp. PCC 7120]				3.5.2.6
2651, 2652	48854173	24	7.00E-09	hutchinsonii	Cytophaga	hypothetical protein Chut02002840 [Cytophaga hutchinsonii]				3.2.1.13
26512, 26513, 26514	18086516 48856843	36 55	8.00E-28 8.00E-37	Cellvibrio japonicus Cytophaga hutchinsonii		alpha-glucuronidase [Cellvibrio japonicus] COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases [Cytophaga hutchinsonii]				9 6.2.1.1
26515, 26516	56461030	51	4.00E-25	Idiomarina loihensis L2TR		Zn-dependent aminopeptidase [Idiomarina loihensis L2TR] gb AAV82762.1] Zn-dependent aminopeptidase [Idiomarina loihensis L2TR]				
26517, 26518	31195879	54	1.00E-29	Anopheles gambiae		ENSANGP00000000448 [Anopheles gambiae]				2.1.1.34
26521, 26522	48856383	40	1.00E-31	hutchinsonii	Cytophaga	COG0044: Dihydroorotase and related cyclic amidohydrolases [Cytophaga hutchinsonii]				3.5.2.3
26523, 26524	29609430	62	3.00E-79	Streptomyces avermitilis MA-4680		putative sugar ABC transporter ATP-binding protein [Streptomyces avermitilis MA-4680] ref NP_826945.1] putative sugar ABC transporter ATP-binding protein [Streptomyces avermitilis MA-4680]	Streptomyces avermitilis genomic DNA, complete genome, section 24/30		90	2.00E-09 1.8.-
26525, 26526	53715357	28	1.00E-21	YCH46	Bacteroides fragilis	hypothetical protein BF4073 [Bacteroides fragilis YCH46] dbj BAD50815.1] conserved hypothetical protein [Bacteroides fragilis YCH46]				
26527, 26528	48855642	34	6.00E-40	hutchinsonii	Cytophaga	COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii] Uncharacterized conserved secreted protein [Idiomarina loihensis L2TR] gb AAV81692.1] Uncharacterized conserved secreted protein [Idiomarina loihensis L2TR]				5.2.1.8
26529, 26530	56459960	34	3.00E-09	Idiomarina loihensis L2TR						

2653,	48856392	48	1.00E-18	Cytophaga hutchinsonii	COG0419: ATPase Involved in DNA repair [Cytophaga hutchinsonii]				
2654				Rubrivivax	COG1988: Predicted membrane-bound metal-dependent hydrolases				
26531,				gelatinosus PM1	[Rubrivivax gelatinosus PM1]				
26532	47575209	31	2.00E-21	Cytophaga hutchinsonii	COG0265: Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain [Cytophaga hutchinsonii]				3.4.21.-
26533,	48853851	29	6.00E-11	Cytophaga hutchinsonii	COG0602: Organic radical activating enzymes [Cytophaga hutchinsonii]				
26534				Cytophaga hutchinsonii					
26535,	48856308	49	3.00E-30	Cytophaga hutchinsonii					
26536				Bacteroides fragilis YCH46	methionyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD51240.1				6.1.1.10
26537,	53715782	69	1.00E-102	Cytophaga hutchinsonii	COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii]				3.1.-
26538	48855589	44	2.00E-16	Cytophaga hutchinsonii	DNA processing protein DprA, putative [Porphyromonas gingivalis W83] ref NP_904614.1 DNA processing protein DprA, putative [Porphyromonas gingivalis W83]				
26541,	34396447	43	4.00E-60	Porphyromonas gingivalis W83	COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii]				4.1.3.-
26542	48856398	53	5.00E-41	Cytophaga hutchinsonii					
26545,	31195945	40	3.00E-26	Anopheles gambiae	ENSANGP00000000452 [Anopheles gambiae]				
26546	AAV3438	2	5.00E-25	Bacteroides fragilis YCH46	Desc:Porphyromonas gingivalis protein PG48. Org:Porphyromonas gingivalis				
26547,	53713702	52	1.00E-78	Bacteroides fragilis YCH46	DNA gyrase A subunit [Bacteroides fragilis YCH46] dbj BAD49160.1 DNA gyrase A subunit [Bacteroides fragilis YCH46]				5.99.1.3
26548				Bacteroides fragilis YCH46	ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] dbj BAD50675.1 ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46]				
26549,	53715217	46	2.00E-50	Anopheles gambiae	ENSANGP000000002020 [Anopheles gambiae]				
26550	31194819	41	6.00E-52	Cytophaga hutchinsonii	COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii]				2.7.7.24
26551,	48853434	68	2.00E-83	Cytophaga hutchinsonii	COG0644: Dehydrogenases (flavoproteins) [Cytophaga hutchinsonii]				1.-
26552	48853677	52	4.00E-58	Cytophaga hutchinsonii	COG1741: Pirin-related protein [Cytophaga hutchinsonii]				
26553,	48856673	65	2.00E-65	Pseudomonas syringae pv. tomato DC3000	ferrochelatase [Pseudomonas syringae pv. tomato str. DC3000] ref NP_790962.1 ferrochelatase [Pseudomonas syringae pv. tomato str. DC3000] sp Q888A2 HEMZ_PSESM Ferrochelatase (Protoheme ferro-lyase) (Heme synthetase)				4.99.1.1
26554	28851580	55	8.00E-23	str. DC3000					

26569, 26570	29346615	69	1.00E-68	Bacteroides thetaiotaomicron VPI-5482	putative ATPase, AAA family [Bacteroides thetaiotaomicron VPI-5482] gb AAO76312.1 putative ATPase, AAA family [Bacteroides thetaiotaomicron VPI-5482]			2.7.7.7
26573, 26574	45659189	43	1.00E-57	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_714399.1 CysC; CysN [Leptospira interrogans serovar Lai str. 56601] gb AAAN51417.1 CysN; CysC [Leptospira interrogans serovar lai str. 56601] gb AAS71912.1 sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			2.7.7.4
26575, 26576	53759913	38	4.00E-34	Methylobacillus flagellatus KT	COG0232: dGTP triphosphohydrolase [Methylobacillus flagellatus KT]			3.1.5.1
26577, 26578	53765021	44	8.00E-41	Anabaena variabilis ATCC 29413	COG0732: Restriction endonuclease S subunits [Anabaena variabilis ATCC 29413]			3.1.21.3
26579, 26580	48856952	50	6.00E-67	Cytophaga hutchinsonii	COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii]			4.1.3.27
26581, 26582	39545768	24	2.00E-09	Aeromonas hydrophila	putative ADP-heptose:LPS [Aeromonas hydrophila]			
26583, 26584	34398084	60	5.00E-39	Porphyromonas gingivalis W83	conserved hypothetical protein TIGR00250 [Porphyromonas gingivalis W83] ref NP_906245.1 conserved hypothetical protein TIGR00250 [Porphyromonas gingivalis W83]			
26589, 26590	32477598	47	3.00E-35	Rhodopirella baltica SH 1	hypothetical protein RB12586 [Rhodopirella baltica SH 1] emb CAD77669.1 hypothetical protein [Pirellula sp.]			
2659, 2660	15076967	50	2.00E-23	Myxococcus xanthus	response regulator HsfA [Myxococcus xanthus]			2.7.--
26595, 26596	53711678	34	1.00E-09	Bacteroides fragilis YCH46	putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD47136.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46]			
26601, 26602	54024396	47	8.00E-07	Nocardia farcinica IFM 10152	putative peptidase [Nocardia farcinica IFM 10152] dbj BAD57274.1 putative peptidase [Nocardia farcinica IFM 10152]			3.4.17.1 1
26605, 26606	53711487	66	2.00E-68	Bacteroides fragilis YCH46	cysteinyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD46945.1 cysteinyl-tRNA synthetase [Bacteroides fragilis YCH46]			6.1.1.16
2661, 2662	48853597	56	2.00E-67	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]			2.4.1.83
26611, 26612	ABG3170	7	5.00E-14		Desc:Beta 1,3-galactose transferase protein #6. Org:Streptococcus agalactiae			2.--
26613, 26614	17940055	31	1.00E-23	Leptospira interrogans	unknown [Leptospira interrogans]			2.4.--

26615,	48853782	54	4.00E-29	Cytophaga hutchinsonii	COG0389: Nucleotidyltransferase/DNA polymerase involved in DNA repair [Cytophaga hutchinsonii]			2.7.7.7
26616								
26617,	48854964	50	2.00E-26	Cytophaga hutchinsonii	COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii]			
26618								
26621,								
26622	34397409	28	2.00E-07	Porphyromonas gingivalis W83	DNA polymerase III, gamma and tau subunits [Porphyromonas gingivalis W83] ref[NP_905573.1] DNA polymerase III, gamma and tau subunits [Porphyromonas gingivalis W83]			
26623,								
26624	21673423	62	2.00E-46	Chlorobium tepidum TLS	cytosine deaminase [Chlorobium tepidum TLS] gb AAM71830.1 cytosine deaminase [Chlorobium tepidum TLS]			3.5.4.1
26627,								
26628	48856903	32	1.00E-35	Cytophaga hutchinsonii	COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii]			
26631,								
26632	34556815	31	6.00E-34	Wolinella succinogenes DSM 1740	NRF1 PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09530.1 NRF1 PROTEIN [Wolinella succinogenes]			
26633,								
26634	48854753	40	7.00E-13	Cytophaga hutchinsonii	COG1078: HD superfamily phosphohydrolases [Cytophaga hutchinsonii]			
26635,								
26636	53712200	51	4.00E-36	3-hydroxymyristoyl	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Bacteroides fragilis YCH46] dbj BAD47688.1 UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [Bacteroides fragilis YCH46]			2.3.1.-
26639,								
26640	48856260	29	5.00E-19	Cytophaga hutchinsonii	COG0489: ATPases involved in chromosome partitioning [Cytophaga hutchinsonii]			
26641,								
26642	AAR5666	7	8.00E-37		Desc:Bacteroides fragilis RprX regulatory response protein. Org:Bacteroides fragilis			2.7.3.-
26643,								
26644	48854369	45	7.00E-21	Cytophaga hutchinsonii	COG0608: Single-stranded DNA-specific exonuclease [Cytophaga hutchinsonii]			3.1.-
26645,								
26646	57167881	32	2.00E-13	Campylobacter coli RM2228	DnaJ domain protein [Campylobacter coli RM2228] gb EAL57667.1 DnaJ domain protein [Campylobacter coli RM2228]			
				Legionella pneumophila subsp. pneumophila str.	reverse transcriptase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27167.1 reverse transcriptase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			2.7.7.49
26649,								
26650	52841315	56	7.00E-86	Philadelphina 1	glycosyltransferase [Bacillus clausii KSM-K16] dbj BAD65699.1 glycosyltransferase [Bacillus clausii KSM-K16]			
26651,								
26652	56964929	50	9.00E-11	KSM-K16	glycosyltransferase [Bacillus clausii KSM-K16]			
26653,								
26654	29345890	54	6.00E-26	Bacteroides thetaiotaomicron VPI-5482	glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75587.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.-.-
26655,								
26656	23114616	29	4.00E-09	Desulfotobacterium hafnense DCB-2	COG1196: Chromosome segregation ATPases [Desulfotobacterium hafnense DCB-2]			

26657,	29347919	28	4.00E-13	Bacteroides thetaiotaomicron VPI-5482	putative transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482] gb AAO77616.1 putative transcriptional regulator [Bacteroides thetaiotaomicron VPI-5482]				
26658	48856481	56	4.00E-43	Cytophaga hutchinsonii	COG1225: Peroxiredoxin [Cytophaga hutchinsonii]				1.11.1.-
26659,						Photobacterium profundum SS9 chromosome 2; segment 3/7			
26660	54302486	72	1.00E-98	Photobacterium profundum SS9	hypothetical maturase [Photobacterium profundum SS9] emb CAG22679.1 hypothetical maturase [Photobacterium profundum] excinuclease ABC, C subunit [Porphyromonas gingivalis W83] ref NP_906065.1 excinuclease ABC, C subunit [Porphyromonas gingivalis W83]		83	2.00E-16	2.7.7.49
26663,	34397903	60	1.00E-60	Porphyromonas gingivalis W83	1-deoxy-D-xylulose 5-phosphate synthase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO79204.1 1-deoxy-D-xylulose 5-phosphate synthase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A0C2 DXS_BACTN 1-deoxy- D-xylulose-5-phosphate synthase (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS)				4.1.3.37
26669,	29349507	49	1.00E-19	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BF4373 [Bacteroides fragilis YCH46] db BAD51111.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
26670	53715653	47	4.00E-21	Bacteroides fragilis YCH46	Desc:Human polypeptide SEQ ID NO 1661. Org:Homo sapiens				
26671,	ABP6961	4	6.00E-15						
26672	48853518	44	4.00E-59	Cytophaga hutchinsonii	COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii]				
26673,	48825076	54	2.00E-37	Enterococcus faecium	COG0637: Predicted phosphatase/phosphohexomutase [Enterococcus faecium]				5.4.2.6
26677,	48853471	36	4.00E-07	Cytophaga hutchinsonii	COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii]				
26678	48854367	46	2.00E-40	Cytophaga hutchinsonii	hypothetical protein Chut02003040 [Cytophaga hutchinsonii]				
26683,	48854415	59	3.00E-80	Cytophaga hutchinsonii	COG3279: Response regulator of the LytR/AigR family [Cytophaga hutchinsonii]				2.7.3.-
26684									
26685,	53715653	51	5.00E-21	Bacteroides fragilis YCH46	hypothetical protein BF4373 [Bacteroides fragilis YCH46] db BAD51111.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
26686	20090134	49	1.00E-21	Methanosarcina acetivorans C2A	sensory transduction histidine kinase [Methanosarcina acetivorans C2A] gb AAM04689.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A]				2.7.3.-
26687,									
26688	34105334	37	3.00E-13	Chromobacterium violaceum ATCC 12472	N-acetylneuraminase cytidyltransferase [Chromobacterium violaceum ATCC 12472] ref NP_903698.1 N-acetylneuraminase cytidyltransferase [Chromobacterium violaceum ATCC 12472]				2.7.7.43

26697,	AAW9314	43	2.00E-10		Desc:P. fluorescens xylanase protein Pseyna. Org:Pseudomonas fluorescens			
26698	1							
26699,				Cytophaga hutchinsonii	hypothetical protein Chut02002032 [Cytophaga hutchinsonii]			
26700	48854974	33	7.00E-10					
				Photorhabdus luminescens subsp. laumondii	hypothetical protein plu3505 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15878.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1]			2.3.1.12
267,								8
268	37527378	31	2.00E-16					
26701,				Cytophaga hutchinsonii	COG0841: Cation/multidrug efflux pump [Cytophaga hutchinsonii]			
26702	48856922	43	7.00E-52					
26703,				Cytophaga hutchinsonii	COG2227: 2-polyphenyl-3-methyl-5-hydroxy-6-methoxy-1,4-benzoquinol methylase [Cytophaga hutchinsonii]			
26704	48854245	31	4.00E-21					
2671,				Gossypium hirsutum	reversibly glycosylated polypeptide [Gossypium hirsutum]			
2672	18077708	38	7.00E-25					
				Thermotoga maritima MSB8	hypothetical protein TM0519 [Thermotoga maritima MSB8] gb AAD35604.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir E72365 conserved hypothetical protein - Thermotoga maritima (strain MSB8)			
26713,								
26714	15643285	53	2.00E-18					
26715,				Bacteroides fragilis	hypothetical protein BF0053 [Bacteroides fragilis YCH46] db BAD46802.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
26716	53711344	41	4.00E-35	YCH46				
				Porphyromonas gingivalis W83	glycogen synthase-related protein [Porphyromonas gingivalis W83] ref NP_905929.1 glycogen synthase-related protein [Porphyromonas gingivalis W83]			2.4.1.21
26717,								
26718	34397767	49	2.00E-64					
				Bacteroides thetaiotaomicron VPI-5482	putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79696.1 putative nitrogen utilization substance protein [Bacteroides thetaiotaomicron VPI-5482]			
26723,								
26724	29349999	40	1.00E-32					
				Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0948 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76055.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
26725,								
26726	29346358	52	6.00E-46					
				Clostridium thermocellum ATCC 27405	COG0842: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405]			2.7.3.-
26727,								
26728	48859543	36	8.00E-34					
				Enterococcus faecium	COG1134: ABC-type polysaccharide/polyol phosphate transport system, ATPase component [Enterococcus faecium]			1.8.-
2673,								
2674	48824414	47	2.00E-36					
				Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VP0504 [Vibrio parahaemolyticus RIMD 2210633] sp Q87SC0 Y504_VIBPA Hypothetical UPF0246 protein VP0504 db BAC58767.1 conserved hypothetical protein [Vibrio parahaemolyticus]			
26733,								
26734	28897278	54	1.00E-61					

26735, 26736	34396372	60	4.00E-80	Porphyromonas gingivalis W83	peptide chain release factor 3 [Porphyromonas gingivalis W83] ref NP_904540.1 peptide chain release factor 3 [Porphyromonas gingivalis W83]			3.6.1.48
26739, 26740	23099975	30	4.00E-20	Oceanobacillus theysensis HTE831	two-component sensor histidine kinase [Oceanobacillus theysensis HTE831] dbj BAC14476.1 two-component sensor histidine kinase involved in degradative enzyme [Oceanobacillus theysensis HTE831]			2.7.3.-
26741, 26742	48855092	30	5.00E-11	Cytophaga hutchinsonii	COG4564: Signal transduction histidine kinase [Cytophaga hutchinsonii] putative two-component system sensor protein histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79072.1 putative two-component system sensor protein histidine kinase [Bacteroides thetaiotaomicron VPI- 5482]			2.7.3.-
26743, 26744	29349375	40	8.00E-39	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein VP2972 [Vibrio parahaemolyticus RIMD 2210633] dbj BAC61235.1 conserved hypothetical protein [Vibrio parahaemolyticus]			2.7.3.-
26745, 26746	28999746	42	2.00E-58	Vibrio parahaemolyticus RIMD 2210633	Desc:Beta-1,3-glucanase. Org:Bacillus sp			3.2.1.-
26747, 26748	AAR1159 9	49	1.00E-29	Shewanella oneidensis MR-1	hypothetical protein SO0125 [Shewanella oneidensis MR-1] gb AAN532.12.1 conserved hypothetical protein [Shewanella oneidensis MR-1]			
26751, 26752	45657308	30	1.00E-25	Leptospira interrogans serovar Copenhagen str. Ficruz L1-130	histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhagen str. Ficruz L1-130] gb AAS70031.1 histidine kinase response regulator hybrid protein [Leptospira interrogans serovar Copenhagen str. Ficruz L1-130]			2.7.3.-
26753, 26754	46446644	46	1.00E-47	Parachlamydia sp. UWE25	hypothetical protein pc1010 [Parachlamydia sp. UWE25] emb CAF23734.1 conserved hypothetical protein [Parachlamydia sp. UWE25]			
26755, 26756	54309979	35	1.00E-19	Photobacterium profundum SS9	hypothetical protein PBPA2825 [Photobacterium profundum SS9] emb CAG21197.1 hypothetical protein [Photobacterium profundum]			
26759, 26760	49235400	38	1.00E-22	Moorella thermoacetica ATCC 39073	COG0860: N-acetylmuramoyl-L-alanine amidase [Moorella thermoacetica ATCC 39073]			3.5.1.28
26761, 26762	48783200	31	2.00E-16	Burkholderia fungorum LB400	COG0438: Glycosyltransferase [Burkholderia fungorum LB400] glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75587.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI- 5482]			
26763, 26764	29345890	36	2.00E-43	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT1257 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76364.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			2.-.-.-
26765, 26766	29346667	62	2.00E-36	Bacteroides thetaiotaomicron VPI-5482				

26767, 26768	55377565	28	7.00E-09	Haloarcula marismortui ATCC 43049	universal stress protein [Haloarcula marismortui ATCC 43049]			
26769, 26770	53711775	45	3.00E-51	Bacteroides fragilis YCH46	glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD47233.1 glycosyltransferase [Bacteroides fragilis YCH46]			
2677, 2678	57233779	27	1.00E-08	Dehalococcoides ethenogenes 195	peptidase, M16 family [Dehalococcoides ethenogenes 195] gb AAW39284.1 peptidase, M16 family [Dehalococcoides ethenogenes 195]			3.4.99.-
26771, 26772	53797086	34	4.00E-40	Chloroflexus aurantiacus	COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Chloroflexus aurantiacus]			
26777, 26778	26988659	27	3.00E-14	Pseudomonas putida KT2440	hypothetical protein PP1931 [Pseudomonas putida KT2440] gb AAN67548.1 conserved hypothetical protein [Pseudomonas putida KT2440]			
26789, 26790	53687786	43	3.00E-14	Nostoc punctiforme PCC 73102	hypothetical protein Npun02004704 [Nostoc punctiforme PCC 73102] putative biotin--(acetyl-CoA carboxylase) synthetase [Bacteroides thetataoiaomicron VPI-5482] gb AAO77345.1 putative biotin--(acetyl-CoA carboxylase) synthetase [Bacteroides thetaiotaomicron VPI-5482]			6.3.4.15
2679, 2680	29347648	35	4.00E-26	Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293				
26793, 26794	23025146	31	7.00E-17	Bdellovibrio bacteriovorus HD100	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]			2.1.1.-
26799, 26800	42524558	44	4.00E-53	Bacteroides thetataoiaomicron VPI-5482	hypothetical protein Bd3175 [Bdellovibrio bacteriovorus HD100] emb CAE80931.1 pttB [Bdellovibrio bacteriovorus HD100] two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482] gb AAO78203.1 two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482]			3.4.21.8 3
26803, 26804	29348506	28	4.00E-12	Bacteroides thetataoiaomicron VPI-5482	putative ABC transporter permease [Bacteroides fragilis YCH46] dbj BAD48347.1 putative ABC transporter permease [Bacteroides fragilis YCH46]			
26805, 26806	53712889	46	2.00E-09	Bacteroides fragilis YCH46				
2681, 2682	48854768	30	9.00E-30	Cytophaga hutchinsonii	COG2319: FOG: WD40 repeat [Cytophaga hutchinsonii]			2.7.1.37
26811, 26812	48854548	34	2.00E-12	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]			

26813, 26814	53715360	48	2.00E-51	Bacteroides fragilis YCH46	ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] dbj BAD50818.1 ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46]			3.6.1.-
26815, 26816	23126434	43	7.00E-15	Nostoc punctiforme PCC 73102	COG1112: Superfamily I DNA and RNA helicases and helicase subunits [Nostoc punctiforme PCC 73102]			3.6.1.-
26817, 26818						Vibrio vulnificus CMCP6 chromosome II section 2 of 6 of the complete sequence	89 2.00E-13	
26819, 26820	56963185	28	4.00E-25	Bacillus clausii KSM-K16	hypothetical protein ABC1420 [Bacillus clausii KSM-K16] dbj BAD63955.1 hypothetical protein [Bacillus clausii KSM-K16]			
26821, 26822	18309430	34	2.00E-15	Clostridium perfringens str. 13	probable transcriptional regulator [Clostridium perfringens str. 13] dbj BAB80154.1 probable transcriptional regulator [Clostridium perfringens str. 13]			2.1.1.63
26823, 26824	48730285	54	7.00E-59	Pseudomonas fluorescens Pfo-1	COG1280: Putative threonine efflux protein [Pseudomonas fluorescens Pfo- 1]			
26825, 26826	9654588	36	1.00E-21	Vibrio cholerae O1 biovar eltor str. N16961	hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229841.1 hypothetical protein VC0184 [Vibrio cholerae O1 biovar eltor str. N16961] pir C82355 hypothetical protein VC0184 [imported] - Vibrio cholerae (strain N16961 serogroup O1)			
26829, 26830	48869829	31	3.00E-08	Pediococcus pentosaceus ATCC 25745	COG0615: Cytidylyltransferase [Pediococcus pentosaceus ATCC 25745] L-sorbose dehydrogenase [Gloeobacter violaceus PCC 7421] dbj BAC90384.1 L-sorbose dehydrogenase [Gloeobacter violaceus PCC 7421]			2.7.7.39
2683, 2684	37522012	30	1.00E-08	Gloeobacter violaceus PCC 7421	COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
26835, 26836	48854285	38	8.00E-41	Cytophaga hutchinsonii	hypothetical protein RB4459 [Rhodopirellula baltica SH 1] emb CAD73798.1 conserved hypothetical protein [Pirellula sp.]			
26837, 26838	32473118	30	3.00E-15	Rhodopirellula baltica SH 1	COG1999: Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems [Cytophaga hutchinsonii]			
26841, 26842	48855464	37	1.00E-28	Cytophaga hutchinsonii	hypothetical protein LMO2365_2347 [Listeria monocytogenes str. 4b F2365] gb AAAT05113.1 conserved domain protein [Listeria monocytogenes str. 4b F2365]			2.7.7.49
26843, 26844	48908547	31	2.00E-16	Listeria monocytogenes str. 4b F2365				

26849, 26850	6457709	36	2.00E-13	Deinococcus radiodurans	conserved hypothetical protein [Deinococcus radiodurans] pir F75565 conserved hypothetical protein - Deinococcus radiodurans (strain R1) ref NP_293774.1 hypothetical protein DR0048 [Deinococcus radiodurans R1]					
26851, 26852	549039	42	5.00E-28		Type II restriction enzyme HpaII [Endonuclease HpaII] (R.HpaII) gb AAA20482.1 HpaII restriction endonuclease					
26853, 26854	15995272	39	2.00E-24	Clostridium acetobutylicum ATCC 824	Predicted iron-sulfur flavoprotein [Clostridium acetobutylicum ATCC 824] gb AAK79961.1 Predicted iron-sulfur flavoprotein [Clostridium acetobutylicum ATCC 824] pir F97146 probable iron-sulfur flavoprotein [imported] - Clostridium acetobutylicum					
26859, 26860	53713554	51	6.00E-37	Bacteroides fragilis YCH46	putative carbon-nitrogen hydrolase [Bacteroides fragilis YCH46] dbj BAD49012.1 putative carbon-nitrogen hydrolase [Bacteroides fragilis YCH46]					
26861, 26862	29345937	46	1.00E-30	Bacteroides thetaiotaomicron VPI-5482	tryptophan synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO75634.1 tryptophan synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482]				4.2.1.20	
26863, 26864	19919301	48	2.00E-42	Legionella pneumophila	putative ATP-dependent DNA helicase protein [Legionella pneumophila]					
26867, 26868	53713283	37	2.00E-21	Bacteroides fragilis YCH46	hypothetical protein BF1993 [Bacteroides fragilis YCH46] dbj BAD48741.1 conserved hypothetical protein [Bacteroides fragilis YCH46]					
26869, 26870	48854312	30	4.00E-23	Cytophaga hutchinsonii	COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii]			Chromobacterium violaceum ATCC 12472 section 7 of 16 of the complete genome		
2687, 2688	47573321	90	1.00E-166	Rubrivivax gelatinosus PM1	COG2766: Putative Ser protein kinase [Rubrivivax gelatinosus PM1]			85 #####		
26873, 26874	47526988	25	8.00E-25	Bacillus anthracis str. 'Ames Ancestor'	tpg glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] ref YP_027843.1 TPR glycosyl transferase domain protein [Bacillus anthracis str. Sterne] ref NP_844138.1 TPR glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAP25624.1 TPR glycosyl transferase domain protein [Bacillus anthracis str. Ames] gb AAT30812.1 TPR glycosyl transferase domain protein [Bacillus anthracis str. 'Ames Ancestor'] gb AAT53894.1 TPR glycosyl transferase domain protein [Bacillus anthracis str. Sterne]				2.4.1.-	
26875, 26876	48854156	37	6.00E-36	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]					2.7.3.-

26879,	51245968	47	4.00E-28	Desulfotalea psychrophila LSV54	hypothetical membrane protein [Desulfotalea psychrophila LSV54]			
26880	48856366	53	1.00E-69	Cytophaga hutchinsonii	COG2120: Uncharacterized proteins, LmbE homologs [Cytophaga hutchinsonii]			
26881,	48855439	42	3.00E-52	Cytophaga hutchinsonii	COG0084: Mg-dependent DNase [Cytophaga hutchinsonii]			3.1.21.-
26882,	48856312	28	4.00E-10	Cytophaga hutchinsonii	hypothetical protein Chut02000024 [Cytophaga hutchinsonii]			
26883,				Porphyromonas gingivalis W83	hypothetical protein PG0482 [Porphyromonas gingivalis W83]			
26884	34396610	39	1.00E-22	Acinetobacter sp. ADP1	ref[NP_904777.1] hypothetical protein PG0482 [Porphyromonas gingivalis W83]			
26885,				Cytophaga hutchinsonii	putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1]			4.1.99.4
26886	50083970	49	5.00E-48	Cytophaga hutchinsonii	emb[CAG67658.1] putative D-cysteine desulfhydrase (DcyD) [Acinetobacter sp. ADP1]			
26887,	48856992	53	2.00E-56	Cytophaga hutchinsonii	COG0702: Predicted nucleoside-diphosphate-sugar epimerases [Cytophaga hutchinsonii]			
26888	48855382	59	3.00E-35	Cytophaga hutchinsonii	COG0294: Dihydropteroate synthase and related enzymes [Cytophaga hutchinsonii]			2.5.1.15
26889,	37222114	49	6.00E-48	uncultured bacterium	Uvs065 [uncultured bacterium]			
26890	29346772	47	5.00E-18	Bacteroides thetaiotaomicron VPI-5482	flavoprotein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76469.1			6.3.2.5
26891,				Nostoc punctiforme PCC 73102	COG1020: Non-ribosomal peptide synthetase modules and related proteins [Nostoc punctiforme PCC 73102]			1.2.1.31
26892	23129356	36	2.00E-30	Cytophaga hutchinsonii	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Cytophaga hutchinsonii]			2.1.1.-
26893,	48854545	50	5.00E-59	Cytophaga hutchinsonii	COG1033: Predicted exporters of the RND superfamily [Cytophaga hutchinsonii]			
26894	48854362	41	1.00E-61	Cytophaga hutchinsonii	COG4339: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
26895,	48854285	47	3.00E-55	Cytophaga hutchinsonii	tyrosine-protein kinase [Bacteroides fragilis YCH46]			2.7.1.11
26896	53714061	29	1.00E-26	Bacteroides fragilis YCH46	tyrosine-protein kinase [Bacteroides fragilis YCH46]			2
26897,				Porphyromonas gingivalis W83	glucose-inhibited division protein B [Porphyromonas gingivalis W83]			
26898	34397317	46	8.00E-26	Porphyromonas gingivalis W83	ref[NP_905481.1] glucose-inhibited division protein B [Porphyromonas gingivalis W83] sp Q7MV10 GIDB_PORGI Methyltransferase gldB (Glucose inhibited division protein B)			

2707,	53693278	35	5.00E-08	Pseudomonas syringae pv. syringae B728a	hypothetical protein Psyr03004855 [Pseudomonas syringae pv. syringae B728a]			
2708								
2709,	54031433	24	4.00E-07	Polaromonas sp. JS666	hypothetical protein PJS6w01001809 [Polaromonas sp. JS666]			
2710					probable topoisomerase IV, subunit B [Desulfotalea psychrophila LSV54]			
271,					emb[CAG37009.1] probable topoisomerase IV, subunit B [Desulfotalea psychrophila LSV54]			5.99.1.-
272	51246132	56	8.00E-59	Desulfotalea psychrophila LSV54				
2715,					conserved hypothetical protein [Plasmodium berghei]			
2716	56494344	26	2.00E-07	Plasmodium berghei				
2717,					TonB [Bacteroides thetaiotaomicron VPI-5482] gb AAO79003.1 TonB			
2718	29349306	36	8.00E-15	Bacteroides thetaiotaomicron VPI-5482	[Bacteroides thetaiotaomicron VPI-5482]			
2721,					phosphoribosylglycinamide formyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78466.1 phosphoribosylglycinamide formyltransferase			2.1.2.2
2722	29348769	50	1.00E-24	Bacteroides thetaiotaomicron VPI-5482	[Bacteroides thetaiotaomicron VPI-5482]			
2731,					hypothetical protein SF0994 [Shigella flexneri 2a str. 301] gb AAO42622.2 orf, conserved hypothetical protein [Shigella flexneri 2a str. 301]			
2732	56479791	46	2.00E-31	Shigella flexneri 2a str. 301	ref NP_836701.1 hypothetical protein S1062 [Shigella flexneri 2a str. 24571] gb AAP16507.1 hypothetical protein S1062 [Shigella flexneri 2a str. 24571]			
2733,					hypothetical protein b0992 [Escherichia coli K12] gb AAC74077.1 orf,			
2734	16128958	49	6.00E-54	Escherichia coli K12	hypothetical protein; putative ferredoxin-type protein [Escherichia coli K12] db BAA36134.1 Hypothetical protein in sfa 3'region . [Escherichia coli K12] pir F64840 probable ferredoxin-like protein yccM - Escherichia coli (strain K-12) sp P52636 YCCM_EC01 Putative electron transport protein yccM			
2735,					two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] db BAC48127.1 two-component hybrid sensor and regulator			2.7.3.-
2736	27377973	48	8.00E-22	Bradyrhizobium japonicum USDA 110	[Bradyrhizobium japonicum USDA 110]			
2737,					cysteiny]-lRNA synthetase [uncultured crenarchaeote 74A4]			6.1.1.16
2738	15383990	58	2.00E-58	uncultured crenarchaeote 74A4				
2739,					PREDICTED: hypothetical protein XP_540158 [Canis familiaris]			2.7.1.-
2740	57098579	31	2.00E-08	Canis familiaris	Desc:Arabidopsis thaliana protein fragment SEQ ID NO: 65704.			
2741,	AAG5174				Org:Arabidopsis thaliana			
2742	5	38	1.00E-38					
2743,					COG0706: Preprotein translocase subunit YidC [Cytophaga hutchinsonii]			
2744	48854398	37	4.00E-15	Cytophaga hutchinsonii				

2745,	48854398	45	2.00E-14	Cytophaga hutchinsonii	COG0706: Preprotein translocase subunit YidC [Cytophaga hutchinsonii]				
2746				Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]				
2749,	48855448	30	7.00E-25	Cytophaga hutchinsonii					
2750				Anopheles gambiae	ENSANGP00000000470 [Anopheles gambiae]				2.3.1.-
2751,	31195995	54	1.00E-39		Sensory transduction histidine kinase [Methanococcus maripaludis S2]				2.7.3.-
2752				Methanococcus maripaludis S2	emb[CAF30859.1] Sensory transduction histidine kinase [Methanococcus maripaludis S2]				
2753,	45358866	38	9.00E-33	Cytophaga hutchinsonii	SMC protein [Cytophaga hutchinsonii] ref ZP_00308092.1 COG1196:				
2754				Rhodospirillum rubrum	Chromosome segregation ATPases [Cytophaga hutchinsonii]				
2757,	28375463	71	1.00E-87	Cytophaga hutchinsonii	COG1434: Uncharacterized conserved protein [Rhodospirillum rubrum]				
2758				Cytophaga hutchinsonii	COG2332: Cytochrome c-type biogenesis protein CcmE [Cytophaga hutchinsonii]				
2759,	48766298	37	3.00E-21		two-component hybrid sensor and regulator [Nostoc sp. PCC 7120]				
2760				Nostoc sp. PCC 7120	pir JAG1928 two-component hybrid sensor and regulator aii0878 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB72935.1 two-component hybrid sensor and regulator [Nostoc sp. PCC 7120]				2.7.3.-
2761,	48855401	30	2.00E-07	Shewanella oneidensis MR-1	gamma-glutamyltranspeptidase [Shewanella oneidensis MR-1]				
2762				uncultured archaeon	gblAAN53817.1 gamma-glutamyltranspeptidase [Shewanella oneidensis MR-1]				2.3.2.2
2763,	17228473	41	9.00E-37	Treponema denticola ATCC 35405	hypothetical protein [uncultured archaeon]				
2764				Treponema denticola ATCC 35405	hypothetical protein TDE1723 [Treponema denticola ATCC 35405]				
2769,	24372330	45	1.00E-64	Cytophaga hutchinsonii	gblAAS12238.1 hypothetical protein TDE1723 [Treponema denticola ATCC 35405]				
2770				Cytophaga hutchinsonii	hypothetical protein Chut02000314 [Cytophaga hutchinsonii]				
277,	56295580	47	4.00E-26	Cytophaga hutchinsonii	hypothetical protein Chut02000253 [Cytophaga hutchinsonii]				
278				Cytophaga hutchinsonii	COG0854: Pyridoxal phosphate biosynthesis protein [Cytophaga hutchinsonii]				
2771,	42527229	38	1.00E-36	Bacteroides thetaiotaomicron VPI-5482	tryptophan synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482]				
2775,	48856580	48	3.00E-32	Bacteroides thetaiotaomicron VPI-5482	gblAAO75634.1 tryptophan synthase alpha chain [Bacteroides thetaiotaomicron VPI-5482]				4.2.1.20
2776				Bacteroides fragilis	Na+/H+ antiporter [Bacteroides fragilis YCH46]				
2785,	48856525	42	9.00E-16	Bacteroides fragilis	antiporter [Bacteroides fragilis YCH46]				
2786				Cytophaga hutchinsonii	COG0188: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit [Cytophaga hutchinsonii]				
2787,	48853523	67	4.00E-36						
2788									
2789,	29345937	51	1.00E-39						
2790									
279,	53711736	34	7.00E-14						
280									
2791,	48853743	37	2.00E-16						
2792									

2795,	48855969	59	1.00E-103	Cytophaga hutchinsonii	COG0841: Cation/multidrug efflux pump [Cytophaga hutchinsonii]				
2796				Microbulbifer	COG0749: DNA polymerase I - 3'-5' exonuclease and polymerase domains				2.7.7.7
2803,	48864493	36	2.00E-17	degradans 2-40	[Microbulbifer degradans 2-40]				
2804					two-component system sensor histidine kinase/response regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482]				
2805,	29345776	27	6.00E-13	Bacteroides thetaiotaomicron VPI-5482	gblAAO75473.1 two-component system sensor histidine kinase/response regulator, hybrid ('one component system') [Bacteroides thetaiotaomicron VPI-5482]				
2806					peptidyl-prolyl cis-trans isomerase SurA [Chlorobium tepidum TLS]				
2807,	21675072	35	4.00E-24	Chlorobium tepidum TLS	gblAAM73479.1 peptidyl-prolyl cis-trans isomerase SurA [Chlorobium tepidum TLS]				5.2.1.8
2808									
281,	48855210	48	1.00E-35	Cytophaga hutchinsonii	COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii]				
282					ORF8 [Bacteriophage phi-105] pfl[T13548 hypothetical protein 8 - Bacillus phage phi-105 db][BAA36665.1 ORF8 [Bacteriophage phi-105]				
2811,	22855032	34	8.00E-37	Bacteriophage phi-105					
2812									
2813,				Rubrobacter xylanophilus DSM	COG4585: Signal transduction histidine kinase [Rubrobacter xylanophilus DSM 9941]				2.7.3.-
2814	46106876	31	1.00E-13	9941					
2817,				Bradyrhizobium japonicum USDA	two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj[BAC48127.1] two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110]				2.7.3.-
2818	27377973	53	9.00E-29	110					
2819,				Bradyrhizobium japonicum USDA	two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj[BAC48127.1] two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110]				2.7.3.-
2820	27377973	50	1.00E-43	110					
2821,				Cytophaga hutchinsonii	COG3968: Uncharacterized protein related to glutamine synthetase [Cytophaga hutchinsonii]				6.3.1.2
2822	48856327	58	8.00E-68						
2823,				Novosphingobium aromaticivorans DSM	hypothetical protein Sar02001624 [Novosphingobium aromaticivorans DSM 12444]				
2824	48849513	30	8.00E-18	DSM 12444					
2825,				Listeria monocytogenes str. 4b F2365	hypothetical protein LMO2365_2347 [Listeria monocytogenes str. 4b F2365]				
2826	46908547	31	5.00E-11		gblAAT05113.1 conserved domain protein [Listeria monocytogenes str. 4b F2365]				
					glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gblAAL49448.1 unknown [Leptospira interrogans] gblAAK19913.1 unknown [Leptospira interrogans] gblAAS70700.1 glycosyltransferase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				
2829,				Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130					
2830	45657977	33	8.00E-13						
2833,				Cytophaga hutchinsonii	COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii]				
2834	48854312	57	1.00E-47						

2837, 2838	30248905	34	3.00E-10	Nitrosomonas europaea ATCC 19718	PDZ domain (also known as DHR or GLGF) [Nitrosomonas europaea ATCC 19718] emb CAD84812.1 PDZ domain (also known as DHR or GLGF) [Nitrosomonas europaea ATCC 19718]			3.4.21.-
2841, 2842	29346358	50	1.00E-34	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0948 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76055.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
2843, 2844	56460817	39	5.00E-48	Idiomarina loihiensis L2TR	Predicted amidohydrolase [Idiomarina loihiensis L2TR] gb AAV82549.1 Predicted amidohydrolase [Idiomarina loihiensis L2TR]			
285, 286						Eremothecium gossypii ATCC 10895 chromosome VI, complete sequence	## 5.00E-30	
2851, 2852	48862211	36	9.00E-41	Microbulbifer degradans 2-40	COG2989: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40]			
2853, 2854	15678563	60	8.00E-51	Methanothermobacter thermotrophicus str. Delta H	peptide methionine sulfoxide reductase [Methanothermobacter thermotrophicus str. Delta H] gb AAB8504.1.1 peptide methionine sulfoxide reductase [Methanothermobacter thermotrophicus str. Delta H] pir F69170 peptide methionine sulfoxide reductase - Methanobacterium thermotrophicum (strain Delta H) sp O26635 MSRA_METH Peptide methionine sulfoxide reductase msrA (Protein-methionine-S-oxide reductase) (Peptide Met(O) reductase)		1.8.4.6	
2855, 2856	49658888	50	1.00E-58	Yersinia pseudotuberculosis	hypothetical protein [Yersinia pseudotuberculosis]			
2857, 2858	53715647	43	3.00E-27	Bacteroides fragilis YCH46	putative endo-1,4-beta-xylanase [Bacteroides fragilis YCH46] dbj BAD51105.1 putative endo-1,4-beta-xylanase [Bacteroides fragilis YCH46]			
2859, 2860	48854355	50	2.00E-71	Cytophaga hutchinsonii	COG1200: RecG-like helicase [Cytophaga hutchinsonii]			3.6.1.-
2861, 2862	15678404	55	2.00E-39	Methanothermobacter thermotrophicus str. Delta H	hypothetical protein MTH376 [Methanothermobacter thermotrophicus str. Delta H] gb AAB84882.1 conserved protein [Methanothermobacter thermotrophicus str. Delta H] pir F69148 hypothetical protein MTH376 - Methanobacterium thermotrophicum (strain Delta H)			2.4.1.-
2863, 2864	16329400	42	2.00E-25	Synechocystis sp. PCC 6803	hypothetical protein sir1790 [Synechocystis sp. PCC 6803] sp P72793 YH90_SYNY3 Hypothetical UPF0093 protein sir1790 dbj BAA16808.1 sir1790 [Synechocystis sp. PCC 6803] pir S74656 hypothetical protein sir1790 - Synechocystis sp. (strain PCC 6803)			

2867, 2868	32041369	37	3.00E-41	Pseudomonas aeruginosa UCBPP- PA14	COG1864: DNA/RNA endonuclease G, NUC1 [Pseudomonas aeruginosa UCBPP-PA14]				
287, 288						Eremothecium gossypii ATCC 10895 chromosome VI, complete sequence	98	8.00E-26	
2881, 2882	48855793	28	5.00E-12	Cytophaga hutchinsonii	hypothetical protein Chut02001004 [Cytophaga hutchinsonii]				
2883, 2884	56678821	35	7.00E-08	Silicibacter pomeroi DSS-3	von Willebrand factor type A domain protein [Silicibacter pomeroi DSS-3] ref YP_167447.1 von Willebrand factor type A domain protein [Silicibacter pomeroi DSS-3]				
2885, 2886	27375314	28	2.00E-08	Bradyrhizobium japonicum USDA 110	hypothetical protein bli0203 [Bradyrhizobium japonicum USDA 110] db BAC45468.1 bli0203 [Bradyrhizobium japonicum USDA 110] conserved hypothetical protein 455 - Odontella sinensis chloroplast emb CAA91669.1 ORF455, homologous to Porphyra ORF565 [Odontella sinensis] ref NP_043637.1 ORF455 [Odontella sinensis] sp P49540 YC45_ODOSI HYPOTHETICAL 51.9 KD PROTEIN YCF45 (ORF455)				
289, 290	7484312	33	1.00E-16	Odontella sinensis		Cylindrotheca sp. chloroplast acyl carrier protein (ACP) gene, complete cds	83	1.00E-12	
2891, 2892	20090585	82	5.00E-62	Methanosarcina acetivorans C2A	hypothetical protein MA1733 [Methanosarcina acetivorans C2A] gb AA05140.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A]	Methanosarcina mazel strain Goe1, section 291 of 379 of the complete genome	84	4.00E-81	
2895, 2896	45917111	47	9.00E-29	Mesorhizobium sp. BNC1	COG3618: Predicted metal-dependent hydrolase of the TIM-barrel fold [Mesorhizobium sp. BNC1]			2.4.2.-	
2897, 2898	53712889	33	2.00E-20	Bacteroides fragilis YCH46	putative ABC transporter permease [Bacteroides fragilis YCH46] db BAD48347.1 putative ABC transporter permease [Bacteroides fragilis YCH46]				
2903, 2904	48855091	37	7.00E-36	Cytophaga hutchinsonii	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii]				3.1.1.61
2905, 2906	16331101	33	7.00E-42	Synechocystis sp. PCC 6803	hemolysin [Synechocystis sp. PCC 6803] sp P74409 Y260_SYNY3 Hypothetical UPF0053 protein sl0260 db BAA18507.1 hemolysin [Synechocystis sp. PCC 6803] pir IS76248 hemolysin, 49K - Synechocystis sp. (strain PCC 6803)				

2907, 2908	16077350	43	8.00E-18	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU02810 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12075.1 ycdD [Bacillus subtilis subsp. subtilis str. 168] pir F69755 L-alanyl-D-glutamate peptidase homolog ycdD - Bacillus subtilis dbj BAA22242.1 YcdD [Bacillus subtilis]				
2913, 2914	48855609	79	7.00E-67	Cytophaga hutchinsonii	COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii]		Bacteroides fragilis YCH46 DNA, complete genome	93	4.00E-07
2919, 2920	48860303	46	4.00E-43	Clostridium thermocellum ATCC 27405	COG0124: Histidyl-tRNA synthetase [Clostridium thermocellum ATCC 27405]				6.1.1.21
2923, 2924	48853834	69	2.00E-82	Cytophaga hutchinsonii	COG0536: Predicted GTPase [Cytophaga hutchinsonii]				
2925, 2926	42548894	40	1.00E-26	Gibberella zeae PH-1	hypothetical protein FG03048.1 [Gibberella zeae PH-1] ref XP_383224.1 hypothetical protein FG03048.1 [Gibberella zeae PH-1]				5.1.3.2
2931, 2932	21227192	46	3.00E-57	Methanosarcina mazel Go1	putative DNA integration/recombination/inversion protein [Methanosarcina mazel Go1] gb AAM30786.1 putative DNA integration/recombination/inversion protein [Methanosarcina mazel Goe1]				
2933, 2934	48854286	33	4.00E-38	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]				
2935, 2936	54303474	31	3.00E-11	Photobacterium profundum SS9	hypothetical protein PBPRB1809 [Photobacterium profundum SS9] emb CAG23667.1 hypothetical protein [Photobacterium profundum]				
2937, 2938	18977621	32	7.00E-30	Pyrococcus furfosus DSM 3638	putative ABC transporter [Pyrococcus furiosus DSM 3638] gb AAL81373.1 putative ABC transporter (ATP-binding protein) [Pyrococcus furiosus DSM 3638]				1.8.-
2939, 2940	45659189	48	7.00E-58	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_714399.1 CysC; CysN [Leptospira interrogans serovar Lai str. 56601] gb AAN51417.1 CysN; CysC [Leptospira interrogans serovar lai str. 56601] gb AAS71912.1 sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				2.7.7.4
2943, 2944	53757295	77	7.00E-61	Methylococcus capsulatus str. Bath	conserved hypothetical protein TIGR00149 [Methylococcus capsulatus str. Bath] ref YP_114605.1 conserved hypothetical protein TIGR00149		Legionella pneumophila subsp. pneumophila str. Philadelphia 1, complete genome	83	2.00E-12
2945, 2946	48853426	57	4.00E-51	Cytophaga hutchinsonii	COG2140: Thermophilic glucose-6-phosphate isomerase and related metalloenzymes [Cytophaga hutchinsonii]				1.13.11. 6

2947, 2948	28211859	47	8.00E-37	Clostridium tetani E88	succinoglycan biosynthesis protein exoA [Clostridium tetani E88] gb AAO36740.1 succinoglycan biosynthesis protein exoA [Clostridium tetani E88]			2.4.1.-
2953, 2954	53713424	35	1.00E-37	Bacteroides fragilis YCH46	ATP-dependent helicase [Bacteroides fragilis YCH46] dbj BAD48882.1 ATP-dependent helicase [Bacteroides fragilis YCH46] putative protein [Arabidopsis thaliana] emb CAA18134.1 putative protein [Arabidopsis thaliana] pIr T04597 hypothetical protein F23E13.170 - Arabidopsis thaliana			3.1.11.5
2955, 2956	7270581	39	4.00E-07	Arabidopsis thaliana	Arabidopsis thaliana			
2957, 2958	29350162	58	3.00E-97	Bacteroides thetataoamicon	putative cytosine-specific methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79859.1 putative cytosine-specific methyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.1.1.73
2959, 2960	34397767	54	1.00E-81	Porphyrromonas gingivalis W83	glycogen synthase-related protein [Porphyrromonas gingivalis W83] ref NP_905929.1 glycogen synthase-related protein [Porphyrromonas gingivalis W83]			2.4.1.21
2965, 2966	29349967	61	3.00E-37	Bacteroides thetataoamicon	hypothetical protein BT4559 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79664.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
2967, 2968	48853419	59	2.00E-37	Cytophaga hutchinsonii	COG0251: Putative translation initiation inhibitor, yjgF family [Cytophaga hutchinsonii]			
2969, 2970	48858374	51	7.00E-08	Clostridium thermocellum	COG2908: Uncharacterized protein conserved in bacteria [Clostridium thermocellum ATCC 27405]			
297, 298	48854724	46	3.00E-17	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-
2971, 2972	48835731	57	4.00E-30	Thermobifida fusca	COG0031: Cysteine synthase [Thermobifida fusca]			4.2.1.22
2973, 2974	53764771	32	1.00E-32	Anabaena variabilis ATCC 29413	COG0031: Cysteine synthase [Anabaena variabilis ATCC 29413]			4.2.1.22
2975, 2976	21227784	30	5.00E-25	Methanosarcina mazel Go1	DNA mismatch repair protein [Methanosarcina mazel Go1] gb AAM31378.1 DNA mismatch repair protein [Methanosarcina mazel Go1]			
2977, 2978	56680238	33	3.00E-16	Silicibacter pomeroi DSS-3	conserved hypothetical protein [Silicibacter pomeroi DSS-3] ref YP_168877.1 hypothetical protein SPO3682 [Silicibacter pomeroi DSS-3]			
2979, 2980	48856934	46	1.00E-69	Cytophaga hutchinsonii	COG1058: Predicted nucleotide-utilizing enzyme related to molybdopterin-biosynthesis enzyme MoeA [Cytophaga hutchinsonii]			
2981, 2982	41205694	41	4.00E-59	Geobacillus stearothermophilus	putative rhamnosyltransferase [Geobacillus stearothermophilus]			2.4.-.-

2983,	56783477	63	4.00E-96	Campylobacter jejuni	nucleotidyl-sugar pyranose mutase [Campylobacter jejuni]			4.2.1.46
2984				Cytophaga hutchinsonii	COG3021: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
2985,	48853539	32	7.00E-25	Cytophaga hutchinsonii				
2986				Cytophaga hutchinsonii	COG2217: Cation transport ATPase [Cytophaga hutchinsonii]			3.6.1.-
299,	48854664	44	6.00E-38	Cytophaga hutchinsonii	COG0034: Glutamine phosphoribosylpyrophosphate amidotransferase [Cytophaga hutchinsonii]			
2993,	48854452	56	3.00E-57	Cytophaga hutchinsonii				
2994				Cytophaga hutchinsonii	COG1109: Phosphomannomutase [Cytophaga hutchinsonii]			5.4.2.8
2995,	48854793	58	5.00E-75	Cytophaga hutchinsonii	related to O-succinylbenzoic acid-CoA ligase (MenE) [Desulfotalea psychrophila LSV54]			
2997,				Desulfotalea psychrophila LSV54	CoA ligase (MenE) [Desulfotalea psychrophila LSV54]			6.2.1.1
2998	51244102	35	1.00E-10	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3469 [Bacteroides thetaiotaomicron VPI-5482]			
2999,				Bacteroides thetaiotaomicron VPI-5482	gb AAO78575.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
3000	29348878	35	1.00E-18	Cytophaga hutchinsonii	COG0793: Periplasmic protease [Cytophaga hutchinsonii]			
3001,	48856115	34	2.00E-29	Cytophaga hutchinsonii				
3002				Desulfotalea psychrophila LSV54	COG4636: Uncharacterized protein conserved in cyanobacteria [Desulfotalea psychrophila LSV54]			
3003,				Desulfotalea psychrophila LSV54				
3004	23112865	40	3.00E-29	Desulfotalea psychrophila LSV54				
				Agrobacterium tumefaciens str. C58	GTP-binding elongation factor [Agrobacterium tumefaciens str. C58]			
3009,				Agrobacterium tumefaciens str. C58	gb AAL41263.1 GTP-binding elongation factor [Agrobacterium tumefaciens str. C58]			
3010	17934157	45	1.00E-78	Agrobacterium tumefaciens str. C58	C58] sp Q8UIQ2 LEPA_AGR15 GTP-binding protein lepA ref NP_353272.1			
				Mus musculus	hypothetical protein AGR_C_411 [Agrobacterium tumefaciens str. C58]			
301,				Mus musculus	pir A12605 GTP-binding elongation factor lepA [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir H97387 GTP-binding protein lepA [imported] - Agrobacterium tumefaciens (strain C58, Cereon)			
302	28077051	43	9.00E-28	Mus musculus	neurolysin (metallopeptidase M3 family) [Mus musculus] gb AAH16224.1			3.4.24.1
3011,				Mesorhizobium loti MAFF303099	Neurolysin (metallopeptidase M3 family) [Mus musculus] dbj BAC37533.1			6
3012	13471565	43	1.00E-38	Mesorhizobium loti MAFF303099	uncharacterized protein product [Mus musculus]			
3015,				Cytophaga hutchinsonii	hypothetical protein mif1575 [Mesorhizobium loti MAFF303099]			2.1.1.-
3016	48856245	54	2.00E-89	Cytophaga hutchinsonii	dbj BAB48917.1 mif1575 [Mesorhizobium loti MAFF303099]			
				Brucella suis 1330	COG1408: Predicted phosphohydrolases [Cytophaga hutchinsonii]			
3017,				Brucella suis 1330	type I restriction-modification system, M subunit [Brucella suis 1330]			
3018	23500570	43	1.00E-38	Brucella suis 1330	gb AAN34015.1 type I restriction-modification system, M subunit [Brucella suis 1330]			2.1.1.72

3019, 3020	48863731	30	1.00E-09	Microbulbifer degradans 2-40	COG0840: Methyl-accepting chemotaxis protein [Microbulbifer degradans 2-40]				
3021, 3022	37676553	45	4.00E-57	Vibrio vulnificus YJ016	methyl-accepting chemotaxis protein [Vibrio vulnificus YJ016] dbj BAC96919.1 methyl-accepting chemotaxis protein [Vibrio vulnificus YJ016]				
3025, 3026	15605828	28	8.00E-30	Aquifex aeolicus VF5	hypothetical protein ag_296 [Aquifex aeolicus VF5] gb AAC06608.1 hypothetical protein [Aquifex aeolicus VF5] pir A70327 conserved hypothetical protein ag_296 - Aquifex aeolicus				
3029, 3030	29346937	36	2.00E-42	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT1527 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76634.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
303, 304	53713020	41	3.00E-37	Bacteroides fragilis YCH46	slolate O-acetyltransferase [Bacteroides fragilis YCH46] dbj BAC56897.1 slolate O-acetyltransferase [Bacteroides fragilis YCH46] dbj BAD48478.1 slolate O-acetyltransferase [Bacteroides fragilis YCH46]				3.1.1.47
3031, 3032	48855460	32	2.00E-23	Cytophaga hutchinsonii	hypothetical protein Chut02001797 [Cytophaga hutchinsonii]				
3035, 3036	48853913	41	1.00E-24	Cytophaga hutchinsonii	COG0018: Arginyl-tRNA synthetase [Cytophaga hutchinsonii]				6.1.1.19
3039, 3040	48853471	32	7.00E-30	Cytophaga hutchinsonii	COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii]				
3041, 3042	30021268	37	5.00E-28	Bacillus cereus ATCC 14579	Pyrimidine Reductase [Bacillus cereus ATCC 14579] gb AAP10100.1 Pyrimidine Reductase [Bacillus cereus ATCC 14579]				
3043, 3044	34397897	50	1.00E-21	Porphyromonas gingivalis W83	CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83] ref NP_906059.1 CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83]				
3045, 3046	34397897	40	5.00E-34	Porphyromonas gingivalis W83	CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83] ref NP_906059.1 CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83]				
3047, 3048	41409487	34	3.00E-14	Mycobacterium avium subsp. paratuberculosis str. k10	hypothetical protein MAP3389c [Mycobacterium avium subsp. paratuberculosis str. k10] gb AA050939.1 hypothetical protein MAP3389c [Mycobacterium avium subsp. paratuberculosis str. k10]				2.7.3.-
305, 306	48854966	74	1.00E-51	Cytophaga hutchinsonii	COG0013: Alanyl-tRNA synthetase [Cytophaga hutchinsonii]	Aspergillus nidulans FGSC A4, AN9419.2 predicted mRNA	90	7.00E-08	6.1.1.7
3051, 3052	48771971	26	3.00E-14	Ralstonia metallidurans CH34	hypothetical protein Reu02000722 [Ralstonia metallidurans CH34]				

3053, 3054	29349375	35	4.00E-25	Bacteroides thetaiotaomicron VPI-5482	putative two-component system sensor protein histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79072.1 putative two-component system sensor protein histidine kinase [Bacteroides thetaiotaomicron VPI- 5482]				2.7.3.-
3057, 3058	48864231	27	1.00E-18	Microbulbifer degradans 2-40	COG0577: ABC-type antimicrobial peptide transport system, permease component [Microbulbifer degradans 2-40]				
3069, 3070	15644598	29	2.00E-19	Thermotoga maritima MSB8	sugar ABC transporter, periplasmic sugar-binding protein, putative [Thermotoga maritima MSB8] gb AAD36917.1 sugar ABC transporter, periplasmic sugar-binding protein, putative [Thermotoga maritima MSB8] pir H72203 hypothetical protein TM1855 - Thermotoga maritima (strain MSB8)				
307, 3071, 3072	48856298	45	2.00E-39	Cytophaga hutchinsonii	COG0317: Guanosine polyphosphate pyrophosphohydrolases/synthetases [Cytophaga hutchinsonii]				2.7.6.5
3073, 3074	48855418	64	1.00E-87	Cytophaga hutchinsonii	COG0535: Predicted Fe-S oxidoreductases [Cytophaga hutchinsonii]				
3075, 3076	48854274	40	6.00E-30	Cytophaga hutchinsonii	COG3239: Fatty acid desaturase [Cytophaga hutchinsonii]				1.14.99. 25
3077, 3078	54308824	47	3.00E-34	Photobacterium profundum SS9	Hypothetical acyltransferase family protein [Photobacterium profundum SS9] emb CAG20042.1 Hypothetical acyltransferase family protein [Photobacterium profundum]				2.3.1.51
3079, 3080	48839924	57	6.00E-45	Methanosarcina barkeri str. fusaro	COG5316: Uncharacterized conserved protein [Methanosarcina barkeri str. fusaro]				
3081, 3082	46907208	53	3.00E-13	Listeria monocytogenes str. 4b F2365	ribose 5-phosphate isomerase A [Listeria monocytogenes str. 4b F2365] gb AA103774.1 ribose 5-phosphate isomerase A [Listeria monocytogenes str. 4b F2365]				5.3.1.6
3083, 3084	30021199	33	2.00E-17	Bacillus cereus ATCC 14579	Phosphoenolpyruvate synthase [Bacillus cereus ATCC 14579] gb AAP10031.1 Phosphoenolpyruvate synthase [Bacillus cereus ATCC 14579]				2.7.9.2
3085, 3086	48853753	56	9.00E-65	Cytophaga hutchinsonii	COG0225: Peptide methionine sulfoxide reductase [Cytophaga hutchinsonii] putative oxidoreductase [Streptomyces avermitilis MA-4680] ref NP_822862.1 putative oxidoreductase [Streptomyces avermitilis MA- 4680]				1.8.4.6
3087, 3088	29605330	28	2.00E-15	Streptomyces avermitilis MA-4680	hypothetical protein [Pseudoalteromonas haloplanktis] putative N6-adenine-specific DNA methylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78361.1 putative N6-adenine-specific DNA methylase [Bacteroides thetaiotaomicron VPI-5482]				2.1.1.52
309, 310	2879819	34	2.00E-30	Pseudoalteromona s haloplanktis	hypothetical protein BT4447 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78552.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
3097, 3098	29348664	48	3.00E-12	Bacteroides thetaiotaomicron VPI-5482					
3097, 3098	29349855	38	5.00E-30	Bacteroides thetaiotaomicron VPI-5482					

3099, 3100	28211514	41	5.00E-14	cytochrome c-553	alcohol dehydrogenase [Cytochrome c-553], gamma chain-like protein [Clostridium tetani E88] gb AAO36395.1 alcohol dehydrogenase [cytochrome c-553], gamma chain-like protein [Clostridium tetani E88]			
3101, 3102	28211514	40	4.00E-14	cytochrome c-553	alcohol dehydrogenase [cytochrome c-553], gamma chain-like protein [Clostridium tetani E88] gb AAO36395.1 alcohol dehydrogenase [cytochrome c-553], gamma chain-like protein [Clostridium tetani E88]			
3103, 3104	48855539	54	6.00E-68	Cytophaga hutchinsonii	COG0142: Geranylgeranyl pyrophosphate synthase [Cytophaga hutchinsonii]			2.5.1.1
3105, 3106	48854339	56	2.00E-79	Cytophaga hutchinsonii	COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii]			
3109, 3110	48854025	47	2.00E-24	Cytophaga hutchinsonii	hypothetical protein Chut02003116 [Cytophaga hutchinsonii]			
311, 312	15679640	27	2.00E-11	Methanothermobacter thermautotrophicus str. Delta H	ABC transporter [Methanothermobacter thermautotrophicus str. Delta H] gb AAB86118.1 ABC transporter [Methanothermobacter thermautotrophicus str. Delta H] pir H69086 ABC transporter - Methanobacterium thermoautotrophicum (strain Delta H)			
3111, 3112	48891492	35	6.00E-33	Trichodesmium erythraeum IMS101	COG1110: Reverse gyrase [Trichodesmium erythraeum IMS101]			
3115, 3116	45531581	52	7.00E-19	Exiguobacterium sp. 255-15	COG0024: Methionine aminopeptidase [Exiguobacterium sp. 255-15]			3.4.11.1 8
3123, 3124	45358866	37	6.00E-33	Methanococcus maripaludis S2	Sensory transduction histidine kinase [Methanococcus maripaludis S2] emb CAF30859.1 Sensory transduction histidine kinase [Methanococcus maripaludis S2]			2.7.3.-
3125, 3126	48855162	44	1.00E-12	Cytophaga hutchinsonii	COG4095: Uncharacterized conserved protein [Cytophaga hutchinsonii]			
3127, 3128	39995705	40	7.00E-22	Geobacter sulfurreducens PCA	sigma-54 dependent DNA-binding response regulator [Geobacter sulfurreducens PCA] gb AAR33928.1 sigma-54 dependent DNA-binding response regulator [Geobacter sulfurreducens PCA]			2.7.3.-
3135, 3136	37519844	29	8.00E-25	Gloeobacter violaceus PCC 7421	hypothetical protein glr0275 [Gloeobacter violaceus PCC 7421] dbj BAC88216.1 glr0275 [Gloeobacter violaceus PCC 7421]			
3137, 3138	29349121	40	1.00E-31	Bacteroides thetaiotaomicron VPI-5482	D-alanine--D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78818.1 D-alanine--D-alanine ligase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A1F3 DDL_BACTN D-alanine--D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase)			6.3.2.4
3139, 3140	29345890	51	9.00E-53	Bacteroides thetaiotaomicron VPI-5482	glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75587.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.7.8.6
3147, 3148	31195951	48	2.00E-23	Anopheles gambiae	ENSANGP00000000471 [Anopheles gambiae]			1.1.1.95

3153, 3154	45656356	47	1.00E-28	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	hypothetical protein LIC10458 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_713968.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar Lai str. 56601] gb AAN50986.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar lai str. 56601] gb AAS69079.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				3.1.-
3155, 3156	53715428	58	8.00E-76	Bacteroides fragilis YCH46	histidine ammonia-lyase [Bacteroides fragilis YCH46] db BAD50886.1 histidine ammonia-lyase [Bacteroides fragilis YCH46]				4.3.1.3
3157, 3158	AAM5260	8	7.00E-93		Desc:Aquifex pyrophilus DNA ligase. Org:Aquifex pyrophilus				6.5.1.2
3161, 3162	48854685	47	2.00E-36	Cytophaga hutchinsonii	COG3832: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
3167, 3168	23297087	40	6.00E-07	Arabidopsis thaliana	unknown protein [Arabidopsis thaliana] ref NP_563980.2 leucine-rich repeat family protein [Arabidopsis thaliana]				
3169, 3170	53711736	34	3.00E-12	Bacteroides fragilis YCH46	Na+/H+ antiporter [Bacteroides fragilis YCH46] db BAD47194.1 Na+/H+ antiporter [Bacteroides fragilis YCH46]				
317, 318	29346409	28	4.00E-11	Bacteroides thetataomicron VPI-5482	putative acetyltransferase [Bacteroides thetataomicron VPI-5482] gb AAO76106.1 putative acetyltransferase [Bacteroides thetataomicron VPI-5482]				2.3.1.12 8
3171, 3172	51246614	29	9.00E-22	Desulfotalea psychrophila Lsv54	hypothetical protein DP2762 [Desulfotalea psychrophila Lsv54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila Lsv54]				2.1.1.14 4
3173, 3174	51246614	29	1.00E-21	Desulfotalea psychrophila Lsv54	hypothetical protein DP2762 [Desulfotalea psychrophila Lsv54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila Lsv54]				2.1.1.14 4
3175, 3176	48836108	56	7.00E-67	Thermobifida fusca	COG2268: Uncharacterized protein conserved in bacteria [Thermobifida fusca]				
3179, 3180	56459231	29	2.00E-34	Idiomarina loliensis L2TR	Membrane-associated protein [Idiomarina loliensis L2TR] gb AAV80963.1 Membrane-associated protein [Idiomarina loliensis L2TR]				2.4.1.15 1
3181, 3182	53712767	72	1.00E-31	Bacteroides fragilis YCH46	dioxygenase [Bacteroides fragilis YCH46] db BAD48225.1 dioxygenase [Bacteroides fragilis YCH46]				1.3.1.9
3185, 3186	48854993	39	6.00E-16	Cytophaga hutchinsonii	COG2989: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
3187, 3188	21674674	34	2.00E-43	Chlorobium tepidum TLS	hypothetical protein CT1862 [Chlorobium tepidum TLS] gb AAM73081.1 conserved hypothetical protein [Chlorobium tepidum TLS]				

3191, 3192	29348773	42	1.00E-21	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3364 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78470.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
3193, 3194	53715112	37	1.00E-59	Bacteroides fragilis YCH46	4-alpha-glucanotransferase [Bacteroides fragilis YCH46] dbj BAD50570.1 4-alpha-glucanotransferase [Bacteroides fragilis YCH46]				2.4.1.25
3203, 3204	31790364	45	6.00E-47	uncultured Acidobacteria bacterium Yersinia	putative glutamine cyclotransferase [uncultured Acidobacteria bacterium] putative DNA methyltransferase [Yersinia pseudotuberculosis IP 32953] emb CAH21036.1 putative DNA methyltransferase [Yersinia pseudotuberculosis IP 32953]				
3207, 3208	51596132	33	2.00E-31	pseudotuberculosis IP 32953	hypothetical protein HI0554 [Haemophilus influenzae Rd KW20] gb AAC22217.1 H. influenzae predicted coding region HI0554 [Haemophilus influenzae Rd KW20] pir E64009 hypothetical protein HI0554 - Haemophilus influenzae (strain Rd KW20) sp P44014 Y554_HAEIN Hypothetical protein HI0554				2.1.1.11 3
3209, 3210	16272498	35	9.00E-21	Haemophilus influenzae Rd KW20	COG0416: Fatty acid/phospholipid biosynthesis enzyme [Cytophaga hutchinsonii]				
3211, 3212	48853959	46	8.00E-27	Cytophaga hutchinsonii	COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii]				
3213, 3214	48855683	56	3.00E-36	Cytophaga hutchinsonii					
3215, 3216	AAW9850	4	35	4.00E-09	Desc:H. pylori GHPO 1224 protein. Org:Helicobacter pylori				2.1.1.72
3217, 3218	AAW9850	4	35	4.00E-09	Desc:H. pylori GHPO 1224 protein. Org:Helicobacter pylori				2.1.1.72
3219, 3220	ABP7901	3	62	2.00E-97	Desc:N. gonorrhoeae amino acid sequence SEQ ID 4556. Org:Neisseria gonorrhoeae				3.1.21.3
3221, 3222	48854777	47	2.00E-56	Cytophaga hutchinsonii	COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii]				
3223, 3224	15606832	35	2.00E-33	Aquifex aeolicus VF5	leucyl-tRNA synthetase beta subunit [Aquifex aeolicus VF5] gb AAC07608.1 leucyl-tRNA synthetase beta subunit [Aquifex aeolicus VF5] pir D70452 leucine-tRNA ligase (EC 6.1.1.4) beta chain - Aquifex aeolicus sp D67646 SYLB_AQUAE Leucyl-tRNA synthetase beta subunit (Leucine- tRNA ligase beta subunit) (LeuRS)				6.1.1.4
3225, 3226	17229731	32	7.00E-37	Nostoc sp. PCC 7120	two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] pir AH2085 two-component hybrid sensor and regulator all2239 [Imported] - Nostoc sp. (strain PCC 7120) dbj BAB73938.1 two-component hybrid sensor and regulator [Nostoc sp. PCC 7120]				2.7.3.-
3227, 3228	48854665	45	7.00E-45	Cytophaga hutchinsonii	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii]				

3237, 3238	9950513	51	5.00E-41	Pseudomonas aeruginosa PAO1	probable phosphate transporter [Pseudomonas aeruginosa PAO1] ref ZP_00137767.1 COG0306: Phosphate/sulphate permeases [Pseudomonas aeruginosa UCBPP-PA14] pir F83109 probable phosphate transporter PA4292 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_252982.1 probable phosphate transporter [Pseudomonas aeruginosa PAO1]				
3239, 3240	48856124	43	2.00E-20	Cytophaga hutchinsonii	COG0770: UDP-N-acetylmuramyl pentapeptide synthase [Cytophaga hutchinsonii]				6.3.2.15
3241, 3242	16125881	32	6.00E-14	Caulobacter crescentus CB15	hypothetical protein CC1635 [Caulobacter crescentus CB15] gb AAK23613.1 conserved hypothetical protein [Caulobacter crescentus CB15] pir A87452 conserved hypothetical protein CC1635 [imported] - Caulobacter crescentus				
3243, 3244	48856104	29	1.00E-07	Cytophaga hutchinsonii	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Cytophaga hutchinsonii]				
3245, 3246	48855273	40	3.00E-24	Cytophaga hutchinsonii	COG4731: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
3249, 3250	29346131	47	4.00E-60	Bacteroides thetaiotaomicron VPI-5482	DNA repair and recombination protein, putative helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75828.1 DNA repair and recombination protein, putative helicase [Bacteroides thetaiotaomicron VPI-5482]				
325, 326	56707295	33	2.00E-10	Francisella tularensis subsp. tularensis Schu 4	DNA helicase II [Francisella tularensis subsp. tularensis Schu 4] emb CAG44754.1 DNA helicase II [Francisella tularensis subsp. tularensis]				3.6.1.-
3251, 3252	1185191	57	6.00E-63	Odontella sinensis Bacillus thuringiensis serovar konkukian str. 97-27	ORF 644 [Odontella sinensis] pir S78301 hypothetical protein 644 - Odontella sinensis chloroplast ref NP_043642.1 ORF 644 [Odontella sinensis] sp P49825 FTSH ODOSI Cell division protein ftsH homolog	Odontella sinensis complete chloroplast genome	89	1.00E-07	3.4.24.-
3261, 3262	49479197	44	2.00E-18	Cytophaga hutchinsonii	alcohol dehydrogenase, zinc containing [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAT61399.1 alcohol dehydrogenase, zinc containing [Bacillus thuringiensis serovar konkukian str. 97-27]				1.1.1.1
3265, 3266	48855616	26	4.00E-22	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]				
3269, 3270	48856849	34	5.00E-25	Cytophaga hutchinsonii	COG0525: Valyl-tRNA synthetase [Cytophaga hutchinsonii]				6.1.1.9
327, 328	21243000	33	9.00E-09	Xanthomonas axonopodis pv. citri str. 306	helicase IV [Xanthomonas axonopodis pv. citri str. 306] gb AAM37118.1 helicase IV [Xanthomonas axonopodis pv. citri str. 306]				3.6.1.-

3279, 3280	52841151	66	2.00E-98	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	penicillin binding protein 3 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_123305.1 Peptidoglycan synthetase FtsI precursor [Legionella pneumophila str. Paris] gb AAU27003.1 penicillin binding protein 3 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH12128.1 Peptidoglycan synthetase FtsI precursor [Legionella pneumophila str. Paris]	2.3.2.-			
3281, 3282	52550184	57	1.00E-95	archaeon GZfos35D7	leucine-rich-repeat protein [uncultured archaeon GZfos35D7]	1.11.1.9			
329, 330	29348151	32	1.00E-13	Bacteroides thetaiotaomicron VPI-5482	integrase, site-specific recombinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77848.1 integrase, site-specific recombinase [Bacteroides thetaiotaomicron VPI-5482]				
3291, 3292	15669150	57	4.00E-63	Methanocaldococcus jannaschii DSM 2661	transaldolase [Methanocaldococcus jannaschii DSM 2661] gb AAB98962.1 transaldolase [Methanocaldococcus jannaschii DSM 2661] sp Q58370 TAL_MET_JA Probable transaldolase pir H64419 transaldolase (EC 2.2.1.2) - Methanococcus jannaschii	2.2.1.2			
3293, 3294	37222112	55	1.00E-63	uncultured bacterium	Uvs063 [uncultured bacterium]				
3301, 3302	53713100	29	5.00E-22	Bacteroides fragilis YCH46	TonB-dependent outer membrane receptor [Bacteroides fragilis YCH46] db BAD48558.1 TonB-dependent outer membrane receptor [Bacteroides fragilis YCH46]				
3307, 3308	52840856	50	3.00E-31	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	glyoxylase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_123011.1 hypothetical protein lpp0673 [Legionella pneumophila str. Paris] gb AAU26708.1 glyoxylase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH11821.1 hypothetical protein [Legionella pneumophila str. Paris]				
3309, 3310	23501343	36	1.00E-49	Brucella suis 1330	ABC transporter, ATP-binding/permease protein [Brucella suis 1330] gb AAN29385.1 ABC transporter, ATP-binding/permease protein [Brucella suis 1330]				
331, 332	48856037	56	2.00E-30	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]				
3313, 3314	56675038	41	9.00E-17	uncultured bacterium	cellulase [uncultured bacterium]				
3315, 3316	21241377	45	5.00E-47	Xanthomonas axonopodis pv. citri str. 306	endonuclease [Xanthomonas axonopodis pv. citri str. 306] gb AAM35495.1 endonuclease [Xanthomonas axonopodis pv. citri str. 306]	3.2.2.23			
3317, 3318	48860907	36	1.00E-28	Microbulbifer degradans 2-40	COG3279: Response regulator of the LysR/AigR family [Microbulbifer degradans 2-40]				

3319, 3320	18313142	29	6.00E-26	Pyrobaculum aerophilum str. IM2	hypothetical protein PAE2159 [Pyrobaculum aerophilum str. IM2] gb AAL63991.1 conserved hypothetical protein [Pyrobaculum aerophilum str. IM2]			1.5.5.-
3321, 3322	29349974	42	2.00E-38	Bacteroides thetataoimicron VPI-5482	two-component system response regulator protein [Bacteroides thetataoimicron VPI-5482] gb AAO79671.1 two-component system response regulator protein [Bacteroides thetataoimicron VPI-5482]			
3323, 3324	48854732	29	3.00E-15	Cytophaga hutchinsonii	COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii]			
3327, 3328	45856536	51	1.00E-21	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	hypothetical protein LIC10638 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS69259.1 conserved hypothetical protein [Leptospira Interrogans serovar Copenhageni str. Flocruz L1-130]			
3329, 3330	29345992	51	1.00E-20	Bacteroides thetataoimicron VPI-5482	hypothetical protein BT0582 [Bacteroides thetataoimicron VPI-5482] gb AAO75689.1 conserved hypothetical protein [Bacteroides thetataoimicron VPI-5482]			
333, 334	37520160	50	6.00E-46	Gloeobacter violaceus PCC 7421	hypothetical protein glr0591 [Gloeobacter violaceus PCC 7421] dbj BAC88532.1 glr0591 [Gloeobacter violaceus PCC 7421]			
3331, 3332	53715217	29	6.00E-18	Bacteroides fragilis YCH46	ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] dbj BAD50675.1 ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46]			3.6.1.-
3335, 3336	23501247	39	6.00E-19	Brucella suis 1330	DNA-binding response regulator, LuxR family [Brucella suis 1330] ref NP_540499.1 TRANSCRIPTIONAL REGULATORY PROTEIN DEGU [Brucella melitensis 16M] gb AAN29289.1 DNA-binding response regulator, LuxR family [Brucella suis 1330] gb AAL52763.1 two-component response regulator [Brucella melitensis 16M] pir AH3449 transcription regulatory protein degU [imported] - Brucella melitensis (strain 16M)			
3337, 3338	48856332	51	3.00E-22	Cytophaga hutchinsonii	hypothetical protein Chut0200044 [Cytophaga hutchinsonii]			
3339, 3340	29346104	56	4.00E-39	Bacteroides thetataoimicron VPI-5482	ABC transporter, ATP-binding protein [Bacteroides thetataoimicron VPI- 5482] gb AAO75801.1 ABC transporter, ATP-binding protein [Bacteroides thetataoimicron VPI-5482]			1.8.-
3341, 3342	28850513	67	3.00E-36	Pseudomonas syringae pv. tomato str. DC3000	helicase domain protein [Pseudomonas syringae pv. tomato str. DC3000] ref NP_789898.1 helicase domain protein [Pseudomonas syringae pv. tomato str. DC3000]			
3345, 3346	48855191	51	9.00E-63	Cytophaga hutchinsonii	COG0842: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-

3349,	48854964	28	5.00E-29	Cytophaga hutchinsonii	COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii]			
3350				Cytophaga hutchinsonii				
3351,	48856102	47	3.00E-42	Cytophaga hutchinsonii	COG2353: Uncharacterized conserved protein [Cytophaga hutchinsonii]			
3352				Campylobacter coli RM2228	type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228] gbl[EAL56262.1] type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228]			2.1.1.72
3353,	57169027	34	7.00E-24	Campylobacter coli RM2228	type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228] gbl[EAL56262.1] type IIS restriction enzyme R and M protein (ECO57IR) [Campylobacter coli RM2228]			2.1.1.72
3355,	57169027	39	6.00E-19	Cytophaga hutchinsonii	COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii]			2.7.3.-
3356	48856489	49	1.00E-24	Geobacter metallireducens GS	COG0417: DNA polymerase elongation subunit (family B) [Geobacter metallireducens GS-15]			2.7.7.7
3357,	48845074	28	5.00E-20	15				
3358				Nostoc punctiforme PCC 73102	COG0514: Superfamily II DNA helicase [Nostoc punctiforme PCC 73102]			3.6.1.-
3363,	23125625	24	2.00E-16	Cytophaga hutchinsonii	hypothetical protein Chut02000134 [Cytophaga hutchinsonii]			
3366	48856416	39	4.00E-35	Mesorhizobium sp. BNC1	COG0057: Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Mesorhizobium sp. BNC1]			1.2.1.12
3369,	45684333	50	1.00E-19	Micromonospora echinospora	putative NAD dependent dehydrogenase [Micromonospora echinospora]			1.1.1.18
337,	45544475	35	2.00E-21	Bradyrhizobium japonicum USDA 110	two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj[BAC48127.1] two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110]			2.7.3.-
3371,	27377973	43	8.00E-34	Dehalococcoides ethenogenes 195	sensory box sensor histidine kinase [Dehalococcoides ethenogenes 195] gblAAW40550.1] sensory box sensor histidine kinase [Dehalococcoides ethenogenes 195]			2.7.3.-
3372	57235045	25	1.00E-19	Nostoc sp. PCC 7120	two-component hybrid sensor and regulator [Nostoc sp. PCC 7120] pir JAG1928 two-component hybrid sensor and regulator all0978 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB72935.1] two-component hybrid sensor and regulator [Nostoc sp. PCC 7120]			2.7.3.-
3375,				Cytophaga hutchinsonii	COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii]			
3376	17228473	41	9.00E-37	Cytophaga hutchinsonii	COG2137: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
3377,	48854312	56	1.00E-45	Cytophaga hutchinsonii				
3378	48854316	45	4.00E-32	Cytophaga hutchinsonii				

3389,	34396834	40	9.00E-33	Porphyrromonas gingivalis W83	D-alanine--D-alanine ligase [Porphyrromonas gingivalis W83] ref NP_905000.1 D-alanine-D-alanine ligase [Porphyrromonas gingivalis W83] sp Q7MWA2 DDL_PORGI D-alanine-D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase)				6.3.2.4
3390				Cytophaga hutchinsonii	hypothetical protein Chuf02001830 [Cytophaga hutchinsonii]				
3391,	48855491	41	1.00E-52	Idiomarina loihiensis L2TR	hypothetical protein IL0571 [Idiomarina loihiensis L2TR] gb AAV81412.1 Uncharacterized conserved protein [Idiomarina loihiensis L2TR]				
3392	56459680	24	3.00E-10	Trichodesmium erythraeum IMS101	COG0566: rRNA methylases [Trichodesmium erythraeum IMS101] hypothetical protein LIC20117 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_714691.1 conserved hypothetical protein [Leptospira interrogans serovar Lai str. 56601] gb AAN51706.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS72145.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				2.1.1.-
3399,	48891870	45	5.00E-51	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	hypothetical protein LIC12133 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70704.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				
3400	45655699	30	3.00E-16	Vibrio vulnificus CMCP6	Transcriptional activator HiyU [Vibrio vulnificus CMCP6] ref NP_933476.1 Transcriptional activator HiyU [Vibrio vulnificus YJ016] gb AAO09030.1 Transcriptional activator HiyU [Vibrio vulnificus CMCP6] dbj BAC93447.1 transcriptional activator [Vibrio vulnificus YJ016]				
3401,				Cytophaga hutchinsonii	COG0644: Dehydrogenases (flavoproteins) [Cytophaga hutchinsonii]				
3402	45657981	34	7.00E-22	Bacteroides thetaotaomicron VPI-5482	DNA primase [Bacteroides thetaotaomicron VPI-5482] gb AAO79037.1 DNA primase [Bacteroides thetaotaomicron VPI-5482]				2.7.7.-
3405,				Bacteroides fragilis YCH46	putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46] dbj BAD47418.1 putative outer membrane protein probably involved in nutrient binding [Bacteroides fragilis YCH46]				
3406	27363975	37	2.00E-10	Cytophaga hutchinsonii	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii]				2.7.3.-
3409,	48854244	44	2.00E-36						
3410	29349340	60	2.00E-31						
3413,									
3414	53711960	28	1.00E-23						
3417,									
3418	48854564	52	2.00E-66						
3423,									
3424									
3425,									
3426									

3427,	53715112	48				Bacteroides fragilis YCH46	4-alpha-glucanotransferase [Bacteroides fragilis YCH46] dbj BAD50570.1 4-alpha-glucanotransferase [Bacteroides fragilis YCH46]	Desc: Genomic sequence of Lactococcus lactis IL1403.	90	2.00E-07	2.4.1.25
3428	48856129	43				Cytophaga hutchinsonii	COG1011: Predicted hydrolase (HAD superfamily) [Cytophaga hutchinsonii]				3.8.1.2
343,	48853894	35				Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]				
3432						Vibrio cholerae O1 biovar eltor str. N16961	hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_232850.1 hypothetical protein VCA0458 [Vibrio cholerae O1 biovar eltor str. N16961] pir A82458 hypothetical protein VCA0458 [Imported] - Vibrio cholerae (strain N16961 serogroup O1)				
3433,	9657860	49				Cytophaga hutchinsonii	COG0327: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
3434	48856395	57				Staphylococcus aureus subsp. aureus COL	orotidine 5'-phosphate decarboxylase [Staphylococcus aureus subsp. aureus COL] ref YP_186079.1 orotidine 5'-phosphate decarboxylase [Staphylococcus aureus subsp. aureus COL]				4.1.1.23
3435,	57285959	48				Bacteroides thetaiotaomicron	ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gbj AAO78949.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]				3.6.1.-
3436	29349252	61				Cytophaga hutchinsonii	COG1250: 3-hydroxyacyl-CoA dehydrogenase [Cytophaga hutchinsonii]	Bacillus cereus ZK, complete genome	##	2.00E-07	1.1.1.35
3437,	48854116	59				Cytophaga hutchinsonii	COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii]				
3438	48853602	54				Cytophaga hutchinsonii	COG1793: ATP-dependent DNA ligase [Cytophaga hutchinsonii]				6.5.1.1
3439,	48853691	41				Cytophaga hutchinsonii	hypothetical protein Chut02002321 [Cytophaga hutchinsonii]				
3440	48854655	33				Cytophaga hutchinsonii	COG1280: Putative threonine efflux protein [Cytophaga hutchinsonii]				
3441,	48854337	27				Anabaena variabilis ATCC 29413	COG3541: Predicted nucleotidyltransferase [Anabaena variabilis ATCC 29413]				
3442						Crocospaera watsonii WH 8501	COG5635: Predicted NTPase (NACHT family) [Crocospaera watsonii WH 8501]				
3443,	50796980	61				Gallus gallus	PREDICTED: similar to Palo protein, partial [Gallus gallus]				

3469,	48856411	53	1.00E-63	Cytophaga hutchinsonii	COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii]				1.8.-
3470					COG2027: D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 4) [Cytophaga hutchinsonii]				3.4.16.4
3471,	48855045	33	2.00E-24	Cytophaga hutchinsonii					
3472									
3473,	23125186	36	4.00E-22	Nostoc punctiforme	hypothetical protein Npun02006402 [Nostoc punctiforme PCC 73102]				
3474				PCC 73102	isopentenyl-diphosphate delta-isomerase, putative [Chlorobium tepidum TLS] gb AAM71503.1 isopentenyl-diphosphate delta-isomerase, putative [Chlorobium tepidum TLS] sp Q8KFR5 ID12_CHLTE isopentenyl-diphosphate delta-isomerase (IPP isomerase) [isopentenyl pyrophosphate isomerase]				5.3.3.2
3475,	21673096	39	6.00E-45	Chlorobium tepidum TLS					
3476									
3477,	48855819	32	5.00E-33	Cytophaga hutchinsonii	COG3361: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
3478					COG4365: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
3479,	48856112	32	3.00E-26	Cytophaga hutchinsonii	putative phosphoacetate hydrolase [Rhodopseudomonas palustris CGA009] emb CAE29178.1 putative phosphoacetate hydrolase [Rhodopseudomonas palustris CGA009]				
3480					tetraacyldisaccharide 4'-kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76987.1 tetraacyldisaccharide 4'-kinase [Bacteroides thetaiotaomicron VPI-5482]				2.7.1.13
3481,	39936798	35	4.00E-10	Rhodopseudomonas palustris CGA009	gp109 [Mycobacteriophage Che9d] ref NP_818074.1 gp109 [Mycobacteriophage Che9d]				0
3482									
3483,	29347290	45	2.00E-66	Bacteroides thetaiotaomicron VPI-5482	Hypothetical Protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA23266.1 Hypothetical Protein [Fusobacterium nucleatum subsp. vincentii ATCC 49256]				
3484									
3485,	29425233	34	1.00E-07	Mycobacteriophage Che9d					
3486									
3487,				Fusobacterium nucleatum subsp. vincentii ATCC 49256					
3488	34764299	28	1.00E-06						
3489,									
3490	48855209	62	1.00E-68	Cytophaga hutchinsonii	COG0357: Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division [Cytophaga hutchinsonii]				
349,									
350	48855170	39	2.00E-35	Cytophaga hutchinsonii	COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii]				2.7.3.-
					glucose-inhibited division protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76252.1 glucose-inhibited division protein [Bacteroides thetaiotaomicron VPI-5482] sp Q8A8M2 GIDB_BACTN Methyltransferase gidB (Glucose inhibited division protein B)				
3493,				Bacteroides thetaiotaomicron VPI-5482					
3494	29346555	76	1.00E-39						

3495, 3496 3497, 3498	48855581 48856245	68 65	1.00E-92 1.00E-77	Cytophaga hutchinsonii Cytophaga hutchinsonii	COG0112: Glycine/serine hydroxymethyltransferase [Cytophaga hutchinsonii] COG1408: Predicted phosphohydrolases [Cytophaga hutchinsonii] guanosine-3,5-bis(diphosphate) 3-pyrophosphohydrolase [Coxiella burnetii RSA 493] gb AAO89860.1 guanosine-3,5-bis(diphosphate) 3- pyrophosphohydrolase [Coxiella burnetii RSA 493]	Photothabdus luminescens subsp. laumondii TTO1 complete genome; segment 12/17	89 5.00E-07	2.1.2.1
3499, 3500	29653654	54	2.00E-98	Coxiella burnetii RSA 493	carboxy-terminal protease [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref YP_122899.1 hypothetical protein lpp0561 [Legionella pneumophila str. Paris] ref YP_125903.1 hypothetical protein lpp0537 [Legionella pneumophila str. Lens] gb AAU26596.1 carboxy-terminal protease [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb CAH14767.1 hypothetical protein [Legionella pneumophila str. Lens] emb CAH11709.1 hypothetical protein [Legionella pneumophila str. Paris] COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Crocospaera watsonii WH 8501]			3.1.7.2
3501, 3502 3503, 3504	52840744 46119993	42 22	5.00E-29 3.00E-07	Legionella pneumophila subsp. pneumophila str. Philadelphia 1 Crocospaera watsonii WH 8501				3.4.2.1- 2.3.1.51
3505, 3506 3507, 3508	39995764 48855704	54 28	4.00E-65 1.00E-21	Geobacter sulfurreducens PCA Cytophaga hutchinsonii	CipB protein [Geobacter sulfurreducens PCA] gb AAR33988.1 CipB protein [Geobacter sulfurreducens PCA] sp Q74FF1 CLPB_GEOSL Chaperone clpB COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii]	Desc.N. meningitidis partial DNA sequence gmm_48 SEQ ID NO:48. Org:Neisseria meningitidis	90 8.00E-09	
3509, 3510	52550522	45	1.00E-55	uncultured archaeon GZfos9D8	BpmI endonuclease-methyltransferase fusion protein type IIG [uncultured archaeon GZfos9D8]			2.1.1.72
351, 352 3513, 3514 3515, 3516	23128081 48854656 48854655	50 54 29	5.00E-22 3.00E-48 1.00E-12	Nostoc punctiforme PCC 73102 Cytophaga hutchinsonii Cytophaga hutchinsonii	COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102] COG0348: Polyferredoxin [Cytophaga hutchinsonii] hypothetical protein Chut02002321 [Cytophaga hutchinsonii]			2.7.3.-

3521,	53688664	33	4.00E-21	Nostoc punctiforme PCC 73102	COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102]				2.7.3.-
3522									
3523,	48854120	58	8.00E-75	Cytophaga hutchinsonii	COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii]				6.2.1.3
3524									
3525,	48853532	28	2.00E-17	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]				
3526									
3529,	48854362	39	6.00E-34	Cytophaga hutchinsonii	COG1033: Predicted exporters of the RND superfamily [Cytophaga hutchinsonii]				
3530									
3531,				Bacteroides thetaiotaomicron	putative type II restriction endonuclease [Bacteroides thetaiotaomicron VPI-5482] gb AAO79119.1 putative type II restriction endonuclease [Bacteroides thetaiotaomicron VPI-5482]				3.1.21.4
3532	29349422	56	4.00E-45	VPI-5482					
3533,									
3534	13507849	28	2.00E-16	Mycoplasma pneumoniae M129	hypothetical protein MPN110 [Mycoplasma pneumoniae M129] gb AAB95692.1 conserved hypothetical protein [Mycoplasma pneumoniae M129] pir S73370 hypothetical protein C09_orf718 - Mycoplasma pneumoniae (strain ATCC 29342) sp P75452 YB10_MYCPN Hypothetical protein MPN110 [C09_orf718]				3.1.21.4
3535,									
3536	53713662	39	5.00E-14	Bacteroides fragilis YCH46	putative ABC transporter permease [Bacteroides fragilis YCH46] dbj BAD49120.1 putative ABC transporter permease [Bacteroides fragilis YCH46]				
3537,									
3538	28209998	36	6.00E-53	Clostridium tetani E88	DNA mismatch repair protein hexA [Clostridium tetani E88] gb AAO34879.1 DNA mismatch repair protein hexA [Clostridium tetani E88]				
3541,									
3542	51893980	65	1.00E-100	Symbiobacterium thermophilum IAM 14863	tyrosine phenol-lyase [Symbiobacterium thermophilum IAM 14863] dbj BAD41827.1 tyrosine phenol-lyase [Symbiobacterium thermophilum IAM 14863]	C.freundii tpi gene for tyrosine phenol-lyase	86	3.00E-18	4.1.99.2
3543,									
3544	42523437	32	4.00E-22	Bdellovibrio bacteriovorus HD100	hypothetical protein Bd1960 [Bdellovibrio bacteriovorus HD100] emb CAE79810.1 hypothetical protein predicted by Glimmer/Critica [Bdellovibrio bacteriovorus HD100]				
3545,									
3546	29349485	44	2.00E-41	Bacteroides thetaiotaomicron VPI-5482	endo-1,4-beta-xylanase Z precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79182.1 endo-1,4-beta-xylanase Z precursor [Bacteroides thetaiotaomicron VPI-5482]				
3547,									
3548	21674468	71	3.00E-44	Chlorobium tepidum TLS	leucyl-tRNA synthetase [Chlorobium tepidum TLS] gb AAM72875.1 leucyl-tRNA synthetase [Chlorobium tepidum TLS] sp Q8KBY2 SYL_CHL TE Leucyl-tRNA synthetase (Leucine-tRNA ligase) (LeuRS)				6.1.1.4
3549,									
3550	19704204	27	4.00E-07	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Hydrolase (HAD superfamily) [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95065.1 Hydrolase (HAD superfamily) [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]				

3551, 3552	29654168	27	2.00E-26	Coxiella burnetii RSA 493	asparagine synthetase B, glutamine-hydrolyzing [Coxiella burnetii RSA 493] gb AAO90374.1 asparagine synthetase B, glutamine-hydrolyzing [Coxiella burnetii RSA 493]				6.3.5.4
3553, 3554	29349611	49	1.00E-22	Bacteroides thetaiotaomicron VPI-5482	tRNA delta(2)-isopentenylpyrophosphate transferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79308.1 tRNA delta(2)- isopentenylpyrophosphate transferase [Bacteroides thetaiotaomicron VPI- 5482] sp Q8A018 MIAA_BACTN tRNA delta(2)-isopentenylpyrophosphate transferase (IPP transferase) (isopentenyl-diphosphate:tRNA isopentenyltransferase) (IPTase) (PPT)				2.5.1.8
3555, 3556	53714925	59	1.00E-48	Bacteroides fragilis YCH46	tRNA nucleotidyltransferase [Bacteroides fragilis YCH46] dbj BAD50383.1 tRNA nucleotidyltransferase [Bacteroides fragilis YCH46]				2.7.7.19
3561, 3562	29348110	67	3.00E-87	Bacteroides thetaiotaomicron VPI-5482	DNA-directed RNA polymerase alpha chain [Bacteroides thetaiotaomicron VPI-5482] gb AAO77807.1 DNA-directed RNA polymerase alpha chain [Bacteroides thetaiotaomicron VPI-5482] sp Q8A4A2 RPOA_BACTN DNA- directed RNA polymerase alpha chain (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit)				2.7.7.6
3563, 3564	21233830	63	2.00E-41	Proteus vulgaris	hypothetical protein Rts1_167 [Proteus vulgaris] dbj BAB93730.1				
3567, 3568	48855784	49	3.00E-62	Cytophaga hutchinsonii	COG1741: Pirin-related protein [Cytophaga hutchinsonii]				
357, 358	42557781	88	7.00E-95	uncultured crenarchaeote	putative valyl tRNA synthetase [uncultured crenarchaeote]	Uncultured crenarchaeote genomic fragment 54d9	93		0 6.1.1.9
3571, 3572	48853634	42	2.00E-19	Cytophaga hutchinsonii	COG0564: Pseudouridylyl synthases, 23S RNA-specific [Cytophaga hutchinsonii] conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228]				4.2.1.70
3573, 3574	57169084	54	1.00E-22	Campylobacter coli RM2228	putative ABC transporter permease [Bacteroides fragilis YCH46] dbj BAD48347.1 putative ABC transporter permease [Bacteroides fragilis YCH46]				
3575, 3576	53712889	28	2.00E-20	Bacteroides fragilis YCH46	COG0608: Single-stranded DNA-specific exonuclease [Cytophaga hutchinsonii]				3.1.--
3579, 3580	48854369	36	3.00E-19	Cytophaga hutchinsonii	ENSANGP00000013062 [Anopheles gambiae]				
3581, 3582	31211505	32	3.00E-07	Anopheles gambiae	COG0156: 7-keto-8-aminopelargonate synthetase and related enzymes [Cytophaga hutchinsonii]				2.3.1.47
3583, 3584	48855098	68	1.00E-82	Cytophaga hutchinsonii					

3585, 3586	53795203	45	2.00E-40	Chloroflexus aurantiacus	COG1680: Beta-lactamase class C and other penicillin binding proteins [Chloroflexus aurantiacus]			3.5.2.6
3589, 3590	23003059	34	1.00E-14	Lactobacillus gasseri	COG0266: Formamidopyrimidine-DNA glycosylase [Lactobacillus gasser]			3.2.2.23
359, 360	24214122	39	4.00E-28	Leptospira interrogans serovar Lai str. 56601	Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gbl AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601]			
3591, 3592	48855418	64	9.00E-99	Cytophaga hutchinsonii	COG0535: Predicted Fe-S oxidoreductases [Cytophaga hutchinsonii]			
3593, 3594	48845408	47	4.00E-21	Geobacter metallireducens GS-15	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Geobacter metallireducens GS-15] conserved hypothetical protein [Neisseria meningitidis MC58] pir [G81000 conserved hypothetical protein NMB2153 [imported] - Neisseria meningitidis (strain MC58 serogroup B) ref NP_275138.1 hypothetical protein NMB2153 [Neisseria meningitidis MC58]			3.4.13.9
3597, 3598	7227411	47	5.00E-47	Neisseria meningitidis MC58	SrA-binding protein [Bacteroides thetaiotaomicron VPI-5482] gbl AAO75286.1 SrA-binding protein [Bacteroides thetaiotaomicron VPI-5482] sp [Q8ABD1 SSRP_BACTN SrA-binding protein sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_714399.1 CysC; CysN [Leptospira interrogans serovar Lai str. 56601] gbl AAN51417.1 CysN; CysC [Leptospira interrogans serovar lai str. 56601] gbl AAS71912.1 sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			2.7.7.4
3603, 3604	45659189	50	3.00E-74	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	COG2895: GTPases - Sulfate adenylyltransferase subunit 1 [Cytophaga hutchinsonii]			2.7.7.4
3605, 3606	48856062	56	3.00E-82	Cytophaga hutchinsonii	COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Cytophaga hutchinsonii]			
3609, 3610	48853493	29	4.00E-11	Cytophaga hutchinsonii	Glu-tRNA amidotransferase, subunit B (gatB-1) [Archaeoglobus fulgidus DSM 4304] gbl AAB89807.1 Glu-tRNA amidotransferase, subunit B (gatB-1) [Archaeoglobus fulgidus DSM 4304] pir [G69429 Glu-tRNA amidotransferase, subunit B (gatB-1) homolog - Archaeoglobus fulgidus sp O28832 GATE_ARCFU Glutaryl-tRNA(Gln) amidotransferase subunit E (Glu-ADT subunit E)]			6.3.5.-
361, 362	11499035	32	9.00E-19	Archaeoglobus fulgidus DSM 4304	Methanosarcina mazel strain Goe1, section 214 of 379 of the complete genome			82 1.00E-16 2.1.1.-
3611, 3612	21228051	77	5.00E-70	Methanosarcina mazel Go1				

3613, 3614	21228051	70	4.00E-46	Methanosarcina mazel Go1	methyltransferase [Methanosarcina mazel Go1] gb AAM31645.1]	Methanosarcina mazel strain Goe1, section 214 of 379 of the complete genome	82	8.00E-17	2.1.1.1.-
3615, 3616	51892431	32	2.00E-25	Symbiobacterium thermophilum IAM 14863	hypothetical protein STH1293 [Symbiobacterium thermophilum IAM 14863] dbj BAD40278.1] conserved hypothetical protein [Symbiobacterium thermophilum IAM 14863]				
3617, 3618	20808965	45	5.00E-29	Thermoanaerobacter tengcongensis MB4	Homoserine dehydrogenase [Thermoanaerobacter tengcongensis MB4] gb AAM25740.1] Homoserine dehydrogenase [Thermoanaerobacter tengcongensis MB4]			1.1.1.3	
3619, 3620	15613411	41	2.00E-18	Bacillus halodurans C-125	hypothetical protein BH0848 [Bacillus halodurans C-125] dbj BAB04567.1] BH0848 [Bacillus halodurans C-125] pir H83755 hypothetical protein BH0848 [imported] - Bacillus halodurans (strain C-125)				
3621, 3622	48863150	39	3.00E-22	Microbulbifer degradans 2-40	COG4166: ABC-type oligopeptide transport system, periplasmic component [Microbulbifer degradans 2-40]				
3623, 3624	55246932	45	4.00E-35	Anopheles gambiae str. PEST	ENSANGP00000029270 [Anopheles gambiae str. PEST] ref XP_561015.1] ENSANGP00000029270 [Anopheles gambiae str. PEST]			4.2.1.46	
3625, 3626	27380888	48	5.00E-26	Bradyrhizobium japonicum USDA 110	hypothetical protein bfr5777 [Bradyrhizobium japonicum USDA 110] dbj BAC51042.1] bfr5777 [Bradyrhizobium japonicum USDA 110]				
3627, 3628	49235065	28	1.00E-12	Moorella thermoacetica ATCC 39073	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Moorella thermoacetica ATCC 39073]				
363, 364	54310134	43	3.00E-42	Photobacterium profundum SS9	putative chorismate mutase/prephenate dehydratase [Photobacterium profundum SS9] emb CAG21352.1] putative chorismate mutase/prephenate dehydratase [Photobacterium profundum]			4.2.1.51	
3633, 3634	13473959	39	6.00E-09	Mesorhizobium loti MAFF303099	hypothetical protein mlr4723 [Mesorhizobium loti MAFF303099] dbj BAB51313.1] mlr4723 [Mesorhizobium loti MAFF303099]				
3635, 3636	48855120	51	4.00E-32	Cytophaga hutchinsonii	COG0495: Leucyl-tRNA synthetase [Cytophaga hutchinsonii]			6.1.1.4	
3637, 3638	30249879	40	2.00E-22	Nitrosomonas europaea ATCC 19718	Sulfate transporter [Nitrosomonas europaea ATCC 19718] emb CAD85838.1] Sulfate transporter [Nitrosomonas europaea ATCC 19718]				
3641, 3642	33862809	29	3.00E-19	Prochlorococcus marinus str. MIT 9313	putative oxidoreductase [Prochlorococcus marinus str. MIT 9313] emb CAE20711.1] putative oxidoreductase [Prochlorococcus marinus str. MIT 9313]			1.---	

3649,					Xanthomonas campestris pv. campestris str. ATCC 33913	hypotheical protein XCC2739 [Xanthomonas campestris pv. campestris str. ATCC 33913] gblAAM42011.1] conserved hypotheical protein [Xanthomonas campestris pv. campestris str. ATCC 33913]				
3650,	21232170	33	2.00E-25		Xanthomonas campestris str. ATCC 33913					
3651,	48853721	35	1.00E-11		Cytophaga hutchinsonii	hypotheical protein Chut02003580 [Cytophaga hutchinsonii]				
3652	AAW7395	37	2.00E-28			Desc:Protoporphyrinogen oxidase protein. Org:Glycine max				1.3.3.4
3661,					Anabaena variabilis ATCC 29413	COG0642: Signal transduction histidine kinase [Anabaena variabilis ATCC 29413]				2.7.3.-
3662	45507334	52	2.00E-24							
3663,					Methanothermobacter thermautotrophicus str. Delta H	hypotheical protein MTH296 [Methanothermobacter thermautotrophicus str. Delta H] gblAAB84802.1] unknown [Methanothermobacter thermautotrophicus str. Delta H] pirl[F69137 hypotheical protein MTH296 - Methanobacterium thermoautotrophicum (strain Delta H)]				
3664	15678324	38	8.00E-14							
3665,					Methanothermobacter thermautotrophicus str. Delta H	hypotheical protein MTH296 [Methanothermobacter thermautotrophicus str. Delta H] gblAAB84802.1] unknown [Methanothermobacter thermautotrophicus str. Delta H] pirl[F69137 hypotheical protein MTH296 - Methanobacterium thermoautotrophicum (strain Delta H)]				
3666	15678324	38	4.00E-14							
3667,					Dechloromonas aromatica RCB	COG3459: Cellulose phosphorylase [Dechloromonas aromatica RCB]				
3668	46140702	37	3.00E-23							
3669,					Porphyromonas gingivalis W83	valyl-tRNA synthetase [Porphyromonas gingivalis W83] ref[NP_905340.1]				
3670	34397176	49	1.00E-61			valyl-tRNA synthetase [Porphyromonas gingivalis W83]			95	5.00E-07 6.1.1.9
3671,					Cytophaga hutchinsonii	COG0118: Glutamine amidotransferase [Cytophaga hutchinsonii]				2.4.2.-
3672	48855136	58	8.00E-33			Desc:Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3679. Org:Staphylococcus epidermidis				
3673,					Archaeoglobus fulgidus DSM 4304	hypotheical protein AF0276 [Archaeoglobus fulgidus DSM 4304]				
3674	ABP3883	43	2.00E-15			gblAAB90956.1] conserved hypotheical protein [Archaeoglobus fulgidus DSM 4304] pirl[D69284 conserved hypotheical protein AF0276 - Archaeoglobus fulgidus sp[O29963]Y276_ARCFU Hypotheical UPF0284 protein AF0276				
3675,	11497892	46	6.00E-58		Archaeoglobus fulgidus DSM 4304					
3676	48856513	48	2.00E-32		Cytophaga hutchinsonii	COG0307: Riboflavin synthase alpha chain [Cytophaga hutchinsonii]				2.5.1.9

3683, 3684	15898659	56	2.00E-24	Sulfolobus solfataricus P2	hypothetical protein SSO1867 [Sulfolobus solfataricus P2] gb AAK42054.1 Conserved hypothetical protein [Sulfolobus solfataricus P2] pir G90349 conserved hypothetical protein [imported] - Sulfolobus solfataricus polysaccharide biosynthesis protein [Shewanella oneidensis MR-1] gb AAN55507.1 polysaccharide biosynthesis protein [Shewanella oneidensis MR-1] putative dehydrogenase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79553.1 putative dehydrogenase [Bacteroides thetaiotaomicron VPI- 5482]				2.1.1.10 7	
3685, 3686	24374020	44	5.00E-40	Shewanella oneidensis MR-1						
3687, 3688	29349856	31	2.00E-31	Bacteroides thetataotaomicron VPI-5482						
369, 370	52841308	46	5.00E-40	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	hypothetical protein lpg1074 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU27160.1 hypothetical protein lpg1074 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]					
3691, 3692	53713591	35	1.00E-39	Bacteroides fragilis YCH46	hypothetical protein BF2302 [Bacteroides fragilis YCH46] dbj BAD49049.1 conserved hypothetical protein [Bacteroides fragilis YCH46]					
3697, 3698	28170110	34	1.00E-10	Vibrio vulnificus	unknown [Vibrio vulnificus]					
3699, 3700	48854153	70	3.00E-37	Cytophaga hutchinsonii	hypothetical protein Chut02003248 [Cytophaga hutchinsonii] putative heptosyltransferase [Bdellovibrio bacteriovorus HD100] emb CAE79382.1 putative heptosyltransferase [Bdellovibrio bacteriovorus HD100]					
37, 38	42523010	26	3.00E-10	Bdellovibrio bacteriovorus HD100						
3705, 3706	29349216	50	5.00E-57	Bacteroides thetataotaomicron VPI-5482	hypothetical protein BT3808 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78913.1 conserved hypothetical protein [Bacteroides thetataotaomicron VPI-5482]					
3707, 3708	21673004	60	3.00E-71	Chlorobium tepidum TLS	alpha oxoglutarate ferredoxin oxidoreductase, alpha subunit [Chlorobium tepidum TLS] gb AAM71411.1 alpha oxoglutarate ferredoxin oxidoreductase, alpha subunit [Chlorobium tepidum TLS]				1.2.7.3	
3709, 3710	56476832	35	1.00E-27	Azoarcus sp. EbN1	hypothetical protein eba2472 [Azoarcus sp. EbN1] emb CAI07520.1 hypothetical protein [Azoarcus sp. EbN1]					
371, 372	16126664	43	5.00E-13	Caulobacter crescentus CB15	hypothetical protein CC2425 [Caulobacter crescentus CB15] gb AAK24396.1 conserved hypothetical protein [Caulobacter crescentus CB15] pir H87549 conserved hypothetical protein CC2425 [imported] - Caulobacter crescentus					
3711, 3712	48856332	45	1.00E-24	Cytophaga hutchinsonii	hypothetical protein Chut02000044 [Cytophaga hutchinsonii]					
3713, 3714	AAB3573 8	48	2.00E-35		Desc:Alpha-galactosidase amino acid sequence SEQ ID 4. Org:Clostridium josui					3.2.1.22

3717, 3718	15896506	55	1.00E-41	Clostridium acetobutylicum ATCC 824	Methylated DNA-protein cysteine methyltransferase [Clostridium acetobutylicum ATCC 824] gb AAK81195.1 Methylated DNA-protein cysteine methyltransferase [Clostridium acetobutylicum ATCC 824] pir H97300 methylated DNA-protein cysteine methyltransferase [imported] - Clostridium acetobutylicum	2.1.1.63
3719, 3720	29348575	35	2.00E-18	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3166 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78272.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]	
3721, 3722	56461500	39	1.00E-47	Idiomarina loihensis L2TR	Capsular polyglutamate biosynthesis secreted protein CapB, ATP- dependent mur ligase family [Idiomarina loihensis L2TR] gb AAV83232.1 Capsular polyglutamate biosynthesis secreted protein CapB, ATP- dependent mur ligase family [Idiomarina loihensis L2TR]	6.3.2.-
3723, 3724	45657306	49	1.00E-55	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_712725.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar Lai str. 56601] gb AAN49743.1 Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar lai str. 56601] gb AAS70029.1 alpha/beta hydrolase superfamily [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]	
3725, 3726	23124495	60	3.00E-82	Nostoc punctiforme PCC 73102	COG0667: Predicted oxidoreductases (related to aryl-alcohol dehydrogenases) [Nostoc punctiforme PCC 73102]	1.-.-.-
3727, 3728	48861126	42	1.00E-45	Microbulbifer degradans 2-40	COG2303: Choline dehydrogenase and related flavoproteins [Microbulbifer degradans 2-40]	1.-.-.-
3729, 3730	48859646	40	2.00E-43	Clostridium thermocellum ATCC 27405	COG2189: Adenine specific DNA methylase Mod [Clostridium thermocellum ATCC 27405]	2.1.1.72
373, 374	32477896	39	2.00E-12	Rhodopirellula baltica SH 1	hypothetical protein RB13143 [Rhodopirellula baltica SH 1] emb CAD77988.1 hypothetical protein [Pirellula sp.]	
3731, 3732	39997334	46	5.00E-47	Geobacter sulfurreducens PCA	GTP pyrophosphokinase [Geobacter sulfurreducens PCA] gb AAR35612.1 GTP pyrophosphokinase [Geobacter sulfurreducens PCA]	2.7.6.5
3735, 3736	54295921	38	3.00E-11	Legionella pneumophila str. Paris	hypothetical protein plpp0078 [Legionella pneumophila str. Paris] emb CAH17255.1 hypothetical protein [Legionella pneumophila str. Paris]	

3739, 3740	20807120	69	1.00E-101	Thermoanaerobacter tengcongensis MB4	ATP-dependent protease Clp, ATPase subunit [Thermoanaerobacter tengcongensis MB4] gb AAM23895.1 ATP-dependent protease Clp, ATPase subunit [Thermoanaerobacter tengcongensis MB4] sp Q8RC24 CLPX_THEIN ATP-dependent Clp protease ATP-binding subunit clpX	Azospirillum brasilense trigger factor (tig), heat-shock protein ClpP (clpP), and heat-shock protein ClpX (clpX) genes, complete cds; and Lon protease (lon) gene, partial cds.	85	3.00E-92	3.4.24.-
3741, 3742	20806566	52	3.00E-64	Thermoanaerobacter tengcongensis MB4	Seryl-tRNA synthetase [Thermoanaerobacter tengcongensis MB4] gb AAM23341.1 Seryl-tRNA synthetase [Thermoanaerobacter tengcongensis MB4] sp Q8RDJ5 SYS_THEIN Seryl-tRNA synthetase (Serine--tRNA ligase) (SerRS)				6.1.1.11
3743, 3744	48855590	70	1.00E-116	Cytophaga hutchinsonii	COG1154: Deoxyxylulose-5-phosphate synthase [Cytophaga hutchinsonii]				4.1.3.37
3747, 3748	48856398	51	7.00E-42	Cytophaga hutchinsonii	COG0147: Anthranilate/para-aminobenzoate synthases component I [Cytophaga hutchinsonii]				4.1.3.-
3749, 3750	32473810	47	4.00E-60	Rhodopirellula balitica SH 1	probable aminopeptidase [Rhodopirellula balitica SH 1] emb CAD74344.1 probable aminopeptidase [Pirellula sp.]				
375, 376	48891840	35	1.00E-16	Trichodesmium erythraeum IMS101	COG1232: Protoporphyrinogen oxidase [Trichodesmium erythraeum IMS101]				1.3.3.4
3751, 3752	49235971	54	6.00E-14	Moorella thermoacetica ATCC 39073	COG1555: DNA uptake protein and related DNA-binding proteins [Moorella thermoacetica ATCC 39073]				
3755, 3756	42557743	31	6.00E-12	uncultured crenarchaeote	hypothetical protein [uncultured crenarchaeote]				
3757, 3758	53714487	56	1.00E-43	Bacteroides fragilis YCH46	SsrA-binding protein [Bacteroides fragilis YCH46] dbj BAD49945.1 SsrA-binding protein [Bacteroides fragilis YCH46]				
3759, 3760	48855337	64	3.00E-53	Cytophaga hutchinsonii	COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii]				
3775, 3776	42548894	41	3.00E-27	Gibberella zeae PH-1	hypothetical protein FG03048.1 [Gibberella zeae PH-1] ref XP_383224.1 hypothetical protein FG03048.1 [Gibberella zeae PH-1]				5.1.3.2
3777, 3778	53712889	36	2.00E-32	Bacteroides fragilis YCH46	putative ABC transporter permease [Bacteroides fragilis YCH46] dbj BAD48347.1 putative ABC transporter permease [Bacteroides fragilis YCH46]				
3779, 3780	16802005	34	2.00E-21	Listeria innocua Clp11262	hypothetical protein lin2946 [Listeria innocua Clp11262] emb CAC98171.1 lin2946 [Listeria innocua] p ir AC1800 hypothetical protein lin2946 [imported] Listeria innocua (strain Clp11262)				

3781, 3782, 3783, 3784, 3785, 3786, 3787, 3788, 379, 3793, 3794, 3797, 3798, 3803, 3804, 3805, 3806, 3807, 3808, 3809, 3810, 381, 382, 3813, 3814	53730651 31195995 23112518 48853493 2281663 48854463 53715112 20089111 42523157 53712342 15897361 57169064 39933400	25 54 40 32 57 58 30 69 23 60 35 32 33	1.00E-10 1.00E-39 1.00E-36 2.00E-14 1.00E-43 2.00E-34 5.00E-29 2.00E-53 2.00E-18 4.00E-86 2.00E-11 1.00E-10 4.00E-10	Dechloromonas aromatica RCB Anopheles gambiae Desulfotobacterium hafniense DCB-2 Cytophaga hutchinsonii Flavobacterium johnsoniae Cytophaga hutchinsonii Bacteroides fragilis YCH46 Methanosarcina acetivorans C2A Bdellovibrio bacteriovorus HD100 Bacteroides fragilis YCH46 Sulfolobus solfataricus P2 Campylobacter coli RM2228 Rhodopseudomonas palustris CGA009	COG0438: Glycosyltransferase [Dechloromonas aromatica RCB] ENSANGP00000000470 [Anopheles gambiae] COG1162: Predicted GTPases [Desulfotobacterium hafniense DCB-2] COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Cytophaga hutchinsonii] gliding motility protein [Flavobacterium johnsoniae] pilT44443 gliding motility protein [imported] - Flavobacterium johnsoniae COG0193: Peptidyl-tRNA hydrolase [Cytophaga hutchinsonii] 4-alpha-glucanotransferase [Bacteroides fragilis YCH46] dbj BAD50570.1 4- alpha-glucanotransferase [Bacteroides fragilis YCH46] Xaa-Pro dipeptidase (cobalt-dependent) [Methanosarcina acetivorans C2A] gb AA03666.1 Xaa-Pro dipeptidase (cobalt-dependent) [Methanosarcina acetivorans str. C2A] Sensory box histidine kinase [Bdellovibrio bacteriovorus HD100] emb CAE79530.1 Sensory box histidine kinase [Bdellovibrio bacteriovorus HD100] valyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD47800.1 valyl- tRNA synthetase [Bacteroides fragilis YCH46] HAM1 protein [Sulfolobus solfataricus P2] gb AAK40756.1 HAM1 protein [Sulfolobus solfataricus P2] pir E90187 HAM1 protein [imported] - Sulfolobus solfataricus conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228] Protein of unknown function UPF0102 [Rhodopseudomonas palustris CGA009] emb CAE25767.1 Protein of unknown function UPF0102 [Rhodopseudomonas palustris CGA009]	90 92 92	5.00E-09 6.00E-10 6.1.1.9 2.7.3.- 6.1.1.9 3.6.1.15 3.1.-.-
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3815,	15644379	38	1.00E-09	Thermotoga maritima MSB8	hypothetical protein TM1631 [Thermotoga maritima MSB8] gbl AAD36698.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir G72229				
3816	48856757	31	3.00E-18	Cytophaga hutchinsonii	COG3735: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
3823,	53715867	50	1.00E-46	Bacteroides fragilis YCH46	putative xanthosine triphosphate pyrophosphatase [Bacteroides fragilis YCH46] dbj BAD51325.1 putative xanthosine triphosphate pyrophosphatase [Bacteroides fragilis YCH46]				2.7.7.56
3826	51891981	35	2.00E-39	Symbiobacterium thermophilum IAM 14863	two-component sensor histidine kinase [Symbiobacterium thermophilum IAM 14863] dbj BAD39828.1 two-component sensor histidine kinase [Symbiobacterium thermophilum IAM 14863]				2.7.3.-
3827,	51891981	36	1.00E-38	Symbiobacterium thermophilum IAM 14863	two-component sensor histidine kinase [Symbiobacterium thermophilum IAM 14863] dbj BAD39828.1 two-component sensor histidine kinase [Symbiobacterium thermophilum IAM 14863]				2.7.3.-
3831,	32472461	32	6.00E-19	Rhodopirellula baltica SH 1	conserved hypothetical protein-putative sodium:solute symporter [Rhodopirellula baltica SH 1] emb CAD73139.1 conserved hypothetical protein-putative sodium:solute symporter [Pirellula sp.]				
3833,	56494802	36	1.00E-19	Plasmodium berghel	thymidylate kinase, putative [Plasmodium berghel]				2.7.4.9
3835,	42523044	34	5.00E-43	Bdellovibrio bacteriovorus HD100	hypothetical protein Bd1537 [Bdellovibrio bacteriovorus HD100] emb CAE79417.1 hypothetical protein predicted by Glimmer/Critica				
3837,	45358689	37	9.00E-31	Methanococcus maripaludis S2	putative proliferating-cell nucleolar antigen [Methanococcus maripaludis S2] emb CAF30682.1 putative proliferating-cell nucleolar antigen [Methanococcus maripaludis S2]				2.1.1.-
3839,	48855704	26	3.00E-28	Cytophaga hutchinsonii	COG1629: Outer membrane receptor proteins, mostly Fe transport [Cytophaga hutchinsonii]				
3843,	48853471	38	9.00E-09	Cytophaga hutchinsonii	COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii]				
3845,	48853824	47	3.00E-68	Cytophaga hutchinsonii	COG0859: ADP-heptose:LPS heptosyltransferase [Cytophaga hutchinsonii]				
3849,	33593091	26	7.00E-08	Bordetella pertussis Tohama I	putative lipoprotein [Bordetella pertussis Tohama I] emb CAE42350.1 putative lipoprotein [Bordetella pertussis Tohama I]				
385,	48862505	40	1.00E-35	Microbulifer degradans 2-40	COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Microbulifer degradans 2-40]				2.7.3.-
3851,	48853176	34	2.00E-39	Ferroplasma acidarmanus	COG0624: Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacetylases [Ferroplasma acidarmanus]				3.5.1.16

3853, 3854	52550513	36	2.00E-08	uncultured archaeon GZfos9D8	conserved hypothetical protein [uncultured archaeon GZfos9D8]			
3859, 3860	29345424	24	1.00E-11	Bacteroides thetaitaomicron VPI-5482	rteA, two-component system histidine kinase, with response regulator receiver domain [Bacteroides thetaitaomicron VPI-5482] gb AAO75121.1 rteA, two-component system histidine kinase, with response regulator receiver domain [Bacteroides thetaitaomicron VPI-5482]			2.7.3.-
3861, 3862	53715302	53	2.00E-32	Bacteroides fragilis YCH46	adenylosuccinate lyase [Bacteroides fragilis YCH46] dbj BAD50760.1 adenylosuccinate lyase [Bacteroides fragilis YCH46]			4.3.2.2
3863, 3864	29349999	21	2.00E-10	Bacteroides thetaitaomicron VPI-5482	putative nitrogen utilization substance protein [Bacteroides thetaitaomicron VPI-5482] gb AAO79696.1 putative nitrogen utilization substance protein [Bacteroides thetaitaomicron VPI-5482]			
3865, 3866					Bacteroides fragilis YCH46 DNA, complete genome	90	6.00E-08	
3867, 3868	18314195	24	2.00E-08	Pyrobaculum aerophilum str. IM2	nitrate reductase subunit, conjectural [Pyrobaculum aerophilum str. IM2] gb AAL65044.1 nitrate reductase subunit, conjectural [Pyrobaculum aerophilum str. IM2]			
387, 388	48854286	42	2.00E-30	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]			
3871, 3872	42548911	30	6.00E-27	Gibberella zeae PH- 1	hypothetical protein FG03065.1 [Gibberella zeae PH-1] ref XP_383241.1 hypothetical protein FG03065.1 [Gibberella zeae PH-1]			
3873, 3874	29347149	56	2.00E-83	Bacteroides thetaitaomicron VPI-5482	exonuclease ABC subunit A [Bacteroides thetaitaomicron VPI-5482] gb AAO76846.1 exonuclease ABC subunit A [Bacteroides thetaitaomicron VPI-5482]			1.8.-
3875, 3876	48855211	43	3.00E-55	Cytophaga hutchinsonii	COG4953: Membrane carboxypeptidase/penicillin-binding protein PbpC [Cytophaga hutchinsonii]			2.4.2.-
3877, 3878	53714076	28	2.00E-16	Bacteroides fragilis YCH46	putative glycosyltransferase [Bacteroides fragilis YCH46] dbj BAD49534.1 putative glycosyltransferase [Bacteroides fragilis YCH46]			2.4.1.-
3879, 3880	28211867	40	6.00E-12	Clostridium tetani E88	glycosyl transferase [Clostridium tetani E88] gb AAO36748.1 glycosyl transferase [Clostridium tetani E88]			2.4.1.-
3881, 3882	48854367	38	8.00E-44	Cytophaga hutchinsonii	hypothetical protein Chut02003040 [Cytophaga hutchinsonii]			
3887, 3888	37521381	32	1.00E-09	Gloeobacter violaceus PCC 7421	hypothetical protein gl1812 [Gloeobacter violaceus PCC 7421] dbj BAC89753.1 gl1812 [Gloeobacter violaceus PCC 7421]			

389, 390	48856849	35	2.00E-30	Cytophaga hutchinsonii	COG0525: Valyl-tRNA synthetase [Cytophaga hutchinsonii] AGR_C_2408p [Agrobacterium tumefaciens str. C58] pir[C97518 hypothetical protein AGR_C_2408 [Imported] - Agrobacterium tumefaciens (strain C58, Cereon) ref NP_354315.1 hypothetical protein AGR_C_2408 [Agrobacterium tumefaciens str. C58]	Desc:Listeria monocytogenes 4b contig DNA sequence #315. Org:Listeria monocytogenes 4b	95	6.00E-07	6.1.1.9
3895, 3896	15156362	40	6.00E-16	Agrobacterium tumefaciens str. C58					
3899, 3900	53795436	34	8.00E-40	Chloroflexus aurantiacus					
39, 40	53715011	34	9.00E-32	Bacteroides fragilis YCH46	COG1232: Protoporphyrinogen oxidase [Chloroflexus aurantiacus] (tRNA and rRNA cytosine-C5-methylase [Bacteroides fragilis YCH46] db BAD50469.1 tRNA and rRNA cytosine-C5-methylase [Bacteroides fragilis YCH46]				
3905, 3906	29348744	36	7.00E-36	Bacteroides thetataomicron VPI-5482	hypothetical protein BT3335 [Bacteroides thetataomicron VPI-5482] gb AAO78441.1 hypothetical protein [Bacteroides thetataomicron VPI- 5482]				
3907, 3908	34557103	38	6.00E-59	Wolliella succinogenes DSM 1740	hypothetical protein WS0692 [Wolliella succinogenes DSM 1740] emb CAE09818.1 conserved hypothetical protein [Wolliella succinogenes]				
3909, 3910	48855680	58	2.00E-35	Cytophaga hutchinsonii	COG0071: Molecular chaperone (small heat shock protein) [Cytophaga hutchinsonii] conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_112939.1 hypothetical protein MCA0408 [Methylococcus capsulatus str. Bath]				
3913, 3914	53756150	34	2.00E-29	Methylococcus capsulatus str. Bath					
3915, 3916	45659045	54	3.00E-30	Leptospira interrogans serovar Copenhagani str. Fiocruz L1-130	Inorganic pyrophosphatase [Leptospira interrogans serovar Copenhagani str. Fiocruz L1-130] ref NP_714220.1 Soluble inorganic pyrophosphatase [Leptospira interrogans serovar Lai str. 56601] gb AAN51238.1 Soluble Inorganic pyrophosphatase [Leptospira interrogans serovar lai str. 56601] sp Q8EZ21 IPYR_LEPIN Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (PPase) gb AAS71768.1 Inorganic pyrophosphatase [Leptospira interrogans serovar Copenhagani str. Fiocruz L1-130] ATP-dependent protease Cip, ATPase subunit [Thermoanaerobacter tengcongensis MB4] gb AAM23895.1 ATP-dependent protease Cip, ATPase subunit [Thermoanaerobacter tengcongensis MB4] sp Q8RC24 CLPX_THETN ATP-dependent Cip protease ATP-binding subunit clpX			3.6.1.1	
3917, 3918	20807120	67	2.00E-94	Thermoanaerobact er tengcongensis MB4		Gloebacter violaceus PCC 7421 DNA, complete genome	84	7.00E-19	3.4.24.-

3923, 3924	48870695	41	7.00E-19	Pedococcus pentosaceus ATCC 25745	COG1234: Metal-dependent hydrolases of the beta-lactamase superfamily III [Pedococcus pentosaceus ATCC 25745]			
3925, 3926	28211584	38	4.00E-19	Clostridium tetani E88	histidyl-tRNA synthetase [Clostridium tetani E88] gb AAO36465.1 histidyl- tRNA synthetase [Clostridium tetani E88] sp Q892X7 SYH_CLOTE Histidyl- tRNA synthetase (Histidine-tRNA ligase) (HisRS)			6.1.1.21
3927, 3928	51573655	40	9.00E-10	Borrelia garinii PBI	isoleucyl-tRNA synthetase [Borrelia garinii PBI] ref YP_073272.1 isoleucyl- tRNA synthetase [Borrelia garinii PBI]			6.1.1.5
3929, 3930	13475838	36	8.00E-27	Mesorhizobium loti MAFF303099	hypothetical protein ml7009 [Mesorhizobium loti MAFF303099] dbj BAB53194.1 ml7009 [Mesorhizobium loti MAFF303099]			
393, 394	34397028	62	7.00E-59	Porphyromonas gingivalis W83	prolyl-tRNA synthetase [Porphyromonas gingivalis W83] ref NP_905193.1 prolyl-tRNA synthetase [Porphyromonas gingivalis W83]			6.1.1.15
3931, 3932	45657291	46	1.00E-33	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	acyl-CoA thioesterase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70014.1 acyl-CoA thioesterase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			3.1.2.-
3933, 3934	AAB3573 8	47	8.00E-35		Desc:Alpha-galactosidase amino acid sequence SEQ ID 4. Org:Clostridium josui			3.2.1.22
3937, 3938	23112865	41	1.00E-35	Desulfotobacterium hafnense DCB-2	COG4636: Uncharacterized protein conserved in cyanobacteria [Desulfotobacterium hafnense DCB-2]			
3939, 3940	48856298	62	1.00E-118	Cytophaga hutchinsonii	COG0317: Guanosine polyphosphate pyrophosphohydrolases/synthetases [Cytophaga hutchinsonii]			2.7.6.5
3941, 3942	56542586	31	8.00E-08	Zymomonas mobilis subsp. mobilis ZM4	conserved hypothetical protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_161851.1 hypothetical protein ZMO0116 [Zymomonas mobilis subsp. mobilis ZM4]			
3947, 3948	7489371	33	6.00E-16	Hordeum vulgare subsp. vulgare	endonuclease (EC 3.1.30.-) precursor - barley dbj BAA28942.1 endonuclease [Hordeum vulgare subsp. vulgare]			
3949, 3950	48855592	25	1.00E-17	Cytophaga hutchinsonii	COG1305: Transglutaminase-like enzymes, putative cysteine proteases [Cytophaga hutchinsonii]			
3953, 3954	48845393	49	2.00E-74	Geobacter metallireducens GS 15	COG0504: CTP synthase (UTP-ammonia lyase) [Geobacter metallireducens GS-15]			6.3.4.2
3957, 3958	48853733	30	2.00E-08	Cytophaga hutchinsonii	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii]			
3959, 3960	28170110	34	1.00E-10	Vibrio vulnificus	unknown [Vibrio vulnificus]			

3961,	48855076	67	1.00E-110	Cytophaga hutchinsonii	COG1251: NAD(P)H-nitrite reductase [Cytophaga hutchinsonii]				1.6.6.4
3962					COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii]				2.7.3.-
3963,	48855703	36	3.00E-32	Cytophaga hutchinsonii	excinuclease ABC subunit C [Bacteroides thetaiotaomicron VPI-5482]				
3964				Bacteroides thetaiotaomicron VPI-5482	excinuclease ABC subunit C [Bacteroides thetaiotaomicron VPI-5482]				
3965,	29348675	43	2.00E-73	Bacteroides thetaiotaomicron VPI-5482	deoxypurine kinase subunit [Oceanobacillus theyensis HTE831]				
3966					dbj BAC11971.1 deoxypurine kinase subunit [Oceanobacillus theyensis HTE831]				2.7.1.11 3
3967,	23097470	43	2.00E-40	Oceanobacillus theyensis HTE831					
3968				Geobacter metallireducens GS-15	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]				2.7.3.-
3969,	48846077	29	6.00E-13	uncultured archaeon	FOG TPR repeat [uncultured archaeon GZfos17F1]				
3970				Geobacter metallireducens GS-15					
3971,	52548588	27	3.00E-32	Geobacter metallireducens GS-15	COG0861: Membrane protein TerC, possibly involved in tellurium resistance [Geobacter metallireducens GS-15]				
3972,	48847199	51	8.00E-56	Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482]				
3973,	29347576	44	2.00E-65	Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-
3974,				Haloarcula marismortui ATCC 33049	putative sulfatase [Haloarcula marismortui ATCC 33049]				3.1.6.-
3975,	55377316	27	3.00E-17	Chlorobium tepidum TLS	putative sulfatase [Haloarcula marismortui ATCC 33049]				
3976,	21674674	36	5.00E-43	Chlorobium tepidum TLS	hypothetical protein CT1862 [Chlorobium tepidum TLS]				
3977,				Cytophaga hutchinsonii	conserved hypothetical protein [Chlorobium tepidum TLS]				
3978,	48855011	52	8.00E-54	Cytophaga hutchinsonii	COG0469: Pyruvate kinase [Cytophaga hutchinsonii]				2.7.1.40
3979,				Geobacillus kaustophilus HTA426	ABC transporter (ATP-binding protein) [Geobacillus kaustophilus HTA426]				
3980,	56418775	40	3.00E-32	Geobacillus kaustophilus HTA426	dbj BAD74525.1 ABC transporter (ATP-binding protein) [Geobacillus kaustophilus HTA426]				
3981,	48856688	39	1.00E-14	Cytophaga hutchinsonii	COG0726: Predicted xylanase/chitin deacetylase [Cytophaga hutchinsonii]				3.5.1.-
3982,									
3983,	48855209	49	5.00E-54	Cytophaga hutchinsonii	COG0357: Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division [Cytophaga hutchinsonii]				
3984,				Mannheimia succiniciproducens MBEL55E	hypothetical protein MS1906 [Mannheimia succiniciproducens MBEL55E]				
3985,	52425961	40	1.00E-18	Mannheimia succiniciproducens MBEL55E	dbj AAU38513.1 unknown [Mannheimia succiniciproducens MBEL55E]				3.8.1.2

3999, 4000	13475625	52	5.00E-44	Mesorhizobium loti MAFF303099	long chain acyl-CoA synthetase [Mesorhizobium loti MAFF303099]: dbj BAB52978.1 long chain acyl-CoA synthetase [Mesorhizobium loti MAFF303099]				6.2.1.3
4001, 4002	46445809	38	1.00E-16	Parachlamydia sp. UWE25	hypothetical protein pc0175 [Parachlamydia sp. UWE25] emb CAF22899.1 hypothetical protein [Parachlamydia sp. UWE25]				
4003, 4004	48855817	41	1.00E-14	Cytophaga hutchinsonii	COG0500: SAM-dependent methyltransferases [Cytophaga hutchinsonii]				
4013, 4014	48833968	47	3.00E-56	Magnetococcus sp. MC-1	COG0673: Predicted dehydrogenases and related proteins [Magnetococcus sp. MC-1]				1.1.1.18
4015, 4016	24371751	53	1.00E-53	Shewanella oneidensis MR-1	hypothetical SAM-dependent methyltransferase [Shewanella oneidensis MR- 1] gb AAN53238.1 conserved hypothetical protein [Shewanella oneidensis MR-1]				2.1.1.64
4017, 4018	48856843	56	5.00E-81	Cytophaga hutchinsonii	COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases [Cytophaga hutchinsonii]				6.2.1.1
4021, 4022	56421844	38	2.00E-17	Geobacillus kaustophilus HTA426	serine acetyltransferase [Geobacillus kaustophilus HTA426] dbj BAD77594.1 serine acetyltransferase [Geobacillus kaustophilus HTA426]				2.3.1.30
4023, 4024	45857668	42	5.00E-22	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	dihydroliipoamide dehydrogenase [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAS70391.1 dihydroliipoamide dehydrogenase [Leptospira interrogans serovar Copenhageni str. Flocruz L1- 130]				1.8.1.4
4025, 4026	32471201	38	2.00E-44	Rhodopirellula baltica SH 1	probable hexosyltransferase [Rhodopirellula baltica SH 1] emb CAD71871.1 probable hexosyltransferase [Pirellula sp.]				
4027, 4028	23130298	37	2.00E-25	Nostoc punctiforme PCC 73102	COG2319: FOG: WD40 repeat [Nostoc punctiforme PCC 73102]				2.7.1.37
4029, 4030	48855761	40	7.00E-31	Cytophaga hutchinsonii	COG0248: Exopolyphosphatase [Cytophaga hutchinsonii]				3.6.1.11
403, 404	53885426	33	8.00E-08	Desulfotobacterium hafnense DCB-2	COG1587: Uroporphyrinogen-III synthase [Desulfotobacterium hafnense DCB-2]				2.1.1.10 7
4031, 4032	48855761	41	6.00E-36	Cytophaga hutchinsonii	COG0248: Exopolyphosphatase [Cytophaga hutchinsonii]				3.6.1.11
4039, 4040	7225870	58	9.00E-55	Neisseria meningitidis MC58	inorganic pyrophosphatase [Neisseria meningitidis MC58] ref NP_273684.1 inorganic pyrophosphatase [Neisseria meningitidis MC58] pir F81175 inorganic pyrophosphatase NMB0641 [imported] - Neisseria meningitidis (strain MC58 serogroup B) sp Q9K0G4 IPYR_NEIMB Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (PPase)				3.6.1.1

4041, 4042	21674725	65	2.00E-92	Chlorobium tepidum TLS	DNA methylase, putative [Chlorobium tepidum TLS] gb AAM73132.1 DNA methylase, putative [Chlorobium tepidum TLS]				
4043, 4044	15669283	38	6.00E-40	Methanocaldococ- cus jannaschii DSM 2661	hypothetical protein MJ1095 [Methanocaldococcus jannaschii DSM 2661] gb AAB99098.1 conserved hypothetical protein [Methanocaldococcus jannaschii DSM 2661] pir F64436 hypothetical protein MJ1095 - Methanococcus jannaschii sp Q58495 YA95_METJA Hypothetical protein MJ1095				
4045, 4046	48854971	43	2.00E-32	Cytophaga hutchinsonii	COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii]				
4047, 4048	53764442	46	7.00E-74	Anabaena variabilis ATCC 29413	COG3280: Maltotriose trehalose synthase [Anabaena variabilis ATCC 29413]				2.4.1.-
4051, 4052	15894850	67	1.00E-102	Clostridium acetobutylicum ATCC 824	Fructose-1,6-bisphosphatase (YDE B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] gb AAK79539.1 Fructose-1,6-bisphosphatase (YDE B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] pir H97093 fructose-bisphosphatase (EC 3.1.3.11) [similarity] - Clostridium acetobutylicum	Desc:Staphylococ- cus epidermidis ORF nucleic acid sequence SEQ ID NO:1485. Org:Staphylococcus epidermidis	85	6.00E-13	3.1.3.11
4053, 4054	15894850	67	1.00E-122	Clostridium acetobutylicum ATCC 824	Fructose-1,6-bisphosphatase (YDE B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] gb AAK79539.1 Fructose-1,6-bisphosphatase (YDE B subtilis ortholog) [Clostridium acetobutylicum ATCC 824] pir H97093 fructose-bisphosphatase (EC 3.1.3.11) [similarity] - Clostridium acetobutylicum	Desc:Staphylococ- cus epidermidis ORF nucleic acid sequence SEQ ID NO:1485. Org:Staphylococcus epidermidis	88	5.00E-11	3.1.3.11
4055, 4056	48854003	23	2.00E-10	Cytophaga hutchinsonii	hypothetical protein Chut02003091 [Cytophaga hutchinsonii]				
4057, 4058	48856470	37	2.00E-19	Cytophaga hutchinsonii	COG2932: Predicted transcriptional regulator [Cytophaga hutchinsonii] heat shock protein (dnaJ) [Mycoplasma genitalium G-37] gb AAC71235.1 heat shock protein (dnaJ) [Mycoplasma genitalium G-37] pir A64202 heat shock protein dnaJ - Mycoplasma genitalium sp P47265 DNAJ_MYCGE Chaperone protein dnaJ				
4063, 4064	12044869	35	5.00E-30	Mycoplasma genitalium G-37	COG1472: Beta-glucosidase-related glycosidases [Cytophaga hutchinsonii]				
4065, 4066	48854182	33	2.00E-40	Cytophaga hutchinsonii	COG1472: Beta-glucosidase-related glycosidases [Cytophaga hutchinsonii]				3.2.1.52
4067, 4068	31194343	50	6.00E-48	Anopheles gambiae	ENSANGP00000000181 [Anopheles gambiae]				

4069, 4070	29349624	54	5.00E-45	Bacteroides thetaiotaomicron VPI-5482	ubiquinone/menaquinone biosynthesis methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79321.1 ubiquinone/menaquinone biosynthesis methyltransferase [Bacteroides thetaiotaomicron VPI-5482] sp Q8A005 UBIE_BACTN Menaquinone biosynthesis methyltransferase ubiE				2.1.1.-
407, 408	17549722	31	4.00E-17	Ralstonia solanacearum GM11000	PROBABLE MAJOR ANAEROBICALLY INDUCED OUTER MEMBRANE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum GM11000] emb CAD18654.1 PROBABLE MAJOR ANAEROBICALLY INDUCED OUTER MEMBRANE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum]				1.7.99.3
4073, 4074	53712342	63	1.00E-109	Bacteroides fragilis YCH46	valyl-tRNA synthetase [Bacteroides fragilis YCH46] db BAD47800.1 valyl- tRNA synthetase [Bacteroides fragilis YCH46]				
4075, 4076	21226558	33	2.00E-16	Methanosarcina mazel Go1	hydrolase [Methanosarcina mazel Go1] gb AAM30152.1 hydrolase [Methanosarcina mazel Go1] sp Q8PZN6 PGP_METMA Phosphoglycolate phosphatase (PGP)	Porphyromonas gingivalis W83 section 5 of 8 of the complete genome	92	7.00E-10	6.1.1.9
4077, 4078	15679388	34	2.00E-42	Methanothermobac ter thermautotrophicus str. Delta H	nifS protein [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85866.1 nifS protein [Methanothermobacter thermautotrophicus str. Delta H] pir [G69051 nifS protein - Methanobacterium thermoautotrophicum (strain Delta H) sp O27442 CSD_METTH Probable cysteine desulfurase Desc:Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4464. Org:Staphylococcus epidermidis				4.4.1.-
4079, 4080	ABP3961	23	2.00E-09		Type II restriction enzyme PstI (Endonuclease PstI) (R.PstI) pir INDOFS type II site-specific deoxyribonuclease (EC 3.1.21.4) PstI - Providencia stuartii gb AAA25673.1 PstI restriction endonuclease (PstI)				
4081, 4082	135244	44	2.00E-53	Methylococcus capsulatus str. Bath	TonB-dependent receptor, putative [Methylococcus capsulatus str. Bath] ref YP_114390.1 TonB-dependent receptor, putative [Methylococcus capsulatus str. Bath]				
4087, 4088	53757742	35	8.00E-21	Bacteroides fragilis YCH46	hypothetical protein BF1415 [Bacteroides fragilis YCH46] db BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				

4091, 4092	23501247	38	1.00E-21	Brucella suis 1330	DNA-binding response regulator, LuxR family [Brucella suis 1330] ref NP_540499.1 TRANSCRIPTIONAL REGULATORY PROTEIN DEGU [Brucella melitensis 16M] gb AAN29289.1 DNA-binding response regulator, LuxR family [Brucella suis 1330] gb AAL52763.1 two-component response regulator [Brucella melitensis 16M] pir AH3449 transcription regulatory protein degU [imported] - Brucella melitensis (strain 16M)				
4093, 4094	23501247	39	6.00E-19	Brucella suis 1330	DNA-binding response regulator, LuxR family [Brucella suis 1330] ref NP_540499.1 TRANSCRIPTIONAL REGULATORY PROTEIN DEGU [Brucella melitensis 16M] gb AAN29289.1 DNA-binding response regulator, LuxR family [Brucella suis 1330] gb AAL52763.1 two-component response regulator [Brucella melitensis 16M] pir AH3449 transcription regulatory protein degU [imported] - Brucella melitensis (strain 16M)				
4097, 4098	48860541	25	3.00E-11	Clostridium thermocellum ATCC 27405	COG0417: DNA polymerase elongation subunit (family B) [Clostridium thermocellum ATCC 27405]				
41, 42	48855377	69	9.00E-52	Cytophaga hutchinsonii	COG0413: Ketopantoate hydroxymethyltransferase [Cytophaga hutchinsonii]				2.1.2.11
4103, 4104	56965163	36	6.00E-23	Bacillus clausii KSM-K16	hypothetical protein ABC3401 [Bacillus clausii KSM-K16] dbj BAD65934.1 conserved hypothetical protein [Bacillus clausii KSM-K16]				
4107, 4108	52548310	56	3.00E-54	uncultured archaeon GZfos11A10	conserved hypothetical protein [uncultured archaeon GZfos11A10]	Methanosarcina acetivorans str. C2A, section 412 of 534 of the complete genome	88	#####	
4109, 4110	34397897	36	6.00E-23	Porphyromonas gingivalis W83	CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83] ref NP_906059.1 CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83]				
411, 412	29349046	37	4.00E-33	Bacteroides thetaiotaomicron VPI-5482	Na ⁺ /H ⁺ antiporter [Bacteroides thetaiotaomicron VPI-5482] gb AAO78743.1 Na ⁺ /H ⁺ antiporter [Bacteroides thetaiotaomicron VPI-5482]				
4111, 4112	34397897	42	2.00E-43	Porphyromonas gingivalis W83	CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83] ref NP_906059.1 CRISPR-associated protein, TM1792 family [Porphyromonas gingivalis W83]				
4119, 4120	42761500	44	4.00E-28	Dictyostelium discoideum	hypothetical protein [Dictyostelium discoideum]				2.3.1.-
4121, 4122	48858151	29	3.00E-23	Clostridium thermocellum ATCC 27405	COG0769: UDP-N-acetylmuramyl tripeptide synthase [Clostridium thermocellum ATCC 27405]				6.3.2.13

4123, 4124	48831856	38	7.00E-45	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			2.7.3.-
4125, 4126	48859986	31	2.00E-23	Clostridium thermocellum ATCC 27405	hypothetical protein Cht02000708 [Clostridium thermocellum ATCC 27405]			
4127, 4128	48862089	48	1.00E-84	Microbulifer degradans 2-40	hypothetical protein Mdeg02002723 [Microbulifer degradans 2-40]			
4129, 4130	48853816	36	3.00E-29	Cytophaga hutchinsonii	COG2928: Uncharacterized conserved protein [Cytophaga hutchinsonii]			
413, 414	34396551	45	7.00E-44	Porphyromonas gingivalis W83	ATP-dependent DNA helicase RecQ [Porphyromonas gingivalis W83] ref NP_904718.1 ATP-dependent DNA helicase RecQ [Porphyromonas gingivalis W83]			3.6.1.-
4133, 4134	AAU0488 0	68	4.00E-90		Desc: Micromonospora evernimycin biosynthetic enzyme evbX. Org: Micromonospora carbonacea var africana	Leifsonia xyli subsp. xyli str. CTC807, complete genome	86 2.00E-09	1.2.1.3
4135, 4136	16329496	53	2.00E-53	Synechocystis sp. PCC 6803	hypothetical protein sir1610 [Synechocystis sp. PCC 6803] dbj BAA16904.1 sir1610 [Synechocystis sp. PCC 6803] pir S74753 hypothetical protein sir1610 - Synechocystis sp. (strain PCC 6803)			2.1.1.-
4137, 4138	56421809	34	2.00E-11	Geobacillus kaustophilus HTA426	sugar ABC transporter (sugar-binding protein) [Geobacillus kaustophilus HTA426] dbj BAD77559.1 sugar ABC transporter (sugar-binding protein) [Geobacillus kaustophilus HTA426]			
4139, 4140	46580428	38	3.00E-16	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	hypothetical protein DVU2021 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96496.1 hypothetical protein DVU2021 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			
4141, 4142	46580428	38	4.00E-16	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	hypothetical protein DVU2021 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96496.1 hypothetical protein DVU2021 [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			
4145, 4146	53715217	29	1.00E-28	Bacteroides fragilis YCH46	ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] dbj BAD50675.1 ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46]			
4149, 4150	23619313	23	8.00E-07	Plasmodium falciparum 3D7	hypothetical protein [Plasmodium falciparum 3D7] emb CAD52512.1 hypothetical protein [Plasmodium falciparum 3D7]			
415, 416	32476012	45	5.00E-55	Rhodopirella baltica SH 1	hypothetical protein RB9659 [Rhodopirella baltica SH 1] emb CAD76391.1 conserved hypothetical protein [Pirella sp.]			
4153, 4154	46105872	37	5.00E-29	Rubrobacter xylanophilus DSM 9941	COG0761: Penicillin tolerance protein [Rubrobacter xylanophilus DSM 9941]			

4157, 4158	48855845	61	1.00E-38	Cytophaga hutchinsonii	COG0477: Permeases of the major facilitator superfamily [Cytophaga hutchinsonii]				
4165, 4166	23098317	30	1.00E-10	Oceanobacillus ihayensis HTE831	L-lysine dehydrogenase [Oceanobacillus ihayensis HTE831] dbj BAC12818.1 L-lysine dehydrogenase [Oceanobacillus ihayensis HTE831]				
4167, 4168	48854163	32	2.00E-10	Cytophaga hutchinsonii	COG2234: Predicted aminopeptidases [Cytophaga hutchinsonii]				
4169, 4170	23126274	28	7.00E-16	Nostoc punctiforme PCC 73102	COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102]				2.7.3.-
4171, 4172	49236839	55	1.00E-67	Moorella thermoacetica ATCC 39073	COG1219: ATP-dependent protease Clp, ATPase subunit [Moorella thermoacetica ATCC 39073]				
4173, 4174	48854863	53	3.00E-85	Cytophaga hutchinsonii	COG0358: DNA primase (bacterial type) [Cytophaga hutchinsonii]				2.7.7.-
4175, 4176	21244775	41	1.00E-63	Xanthomonas axonopodis pv. citri str. 306	beta-xylosidase [Xanthomonas axonopodis pv. citri str. 306] gb AAM38893.1 beta-xylosidase [Xanthomonas axonopodis pv. citri str. 306]				3.2.1.37
4183, 4184									
4187, 4188	48831484	40	9.00E-69	Magnetococcus sp. MC-1	COG0550: Topoisomerase IA [Magnetococcus sp. MC-1]				5.99.1.2
4189, 4190	56418811	51	7.00E-66	NAD+	DNA ligase (polydeoxyribonucleotide synthase[NAD+]) [Geobacillus kaustophilus HTA426] dbj BAD74561.1 DNA ligase (polydeoxyribonucleotide synthase[NAD+]) [Geobacillus kaustophilus HTA426]				
419, 420	48855612	40	9.00E-25	Cytophaga hutchinsonii	COG0845: Membrane-fusion protein [Cytophaga hutchinsonii]				6.5.1.2
4195, 4196	23126888	61	2.00E-42	Nostoc punctiforme PCC 73102	COG0784: FOG: CheY-like receiver [Nostoc punctiforme PCC 73102]				2.7.3.-
4197, 4198	48854003	32	5.00E-22	Cytophaga hutchinsonii	hypothetical protein Chut02003091 [Cytophaga hutchinsonii]				
4201, 4202	48853843	65	8.00E-62	Cytophaga hutchinsonii	COG0451: Nucleoside-diphosphate-sugar epimerases [Cytophaga hutchinsonii]				5.1.3.-

4203,	29348773	42	1.00E-21	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3364 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78470.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
4204									
4205,	48855009	45	4.00E-35	Cytophaga hutchinsonii	COG1801: Uncharacterized conserved protein [Cytophaga hutchinsonii] transcriptional regulator, Crp family [Porphyromonas gingivalis W83] ref NP_905705.1 transcriptional regulator, Crp family [Porphyromonas gingivalis W83]				
421,									
422	34397542	40	1.00E-31	Porphyromonas gingivalis W83	hypothetical protein TDE2139 [Treponema denticola ATCC 35405] gb AAS12659.1 hypothetical protein TDE2139 [Treponema denticola ATCC 35405]				
4211,									
4212	42527642	28	4.00E-10	Treponema denticola ATCC 35405	Adenosylhomocysteinase [Gluconobacter oxydans 621H] hypothetical protein Mdeg02002723 [Microbulbifer degradans 2-40] probable cytochrome C-type biogenesis protein [Clostridium perfringens str. 13] dbj BAB80447.1 probable cytochrome C-type biogenesis protein [Clostridium perfringens str. 13]				
4213,									
4214	58001953	79	1.00E-129	Gluconobacter oxydans 621H	glyoxylase family protein [Bacillus anthracis str. Sterne] gb AAT55291.1 glyoxylase family protein [Bacillus anthracis str. Sterne]				
4219,									
4220	48862089	46	6.00E-79	Microbulbifer degradans 2-40	hypothetical protein GKP41 [Geobacillus kaustophilus HTA426] dbj BAD74284.1 hypothetical protein [Geobacillus kaustophilus HTA426] COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii]				6.2.1.3
4221,									
4222	18309723	36	3.00E-18	Clostridium perfringens str. 13	hypothetical protein Chut02002781 [Cytophaga hutchinsonii] hypothetical protein BT3364 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78470.1 hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
4223,									
4224	49185988	35	2.00E-10	Bacillus anthracis str. Sterne	Desc: Putative P. abyssal dihydroorotase #1. Org: Pyrococcus abyssal				3.5.4.2
4225,									
4226	56410478	45	3.00E-27	Geobacillus kaustophilus HTA426	COG1408: Predicted phosphohydrolases [Cytophaga hutchinsonii] unknown [Rattus norvegicus] ref NP_942073.1 chromosome 11 open reading frame 8 [Rattus norvegicus]				
4227,									
4228	48854120	51	2.00E-70	Cytophaga hutchinsonii					
4229,									
4230	48854579	38	2.00E-12	Cytophaga hutchinsonii					
4231,									
4232	29348773	42	1.00E-21	Bacteroides thetaiotaomicron VPI-5482					
4233,	AAB9607								
4234	3	49	5.00E-19						
4245,									
4246	48856245	25	2.00E-07	Cytophaga hutchinsonii					
4249,									
4250	25989494	36	9.00E-11	Rattus norvegicus					

425, 426	13508372	45	3.00E-21	Mycoplasma pneumoniae M129	hypothetical protein MPN633 [Mycoplasma pneumoniae M129] conserved hypothetical protein, see: MPN635 [Mycoplasma pneumoniae M129] pir S73535 hypothetical protein C12_orf247 - Mycoplasma pneumoniae (strain ATCC 29342) sp P75164 YG33_MYCPN Hypothetical protein MPN633 (C12_orf247)				
4251, 4252	42557703	63	3.00E-77	uncultured crenarchaeote	hypothetical protein [uncultured crenarchaeote]				
4253, 4254	48856081	50	4.00E-76	Cytophaga hutchinsonii	COG0513: Superfamily II DNA and RNA helicases [Cytophaga hutchinsonii]				2.7.7.-
4255, 4256	48856514	38	4.00E-31	Cytophaga hutchinsonii	COG2148: Sugar transferases involved in lipopolysaccharide synthesis [Cytophaga hutchinsonii]				2.-.-.-
4261, 4262	17940055	33	3.00E-16	Leptospira interrogans	unknown [Leptospira interrogans]				2.4.-.-
4263, 4264	18310494	31	9.00E-24	Clostridium perfringens str. 13	two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] dbj BAB81218.1 two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13]				
4265, 4266	48856475	45	3.00E-34	Cytophaga hutchinsonii	COG2602: Beta-lactamase class D [Cytophaga hutchinsonii]				3.5.2.6
4267, 4268	16554506	31	3.00E-15	Halobacterium salinarum NRC-1	Predicted kinase [Halobacterium salinarum NRC-1]				2.7.1.12
4269, 4270	57234724	40	1.00E-14	Dehalococcoides ethenogenes 195	hypothetical protein DE10514 [Dehalococcoides ethenogenes 195] gb AAW40229.1 conserved hypothetical protein [Dehalococcoides ethenogenes 195]				2.7.1.12
427, 428	48855641	38	8.00E-23	Cytophaga hutchinsonii	COG0760: Parvulin-like peptidyl-prolyl isomerase [Cytophaga hutchinsonii]				
4271, 4272	53712767	78	2.00E-59	Bacteroides fragilis YCH46	dioxygenase [Bacteroides fragilis YCH46] dbj BAD48225.1 dioxygenase [Bacteroides fragilis YCH46]				1.3.1.9
4281, 4282	48853419	59	2.00E-37	Cytophaga hutchinsonii	COG0251: Putative translation initiation inhibitor, yigF family [Cytophaga hutchinsonii]				
4283, 4284	48858374	33	3.00E-08	Clostridium thermocellum ATCC 27405	COG2908: Uncharacterized protein conserved in bacteria [Clostridium thermocellum ATCC 27405]				
4287, 4288	23126588	29	4.00E-26	Nostoc punctiforme PCC 73102	COG0438: Glycosyltransferase [Nostoc punctiforme PCC 73102]				
4289, 4290	48783455	41	8.00E-24	Burkholderia fungorum LB400	COG5483: Uncharacterized conserved protein [Burkholderia fungorum LB400]				
429, 430	53713709	39	1.00E-25	Bacteroides fragilis YCH46	conserved hypothetical protein BatB [Bacteroides fragilis YCH46] gb AAD30859.1 BatB [Bacteroides fragilis] dbj BAD49167.1 conserved hypothetical protein BatB [Bacteroides fragilis YCH46]				

4293,	48854274	40	6.00E-47	Cytophaga hutchinsonii	COG3239: Fatty acid desaturase [Cytophaga hutchinsonii]			1.14.99.
4294				Geobacter metallireducens GS				25
4297,				15				
4298	48847270	46	3.00E-33	Vibrio vulnificus	COG0796: Glutamate racemase [Geobacter metallireducens GS-15]			5.1.1.3
4299,				CMCP6	Glycosyltransferase [Vibrio vulnificus CMCP6]			
4300	27364227	34	4.00E-16	Bacteroides thetaiotaomicron	Glycosyltransferase [Vibrio vulnificus CMCP6]			2.4.1.-
43, 44	29349049	30	3.00E-18	VPI-5482	hypothetical protein BT3641 [Bacteroides thetaiotaomicron VPI-5482]			
				Bacillus thuringiensis serovar konkukian	gb AAO78748.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
4301,				str. 97-27	conserved hypothetical protein, possible glycosyl transferase [Bacillus thuringiensis serovar konkukian str. 97-27]			
4302	49478938	25	2.00E-07	Aquifex aeolicus VF5	hypothetical protein, possible glycosyl transferase [Bacillus thuringiensis serovar konkukian str. 97-27]			
4303,					dolichol-phosphate mannosyltransferase [Aquifex aeolicus VF5]			
4304	15606924	45	1.00E-66	Aquifex aeolicus VF5	gb AAC07699.1 dolichol-phosphate mannosyltransferase [Aquifex aeolicus VF5] pir G70463 dolichol-phosphate mannosyltransferase - Aquifex aeolicus			2.4.1.83
4305,					dolichol-phosphate mannosyltransferase [Aquifex aeolicus VF5]			
4306	15606924	40	7.00E-27	Aquifex aeolicus VF5	gb AAC07699.1 dolichol-phosphate mannosyltransferase [Aquifex aeolicus VF5] pir G70463 dolichol-phosphate mannosyltransferase - Aquifex aeolicus			2.4.1.83
4307,				Cytophaga hutchinsonii	COG3278: Response regulator of the LysR/AIGR family [Cytophaga hutchinsonii]			
4308	48854415	33	1.00E-10	Clostridium perfringens str. 13	hypothetical protein CPE1285 [Clostridium perfringens str. 13]			
4309,					dbj BAB80991.1 hypothetical protein [Clostridium perfringens str. 13]			
4310	18310267	26	2.00E-16	Bacteroides fragilis YCH46	ABC transporter ATP-binding protein [Bacteroides fragilis YCH46]			
4311,					dbj BAD47773.1 ABC transporter ATP-binding protein [Bacteroides fragilis YCH46]			
4312	53712315	35	8.00E-15	Aspergillus nidulans FGSC A4	hypothetical protein AN6925.2 [Aspergillus nidulans FGSC A4]			
4313,					ref XP_411062.1 hypothetical protein AN6925.2 [Aspergillus nidulans FGSC A4]			
4314	40738490	39	6.00E-12	Geobacter metallireducens GS-15	COG0500: SAM-dependent methyltransferases [Geobacter metallireducens GS-15]			
4315,					COG1092: Predicted SAM-dependent methyltransferases [Cytophaga hutchinsonii]			2.1.1.-
4316	48844445	24	6.00E-11	Cytophaga hutchinsonii	hypothetical protein Chut02001987 [Cytophaga hutchinsonii]			
4323,								
4324	48856165	53	2.00E-70	Cytophaga hutchinsonii				
4325,								
4326	48854930	51	1.00E-60	Vibrio cholerae				6.3.5.4
4327,								
4328	2244692	35	1.00E-31					

433, 434	48832592	46	8.00E-32	Magnetococcus sp. MC-1	COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Magnetococcus sp. MC-1]				
4333, 4334	29349972	64	2.00E-95	Bacteroides thetataoimicron VPI-5482	putative glycosyltransferase [Bacteroides thetataoimicron VPI-5482] gb AAO79669.1 putative glycosyltransferase [Bacteroides thetataoimicron VPI-5482]	Bacteroides thetataoimicron VPI-5482, section 20 of 21 of the complete genome	85	2.00E-07	2.4.1.83
4337, 4338	5578853	30	4.00E-07	Streptomyces coelicolor A3(2)	putative secreted protease [Streptomyces coelicolor A3(2)] pir T35287 probable secreted proteinase - Streptomyces coelicolor ref NP_626424.1 putative secreted protease [Streptomyces coelicolor A3(2)]				3.4.21.-
4339, 4340	53714925	59	3.00E-49	Bacteroides fragilis YCH46	tRNA nucleotidyltransferase [Bacteroides fragilis YCH46] dbj BAD50383.1 tRNA nucleotidyltransferase [Bacteroides fragilis YCH46]				2.7.7.19
4341, 4342	53712197	33	1.00E-13	Bacteroides fragilis YCH46	hypothetical protein BF0904 [Bacteroides fragilis YCH46] dbj BAD47655.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
4343, 4344	34396924	27	1.00E-16	Porphyromonas gingivalis W83	Integrase [Porphyromonas gingivalis W83] ref NP_905090.1 Integrase				
4347, 4348	48854856	53	4.00E-91	Cytophaga hutchinsonii	COG0519: GMP synthase, PP-ATPase domain/subunit [Cytophaga hutchinsonii]				6.3.5.2
4349, 4350	57158267	27	4.00E-15	Thermococcus kodakaraensis	predicted DNA methylase [Thermococcus kodakaraensis] ref YP_182421.1 predicted DNA methylase [Thermococcus kodakaraensis]				
435, 436	48853532	45	4.00E-39	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]				
4351, 4352	20091500	89	1.00E-142	Methanosarcina acetivorans C2A	transposase [Methanosarcina acetivorans C2A] gb AAM06055.1 transposase [Methanosarcina acetivorans str. C2A]	Methanosarcina acetivorans str. C2A, section 309 of 534 of the complete genome	89	0	
4355, 4356	46317628	28	2.00E-12	Burkholderia cepacia R18194	COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Burkholderia cepacia R18194]				
4357, 4358	53713993	27	4.00E-20	Bacteroides fragilis YCH46	transcriptional regulator [Bacteroides fragilis YCH46] dbj BAD49451.1 transcriptional regulator [Bacteroides fragilis YCH46]				
4359, 4360	29346614	27	2.00E-39	Bacteroides thetataoimicron VPI-5482	conserved hypothetical protein, putative outer membrane protein [Bacteroides thetataoimicron VPI-5482] gb AAO76311.1 conserved hypothetical protein, putative outer membrane protein [Bacteroides thetataoimicron VPI-5482]				

4363, 4364	59964719	72	1.00E-55	Bacillus clausii KSM-K16	thymidylate synthase [Bacillus clausii KSM-K16] dbj BAD5489.1 thymidylate synthase [Bacillus clausii KSM-K16]	Coxiella burnetii strain RSA 493, section 5 of 7 of the complete genome	81	1.00E-06	2.1.1.45
4373, 4374	53763896	31	3.00E-25	Anabaena variabilis ATCC 29413	COG0860: N-acetylmuramoyl-L-alanine amidase [Anabaena variabilis ATCC 29413]				3.5.1.28
4375, 4376	48845074	28	7.00E-24	Geobacter metallireducens GS-15	COG0417: DNA polymerase elongation subunit (family B) [Geobacter metallireducens GS-15]				2.7.7.7
4377, 4378	29349976	27	4.00E-21	Bacteroides thetataoamicon VPI-5482	hypothetical protein BT4568 [Bacteroides thetataoamicon VPI-5482] gb AAO79673.1 conserved hypothetical protein [Bacteroides thetataoamicon VPI-5482]				
4381, 4382	21227241	30	4.00E-11	Methanosarcina mazei Go1	Dolichyl-phosphate mannose synthase related protein [Methanosarcina mazei Go1] gb AAM30835.1 Dolichyl-phosphate mannose synthase related protein [Methanosarcina mazei Go1]				2.---
4383, 4384	48839273	62	1.00E-54	Methanosarcina barkeri str. fusaro	COG0732: Restriction endonuclease S subunits [Methanosarcina barkeri str. fusaro]	Methanosarcina acetivorans str. C2A, section 242 of 534 of the complete genome	95	1.00E-54	3.1.21.3
4385, 4386	48838982	67	2.00E-67	Methanosarcina barkeri str. fusaro	COG2043: Uncharacterized protein conserved in archaea [Methanosarcina barkeri str. fusaro]				
4389, 4390	17549722	31	4.00E-17	Ralstonia solanacearum GMI1000	PROBABLE MAJOR ANAEROBICALLY INDUCED OUTER MEMBRANE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum GMI1000] emb CAD18654.1 PROBABLE MAJOR ANAEROBICALLY INDUCED OUTER MEMBRANE TRANSMEMBRANE PROTEIN [Ralstonia solanacearum]				1.7.99.3
439, 440	48856925	32	7.00E-23	Cytophaga hutchinsonii	COG1309: Transcriptional regulator [Cytophaga hutchinsonii]				
4391, 4392	48855725	24	3.00E-11	Cytophaga hutchinsonii	hypothetical protein Chut02000929 [Cytophaga hutchinsonii]				
4393, 4394	48855974	30	3.00E-19	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]				
4395, 4396	46134478	35	3.00E-37	Anabaena variabilis ATCC 29413	COG0642: Signal transduction histidine kinase [Anabaena variabilis ATCC 29413]				2.7.3.-
4397, 4398	6691605	70	1.00E-89	Flavobacterium psychrophilum	gyrase B [Flavobacterium psychrophilum]				5.99.1.-

4399, 4400	53715112	32	2.00E-40	Bacteroides fragilis YCH46	4-alpha-glucanotransferase [Bacteroides fragilis YCH46] dbj BAD50570.1 4-alpha-glucanotransferase [Bacteroides fragilis YCH46]			2.4.1.25
4401,	48853434	68	1.00E-50	Cytophaga hutchinsonii	COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii]			2.7.7.24
4402	48853434	68	1.00E-50	Cytophaga hutchinsonii	putative helicase [Staphylococcus phage K] gb AAO47520.1 ORF71			
4403,	48696459	27	4.00E-12	Staphylococcus phage K	[Staphylococcus phage K]			
4404,	48853532	26	3.00E-18	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]			
4405,	48853532	26	3.00E-18	Cytophaga hutchinsonii	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis			
4406	48854545	52	2.00E-59	Cytophaga hutchinsonii	[Cytophaga hutchinsonii]			2.1.1.-
4407,	48854545	52	2.00E-59	Cytophaga hutchinsonii	hypothetical protein BT0164 [Bacteroides thetaiotaomicron VPI-5482]			
4408	48854545	52	2.00E-59	Cytophaga hutchinsonii	gb AAO75271.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
441,	29345574	38	1.00E-31	Bacteroides thetaitaomicron	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]			
442	48855616	28	2.00E-24	Cytophaga hutchinsonii	hypothetical protein CPE2540 [Clostridium perfringens str. 13]			
4413,	48855616	28	2.00E-24	Cytophaga hutchinsonii	dbj BAB82246.1 conserved hypothetical protein [Clostridium perfringens str. 13]			3.1.2.6
4415,	18311522	31	1.00E-10	Clostridium perfringens str. 13	COG1357: Uncharacterized low-complexity proteins [Cytophaga hutchinsonii]			
4416	18311522	31	1.00E-10	Clostridium perfringens str. 13	putative two-component system sensor histidine kinase, putative heat shock protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79860.1 putative two-component system sensor histidine kinase, putative heat shock protein [Bacteroides thetaiotaomicron VPI-5482]			2.7.3.-
4419,	48854397	48	6.00E-32	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]			
4420	48854397	48	6.00E-32	Cytophaga hutchinsonii	ABC-type sugar/spermidine/putrescine/iron/thiamine transport systems, ATPase component [Thermoanaerobacter tengcongensis MB4]			
4427,	29350163	23	6.00E-13	Bacteroides thetaitaomicron	gb AAM25158.1 ABC-type sugar/spermidine/putrescine/iron/thiamine transport systems, ATPase component [Thermoanaerobacter tengcongensis MB4]			
4428	29350163	23	6.00E-13	Bacteroides thetaitaomicron	COG0325: Predicted enzyme with a TIM-barrel fold [Cytophaga hutchinsonii]			
4431,	48854286	34	2.00E-23	Cytophaga hutchinsonii	transaldolase [Methanocaldococcus jannaschii DSM 2661] gb AAB98982.1 transaldolase [Methanocaldococcus jannaschii DSM 2661]			
4432	48854286	34	2.00E-23	Cytophaga hutchinsonii	sp Q58370 TAL_METJA Probable transaldolase pir H64419 transaldolase [EC 2.2.1.2] - Methanococcus jannaschii			2.2.1.2
4447,	20803383	75	5.00E-99	Thermoanaerobacter tengcongensis				
4448	20803383	75	5.00E-99	Thermoanaerobacter tengcongensis				
4451,	48854499	53	7.00E-48	Cytophaga hutchinsonii				
4452	48854499	53	7.00E-48	Cytophaga hutchinsonii				
4453,	15669150	57	4.00E-63	Methanocaldococcus jannaschii DSM 2661				
4454	15669150	57	4.00E-63	Methanocaldococcus jannaschii DSM 2661				

4457, 4458	29346936	66	8.00E-84	Bacteroides thetaiotaomicron VPI-5482	myo-inositol-1-phosphate synthase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76633.1 myo-inositol-1-phosphate synthase [Bacteroides thetaiotaomicron VPI-5482]				5.5.1.4
4459, 4460	29346936	65	9.00E-86	Bacteroides thetaiotaomicron VPI-5482	myo-inositol-1-phosphate synthase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76633.1 myo-inositol-1-phosphate synthase [Bacteroides thetaiotaomicron VPI-5482]				5.5.1.4
4463, 4464	48853540	35	6.00E-14	Cytophaga hutchinsonii	COG0779: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
4465, 4466	48853541	43	8.00E-23	Cytophaga hutchinsonii	COG0195: Transcription elongation factor [Cytophaga hutchinsonii]				
4467, 4468	50252056	33	3.00E-11	Oryza sativa (japonica cultivar- group)	putative 4-coumarate coenzyme A ligase [Oryza sativa (japonica cultivar- group)]				6.2.1.12
4469, 4470	18920646	28	2.00E-15	Microcystis aeruginosa	McyA [Microcystis aeruginosa]				6.2.1.1
447, 448	53711736	34	6.00E-13	Bacteroides fragilis YCH46	Na ⁺ /H ⁺ antiporter [Bacteroides fragilis YCH46] antiporter [Bacteroides fragilis YCH46]				
4471, 4472	15669064	42	4.00E-42	Methanocaldococ- cus jannaschii DSM 2661	ferric enterobactin transport ATP-binding protein [Methanocaldococcus jannaschii DSM 2661] gb AAB98878.1 ferric enterobactin transport ATP- binding protein [Methanocaldococcus jannaschii DSM 2661] spiQ58283 Y873_METJA Hypothetical ABC transporter ATP-binding protein MJ0873				3.6.3.33
4473, 4474	15613299	41	5.00E-31	Bacillus halodurans C-125	hypothetical protein BH0736 [Bacillus halodurans C-125] db BAB04455.1 BH0736 [Bacillus halodurans C-125] pir H83741 hypothetical protein BH0736 [imported] - Bacillus halodurans (strain C-125)				
4475, 4476	48855819	32	6.00E-33	Cytophaga hutchinsonii	COG3361: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
4477, 4478	39995136	27	2.00E-17	Geobacter sulfurreducens PCA	tolB protein [Geobacter sulfurreducens PCA] gb AAR33360.1 tolB protein [Geobacter sulfurreducens PCA]				
4479, 4480	34396304	36	3.00E-07	Porphyromonas gingivalis W83	mannosyltransferase [Porphyromonas gingivalis W83] ref NP_904472.1 mannosyltransferase [Porphyromonas gingivalis W83]				2.4.1.-
4481, 4482	21226752	39	1.00E-23	Methanosarcina mazel Go1	mannosyltransferase [Methanosarcina mazel Go1] gb AAM30346.1 mannosyltransferase [Methanosarcina mazel Goe1]				2.4.1.-
4485, 4486	53714487	56	3.00E-44	Bacteroides fragilis YCH46	SsrA-binding protein [Bacteroides fragilis YCH46] db BAD49945.1 SsrA- binding protein [Bacteroides fragilis YCH46]				
4487, 4488	49236141	51	4.00E-48	Moorella thermoacetica ATCC 39073	COG0231: Translation elongation factor P (EF-P)/translation initiation factor 5A (eIF-5A) [Moorella thermoacetica ATCC 39073]				

4489, 4490	17231259	45	1.00E-18	7120	Nostoc sp. PCC	two-component sensor histidine kinase [Nostoc sp. PCC 7120] pir AH2276 two-component sensor histidine kinase al 3767 [Imported] - Nostoc sp. (strain PCC 7120) dbj BAB75466.1 two-component sensor histidine kinase [Nostoc sp. PCC 7120]				2.7.3.-
449, 450	20094204	43	3.00E-37		Methanopyrus kandleri AV19	Undecaprenyl pyrophosphate synthase [Methanopyrus kandleri AV19] gb AA01981.1 Undecaprenyl-pyrophosphate synthase [Methanopyrus kandleri AV19] sp Q8TXA7 UPPS_METKA Undecaprenyl pyrophosphate synthetase (UPP synthetase) (Di-trans,poly-cis-decaprenylcistransferase) (Undecaprenyl diphosphate synthase) (UDS)				2.5.1.31
4491, 4492	48856903	39	3.00E-56		Cytophaga hutchinsonii	COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii]				
4493, 4494	48844178	34	4.00E-35	15	Geobacter metallireducens GS	COG0260: Leucyl aminopeptidase [Geobacter metallireducens GS-15]				2.3.1.43
4497, 4498	48854264	69	1.00E-120		Cytophaga hutchinsonii	COG0069: Glutamate synthase domain 2 [Cytophaga hutchinsonii]	Desc:Listeria monocytogenes EGD-e genome sequence. Org:Listeria monocytogenes	87	4.00E-15	1.4.1.13
4499, 4500	48854264	62	1.00E-106		Cytophaga hutchinsonii	COG0068: Glutamate synthase domain 2 [Cytophaga hutchinsonii]				1.4.1.13
4509, 4510	48854452	66	1.00E-109		Cytophaga hutchinsonii	COG0034: Glutamine phosphoribosylpyrophosphate amidotransferase [Cytophaga hutchinsonii]				2.4.2.14
451, 452	48832080	29	6.00E-21		Magnetococcus sp. MC-1	COG1352: Methylase of chemotaxis methyl-accepting proteins [Magnetococcus sp. MC-1]				2.1.1.80
4511, 4512	14520856	43	9.00E-26		Pyrococcus abyssi GE5	transcriptional regulatory protein, AsnC family [Pyrococcus abyssi GE5] emb CAB49562.1 Transcriptional regulatory protein, Lrp-AsnC family [Pyrococcus abyssi] sp Q9V0Y9 REG6_PYRAB Putative HTH-type transcriptional regulator PYRAB06490 pir A75106 transcription regulatory protein, asnc family PAB1938 - Pyrococcus abyssi (strain Orsay)				
4513, 4514	29346036	46	1.00E-71		Bacteroides thetaiotaomicron VPI-5482	phenylalanyl-tRNA synthetase beta chain [Bacteroides thetaiotaomicron VPI- 5482] gb AA075733.1 phenylalanyl-tRNA synthetase beta chain [Bacteroides thetaiotaomicron VPI-5482] sp Q8AA39 SYFB_BACTN Phenylalanyl-tRNA synthetase beta chain (Phenylalanine-tRNA ligase beta chain) (PheRS)				6.1.1.20
4515, 4516	53714672	35	1.00E-26		Bacteroides fragilis YCH46	RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD50130.1 RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46]				

4517, 4518	48856262	56	1.00E-27	Cytophaga hutchinsonii	COG1134: ABC-type polysaccharide/polyol phosphate transport system, ATPase component [Cytophaga hutchinsonii]			1.8.-
4523, 4524	48838433	39	2.00E-47	Methanosarcina barkeri str. fusaro	COG1002: Type II restriction enzyme, methylase subunits [Methanosarcina barkeri str. fusaro]			2.1.1.72
4527, 4528	6968646	42	3.00E-38	Campylobacter jejuni subsp. jejuni NCTC 11168	putative glycolate oxidase subunit D [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282360.1 putative glycolate oxidase subunit D [Campylobacter jejuni subsp. jejuni NCTC 11168] pir G81327 probable glycolate oxidase chain D Cj1213c [imported] - Campylobacter jejuni (strain NCTC 11168)			1.1.3.15
4529, 4530	29349593	60	2.00E-20	Bacteroides thetaiotaomicron VPI-5482	xylosidase/arabinosidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79290.1 xylosidase/arabinosidase [Bacteroides thetaiotaomicron VPI-5482]			
4531, 4532	48893181	29	4.00E-28	Trichodesmium erythraeum IMS101	COG1089: GDP-D-mannose dehydratase [Trichodesmium erythraeum IMS101]			4.2.1.47
4533, 4534	23125015	50	4.00E-29	Nostoc punctiforme PCC 73102	COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102]			2.7.3.-
4535, 4536	48854194	46	1.00E-53	Cytophaga hutchinsonii	COG4464: Capsular polysaccharide biosynthesis protein [Cytophaga hutchinsonii]			
4537, 4538	48854195	32	2.00E-13	Cytophaga hutchinsonii	COG3206: Uncharacterized protein involved in exopolysaccharide biosynthesis [Cytophaga hutchinsonii]			
4539, 4540	23129857	50	1.00E-10	Nostoc punctiforme PCC 73102	COG3920: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102]			2.7.3.-
4541, 4542	57234806	27	1.00E-15	Dehalococcoides ethenogenes 195 uncultured archaeon	conserved hypothetical protein TIGR00147 [Dehalococcoides ethenogenes 195] gb AAW40311.1 conserved hypothetical protein TIGR00147 [Dehalococcoides ethenogenes 195]			
4543, 4544	52548759	50	2.00E-69	GZfos18F2	putative glycosyl transferase [uncultured archaeon GZfos18F2] cadmium resistance protein [Methanocaldococcus jannaschii DSM 2661] gb AAB99335.1 cadmium resistance protein [Methanocaldococcus jannaschii DSM 2661] sp Q58721 YD25_METJA Putative HTH-type transcriptional regulator MJ1325 pir D64465 hypothetical protein MJ1325 - Methanococcus jannaschii			2.-
4547, 4548	15669515	37	4.00E-09	Methanocaldococcus jannaschii DSM 2661	putative GTP-binding protein [Bacteroides fragilis YCH46] dbj BAD50830.1 putative GTP-binding protein [Bacteroides fragilis YCH46]			
455, 456	53715372	48	1.00E-32	Bacteroides fragilis YCH46				

4551, 4552	42524924	63	1.00E-57	Bdellovibrio bacteriovorus HD100	hydroxymethylglutaryl-CoA lyase [Bdellovibrio bacteriovorus HD100] embjCAE80958.1] hydroxymethylglutaryl-CoA lyase [Bdellovibrio bacteriovorus HD100]			4.1.3.4
4559, 4560	48848789	68	1.00E-29	Novosphingobium aromaticivorans DSM 12444	COG0553: Preprotein translocase subunit SecA (ATPase, RNA helicase) [Novosphingobium aromaticivorans DSM 12444]			
4561, 4562	17229604	40	2.00E-19	Nostoc sp. PCC 7120	hypothetical protein alr2112 [Nostoc sp. PCC 7120] dbj BAB73811.1 alr2112 [Nostoc sp. PCC 7120] pir JAB2070 hypothetical protein alr2112 [Imported] - Nostoc sp. (strain PCC 7120)			
4563, 4564	2281663	63	3.00E-68	Flavobacterium johnsoniae	gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding motility protein [Imported] - Flavobacterium johnsoniae			1.8.-.-
4569, 4570	48854858	55	5.00E-29	Cytophaga hutchinsonii	COG0496: Predicted acid phosphatase [Cytophaga hutchinsonii]			3.1.3.2
4571, 4572	48854463	51	2.00E-48	Cytophaga hutchinsonii	COG0193: Peptidyl-RNA hydrolase [Cytophaga hutchinsonii] putative dipeptidyl-peptidase III [Bacteroides thetaiotaomicron VPI-5482] gb AAO76953.1] putative dipeptidyl-peptidase III [Bacteroides thetaiotaomicron VPI-5482]			3.1.1.29
4573, 4574	29347256	56	1.00E-36	Bacteroides thetaiotaomicron VPI-5482	putative peptidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78570.1 putative peptidase [Bacteroides thetaiotaomicron VPI-5482] COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cytophaga hutchinsonii]			
4577, 4578	29348873	26	2.00E-13	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein Chui02003855 [Cytophaga hutchinsonii] COG2137: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
4581, 4582	48853429	46	9.00E-16	Cytophaga hutchinsonii	hypothetical protein nfa2750 [Nocardia farcinica IFM 10152] dbj BAD55117.1 hypothetical protein [Nocardia farcinica IFM 10152]			
4583, 4584	48854316	37	9.00E-22	Cytophaga hutchinsonii	COG0622: Predicted phosphoesterase [Cytophaga hutchinsonii]			
4585, 4586	54022239	25	8.00E-07	Nocardia farcinica IFM 10152	COG0457: FOG: TPR repeat [Trichodesmium erythraeum IMS101] COG4564: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-
4587, 4588	48854510	57	7.00E-46	Cytophaga hutchinsonii	glycosyl transferase [Pyrococcus furiosus DSM 3638] gb AAL81485.1 glycosyl transferase [Pyrococcus furiosus DSM 3638]			2.4.1.-
4595, 4596	48892769	23	5.00E-07	Trichodesmium erythraeum IMS101	VV A18 helicase [Mimivirus] gb AAV50665.1 VV A18 helicase [Mimivirus]			3.6.3.14
4597, 4598	48853443	26	3.00E-11	Cytophaga hutchinsonii				
4599, 4600	18977733	31	1.00E-08	Pyrococcus furiosus DSM 3638				
4603, 4604	55819271	37	3.00E-16	Mimivirus				

4605, 4606	31195963	49	1.00E-59	Anopheles gambiae	ENSANGP00000000454 [Anopheles gambiae] SSU ribosomal protein S13AB (rps13AB) [Sulfolobus solfataricus P2] gb AAK40436.1 SSU ribosomal protein S13AB (rps13AB) [Sulfolobus solfataricus P2] emb CAA69528.1 ribosomal protein S18 [Sulfolobus solfataricus] pir S75414 probable ribosomal protein S18 - Sulfolobus solfataricus sp P95986 RS13_SULSO 30S ribosomal protein S13P			4.2.1.22
4609, 4610	15897041	50	3.00E-35	Sulfolobus solfataricus P2	Desc:N. gonorrhoeae amino acid sequence SEQ ID 4556. Org:Neisseria gonorrhoeae			3.1.21.3
4611, 4612	ABP7901 3	57	2.00E-51		UDP-N-acetylenolpyruvoylglucosamine reductase [EC:1.1.1.158] [Rickettsia conorii str. Malish 7] gb AAL02870.1 UDP-N-acetylenolpyruvoylglucosamine reductase [EC:1.1.1.158] [Rickettsia conorii str. Malish 7] pir D97741 hypothetical protein murB [imported] - Rickettsia conorii (strain Malish 7) COG0286: Type I restriction-modification system methyltransferase subunit [Haemophilus somnus 2336]			1.1.1.15 8
4613, 4614	15892255	32	1.00E-16	EC:1.1.1.158	[Haemophilus somnus 2336] type I restriction-modification system S subunit [Geobacillus kaustophilus HTA426] dbj BAD74829.1 type I restriction-modification system S subunit [Geobacillus kaustophilus HTA426]			3.1.21.3
4615, 4616	46156664	32	2.00E-20	Haemophilus sommus 2336	GTP pyrophosphokinase [Geobacter sulfurreducens PCA] gb AAR35612.1 GTP pyrophosphokinase [Geobacter sulfurreducens PCA]			2.7.6.5
4617, 4618	56418879	35	3.00E-22	Geobacillus kaustophilus HTA426	hypothetical protein Chut02003580 [Cytophaga hutchinsonii] putative exopolysaccharide production protein [Bradyrhizobium japonicum USDA 110] dbj BAC51575.1 bl6310 [Bradyrhizobium japonicum USDA 110]			2.---
4619, 4620	39997334	63	1.00E-102	Geobacter sulfurreducens PCA	COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii] COG1463: ABC-type transport system involved in resistance to organic solvents, periplasmic component [Cytophaga hutchinsonii]			
4623, 4624	48853721	33	2.00E-13	Cytophaga hutchinsonii	hypothetical protein LA1652 [Leptospira interrogans serovar Lai str. 56601] gb AAN48851.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601]			
4629, 4630	27381421	49	3.00E-42	Bradyrhizobium japonicum USDA 110	hypothetical protein UM04845.1 [Ustilago maydis 521] ref XP_402460.1 hypothetical protein UM04845.1 [Ustilago maydis 521]			2.3.1.51
463, 464	48855210	44	4.00E-30	Cytophaga hutchinsonii				
4631, 4632	48853578	31	5.00E-14	Cytophaga hutchinsonii				
4633, 4634	24214352	45	2.00E-36	Leptospira interrogans serovar Lai str. 56601				
4635, 4636	46100876	30	2.00E-13	Ustilago maydis				

4637, 4638	15628781	29	4.00E-13	Myco-plasma pulmonis UAB CTIP	FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY-DNA GLYCOSYLASE) [Mycoplasma pulmonis UAB CTIP] emb[CAC13483.1] FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY-DNA GLYCOSYLASE) [Mycoplasma pulmonis] sp[Q98QQ1]FPG_MYCPU Formamidopyrimidine-DNA glycosylase (FAPY-DNA glycosylase) (DNA- apurinic or apyrimidinic site) lyase mutM (AP lyase mutM) pir[IF90550 hypothetical protein MYP_3100 [Imported] - Mycoplasma pulmonis (strain UAB CTIP)			3.2.2.23
4639, 4640	29348887	37	7.00E-33	Bacteroides thetaiotaomicron VPI-5482	Integrase [Bacteroides thetaiotaomicron VPI-5482] gb[AAO78584.1] Integrase [Bacteroides thetaiotaomicron VPI-5482]			
4643, 4644	48856526	75	3.00E-98	Cytophaga hutchinsonii	COG1899: Deoxyhypusine synthase [Cytophaga hutchinsonii]			2.5.1.46
4645, 4646	48854545	56	7.00E-46	Cytophaga hutchinsonii	COG2226: Methylase involved in ubiquinone/menaquinone biosynthesis [Cytophaga hutchinsonii]			2.1.1.-
4647, 4648	53765097	29	9.00E-22	Anabaena variabilis ATCC 29413	COG0438: Glycosyltransferase [Anabaena variabilis ATCC 29413]			
465, 466	48848776	82	2.00E-58	Novosphingobium aromaticivorans DSM 12444	COG0499: S-adenosylhomocysteine hydrolase [Novosphingobium aromaticivorans DSM 12444]	Mesorhizobium loti MAFF303099 DNA, complete genome	81	8.00E-45
4651, 4652	48856685	30	6.00E-12	Cytophaga hutchinsonii	COG0764: 3-hydroxymyristoyl(3-hydroxydecanoyl)-(acyl carrier protein) dehydratases [Cytophaga hutchinsonii]			3.3.1.1
4655, 4656	45657684	26	2.00E-11	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	hypothetical protein LIC11819 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb[AAS70407.1] conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			
4657, 4658	21227195	38	8.00E-18	Methanosarcina mazei Go1	hypothetical sensory transduction histidine kinase [Methanosarcina mazei Go1] gb[AAM30789.1] hypothetical sensory transduction histidine kinase [Methanosarcina mazei Go1]			2.7.3.-
4659, 4660	17230661	38	2.00E-19	Nostoc sp. PCC 7120	hypothetical protein all3169 [Nostoc sp. PCC 7120] pir[AB2202 hypothetical protein all3169 [Imported] - Nostoc sp. (strain PCC 7120) dbj[BAB74868.1] all3169 [Nostoc sp. PCC 7120]			2.7.1.37
4665, 4666	48853603	51	2.00E-69	Cytophaga hutchinsonii	COG0809: S-adenosylmethionine:tRNA-ribosyltransferase-isomerase (guanine synthetase) [Cytophaga hutchinsonii]			5.---
4667, 4668	48839466	93	1.00E-66	Methanosarcina barkeri str. fusaro	COG1335: Amidases related to nicotinamide [Methanosarcina barkeri str. fusaro]			3.5.1.19

4669, 4670	52548310	52	6.00E-55	uncultured archaeon GZfos11A10	conserved hypothetical protein [uncultured archaeon GZfos11A10]	Methanosarcina acetivorans str. C2A, section 412 of 534 of the complete genome	88	0
467, 468	28553411	45	6.00E-13	Pseudomonas syringae pv. tomato str. DC3000	conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] ref NP_792784.1 hypothetical protein PSPTO2987 [Pseudomonas syringae pv. tomato str. DC3000]			
4673, 4674 4675, 4676	34397317	51	2.00E-45	Porphyrromonas gingivalis W83	glucose-inhibited division protein B [Porphyrromonas gingivalis W83] ref NP_905481.1 glucose-inhibited division protein B [Porphyrromonas gingivalis W83] sp Q7MV10 GIDB_PORGI Methyltransferase gidB (Glucose inhibited division protein B)			
4681, 4682 4683, 4684	48855392	27	9.00E-08	Cytophaga hutchinsonii	endonuclease [EC 3.1.30.-] precursor - barley dbj BA28942.1 endonuclease [Hordeum vulgare subsp. vulgare] COG0823: Periplasmic component of the Tol biopolymer transport system [Cytophaga hutchinsonii]			
	48854977	57	4.00E-89	Cytophaga hutchinsonii	COG0885: 5,10-methylenetetrahydrofolate reductase [Cytophaga hutchinsonii]			1.7.99.5
4685, 4686 4687, 4688	15615605	37	3.00E-30	Bacillus halodurans C-125	glutamate-1-semialdehyde 2,1-aminotransferase [Bacillus halodurans C- 125] dbj BAB06762.1 glutamate-1-semialdehyde 2,1-aminotransferase [Bacillus halodurans C-125] sp Q9K8G3 GSA_BACHD Glutamate-1- semialdehyde 2,1-aminotransferase (GSA) (Glutamate-1-semialdehyde aminotransferase) (GSA-AT) pir C84030 glutamate-1-semialdehyde 2,1- aminotransferase hemL [imported] - Bacillus halodurans (strain C-125) unnamed protein product [Kluyveromyces fragilis] emb CAG9948.1 unnamed protein product [Kluyveromyces fragilis] NRRL Y-1140]			5.4.3.8
4691, 4692 4693, 4694	50308779	37	3.00E-36	Cytophaga hutchinsonii	COG0151: Phosphoribosylamine-glycine ligase [Cytophaga hutchinsonii]			1.---
	48855741	55	8.00E-81	Cytophaga hutchinsonii	COG1408: Predicted phosphohydrolases [Cytophaga hutchinsonii]			6.3.4.13
4697, 4698 4699, 4700	37523515	77	8.00E-77	Gloeobacter violaceus PCC 7421	rifampin ADP-ribosyl transferase [Gloeobacter violaceus PCC 7421] dbj BAC91887.1 rifampin ADP-ribosyl transferase [Gloeobacter violaceus PCC 7421] COG1290: Cytochrome b subunit of the bc complex [Mesorhizobium sp. BNC1]	Gloeobacter violaceus PCC 7421 DNA, complete genome	82	6.00E-81
4701, 4702	45680978	27	3.00E-20	Mesorhizobium sp. BNC1	putative cell-cycle protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76700.1 putative cell-cycle protein [Bacteroides thetaiotaomicron VPI-5482]			1.2.99.5
	29347003	37	5.00E-43	Bacteroides thetaitaomicron VPI-5482				

4703, 4704	20089503	35	1.00E-44	Methanosarcina acetivorans C2A	3-hydroxyisobutyrate dehydrogenase [Methanosarcina acetivorans str. C2A]				1.1.1.31
4705, 4706	48854136	22	2.00E-16	Cytophaga hutchinsonii	COG1566: Multidrug resistance efflux pump [Cytophaga hutchinsonii]				
4707, 4708	37523705	23	4.00E-07	Gloeobacter violaceus PCC 7421	hypothetical protein glt4136 [Gloeobacter violaceus PCC 7421] dbj BAC92077.1 glt4136 [Gloeobacter violaceus PCC 7421]				
4709, 4710	23125049	56	3.00E-32	Nostoc punctiforme PCC 73102	COG1225: Peroxiredoxin [Nostoc punctiforme PCC 73102]				1.6.4.-
471, 472	53713334	24	2.00E-12	Bacteroides fragilis YCH46	putative ABC transporter permease [Bacteroides fragilis YCH46] dbj BAD48792.1 putative ABC transporter permease [Bacteroides fragilis YCH46]				
4711, 4712	48854837	31	8.00E-20	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]				
4715, 4716	48854837	38	6.00E-31	Cytophaga hutchinsonii	COG1595: DNA-directed RNA polymerase specialized sigma subunit, sigma24 homolog [Cytophaga hutchinsonii]				
4717, 4718	53713847	69	1.00E-104	Bacteroides fragilis YCH46	GTP-binding protein [Bacteroides fragilis YCH46] dbj BAD49305.1 GTP- binding protein [Bacteroides fragilis YCH46]	Bacillus halodurans C-125 DNA, complete genome, section 5/14	86	7.00E-19	
4719, 4720	40643170	55	5.00E-94	Leptospira biflexa temperate bacteriophage LE1	unnamed protein product [Leptospira biflexa temperate bacteriophage LE1]				
4721, 4722	48856951	36	3.00E-13	Cytophaga hutchinsonii	COG0019: Diaminopimelate decarboxylase [Cytophaga hutchinsonii]				4.1.1.20
4725, 4726	28212149	48	2.00E-35	Clostridium tetani E88	tRNA pseudouridine synthase A [Clostridium tetani E88] gb AAO37030.1 tRNA pseudouridine synthase A [Clostridium tetani E88] sp Q890R5 TRA2_CLOTE tRNA pseudouridine synthase A 2 (Pseudouridylylase synthase 12) (Pseudouridylylase synthase 12) (Uracil hydrolyase 2)				4.2.1.70
4729, 4730	52840322	47	2.00E-58	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	phosphoribosylglycinamide synthetase ATP-grasp (A) domain protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU26174.1 phosphoribosylglycinamide synthetase ATP-grasp (A) domain protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]				

4731, 4732	29347017	62	4.00E-97	Bacteroides thetaiotaomicron VPI-5482	methylentetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76714.1 methylentetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase [Bacteroides thetaiotaomicron VPI-5482]	1.5.1.5
4733, 4734	48893492	36	1.00E-42	Trichodesmium erythraeum IMS101	COG0587: DNA polymerase III, alpha subunit [Trichodesmium erythraeum IMS101]	2.7.7.7
4735, 4736	48840221	35	4.00E-30	Methanosarcina barkeri str. fusaro	COG0463: Glycosyltransferases involved in cell wall biogenesis [Methanosarcina barkeri str. fusaro]	
4737, 4738	42780089	46	8.00E-21	Bacillus cereus ATCC 10987	hypothetical protein BCE1013 [Bacillus cereus ATCC 10987] gb AAS39944.1 conserved hypothetical protein [Bacillus cereus ATCC 10987]	
4739, 4740	48856971	65	2.00E-94	Cytophaga hutchinsonii	COG0138: AICAR transformylase/IMP cyclohydrolase PurH (only IMP cyclohydrolase domain in Aful) [Cytophaga hutchinsonii]	2.1.2.3
4741, 4742	48854286	35	5.00E-19	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]	
4743, 4744	48853692	53	6.00E-47	Cytophaga hutchinsonii	COG1273: Uncharacterized conserved protein [Cytophaga hutchinsonii]	6.5.1.2
4745, 4746	48847026	34	1.00E-52	Geobacter metallireducens GS 15	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]	Oryza sativa (japonica cultivar- group), mRNA ## 8.00E-07 2.7.3.-
4749, 4750	27904689	35	6.00E-09	Buchnera aphidicola str. Bp (Baizongia pistaciae)	GMP reductase [Buchnera aphidicola str. Bp (Baizongia pistaciae)] gb AAO26920.1 GMP reductase [Buchnera aphidicola str. Bp (Baizongia pistaciae)] sp P59443 GUAC_BUCBP GMP reductase (Guanosine 5'- monophosphate oxidoreductase) (Guanosine monophosphate reductase)	1.6.6.8
4751, 4752	48863265	34	5.00E-09	Microbulifer degradans 2-40	COG0402: Cytosine deaminase and related metal-dependent hydrolases [Microbulifer degradans 2-40]	
4753, 4754	48854732	35	8.00E-36	Cytophaga hutchinsonii	COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii]	
4755, 4756	48853949	67	1.00E-141	Cytophaga hutchinsonii	COG0187: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), B subunit [Cytophaga hutchinsonii]	5.99.1.-
4757, 4758	16329398	34	1.00E-17	Synechocystis sp. PCC 6803	hybrid sensory kinase [Synechocystis sp. PCC 6803] dbj BAA16806.1 hybrid sensory kinase [Synechocystis sp. PCC 6803] pir S74654 sensory transduction histidine kinase sll1672 - Synechocystis sp. (strain PCC 6803)	90 6.00E-07 2.7.3.-
4759, 4760	16329398	34	6.00E-18	Synechocystis sp. PCC 6803	hybrid sensory kinase [Synechocystis sp. PCC 6803] dbj BAA16806.1 hybrid sensory kinase [Synechocystis sp. PCC 6803] pir S74654 sensory transduction histidine kinase sll1672 - Synechocystis sp. (strain PCC 6803)	90 4.00E-07 2.7.3.-

4761,	23125020	25	1.00E-09	Nostoc punctiforme PCC 73102	COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102]			2.7.3.-
4762				Cytophaga	COG1024: Enoyl-CoA hydratase/carnitine racemase [Cytophaga hutchinsonii]			4.2.1.17
4763,	48853568	40	1.00E-45	hutchinsonii				
4764				Geobacter				
4767,				metallireducens GS				
4768	48845451	30	1.00E-33	15	COG0366: Glycosidases [Geobacter metallireducens GS-15]			
477,				Nanoarchaeum	hypothetical protein NEQ511 [Nanoarchaeum equitans Kin4-M]			
478	41615293	35	8.00E-13	equitans Kin4-M	gb AAR39352.1 NEQ511 [Nanoarchaeum equitans Kin4-M]			3.5.1.16
4771,				Bacteroides fragilis	sialate O-acetyltransferase [Bacteroides fragilis YCH46] dbj BAC56897.1			
4772	53713020	41	2.00E-37	YCH46	sialate O-acetyltransferase [Bacteroides fragilis YCH46] dbj BAD48478.1			3.1.1.47
					sialate O-acetyltransferase [Bacteroides fragilis YCH46]			
4773,				Pyrococcus	arginyl-tRNA synthetase [Pyrococcus furiosus DSM 3638] gb AAL81504.1			
4774	18977752	37	2.00E-27	furiosus DSM 3638	arginyl-tRNA synthetase [Pyrococcus furiosus DSM 3638]			
4775,				Cytophaga	sp Q8U149 SYR_PYRFU Arginyl-tRNA synthetase (Arginine--tRNA ligase) (ArgRS)			6.1.1.19
4776	48855955	34	3.00E-32	hutchinsonii				1.11.1.5
4779,				Neisseria	COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii]			
4780	15794814	62	2.00E-60	meningitidis Z2491	DNA-3-methyladenine glycosylase I [Neisseria meningitidis Z2491]			
				Geobacter	emb CAB85151.1 DNA-3-methyladenine glycosylase I [Neisseria meningitidis Z2491] pir A81821 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) NMA1931 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)			3.2.2.20
4781,				metallireducens GS				
4782	48844153	42	1.00E-13	15	hypothetical protein Gmet02003361 [Geobacter metallireducens GS-15]			
4783,				Cytophaga	COG0721: Asp-tRNAAsn/Glu-tRNAAla amidotransferase C subunit			6.3.5.-
4784	48853683	57	2.00E-25	hutchinsonii	[Cytophaga hutchinsonii]			
4787,	AAG4650				Desc:Arabidopsis thaliana protein fragment SEQ ID NO: 58507.			
4788	0	51	3.00E-15		Org:Arabidopsis thaliana			
479,				Clostridium				
480	48860398	28	9.00E-11	thermocellum ATCC 27405	COG1408: Predicted phosphohydrolases [Clostridium thermocellum ATCC 27405]			
4791,				Geobacter				
4792	48846050	34	1.00E-16	metallireducens GS	hypothetical protein Gmet02001503 [Geobacter metallireducens GS-15]			
4793,					COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Cytophaga hutchinsonii]			
4794	48853682	33	2.00E-07	hutchinsonii				

4795, 4796, 4797, 4798	48854564 48854757	53 43	5.00E-67 5.00E-35	Cytophaga hutchinsonii Cytophaga hutchinsonii	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii] COG1131: ABC-type multidrug transport system, ATPase component [Cytophaga hutchinsonii]			2.7.3.- 3.6.3.33
4799, 4800	33594991	36	7.00E-13	Bordetella parapertussis 12822	ferredoxin [Bordetella parapertussis 12822] ref NP_879432.1 ferredoxin [Bordetella pertussis Tohama I] ref NP_886828.1 ferredoxin [Bordetella bronchiseptica RB50] emb CAE30777.1 ferredoxin [Bordetella bronchiseptica RB50] emb CAE40017.1 ferredoxin [Bordetella parapertussis] emb CAE44914.1 ferredoxin [Bordetella pertussis Tohama I]		1.-.-.-	
4803, 4804	48855541	79	2.00E-62	Cytophaga hutchinsonii	COG1875: Predicted ATPase related to phosphate starvation-inducible protein PhoH [Cytophaga hutchinsonii]	Chlamydia muridarum section 27 of 85 of the complete genome	93 1.00E-06	
4809, 4810	48853628	48	1.00E-41	Cytophaga hutchinsonii	COG0006: Xaa-Pro aminopeptidase [Cytophaga hutchinsonii]		3.4.11.9	
481, 482	48856298	68	3.00E-43	Cytophaga hutchinsonii	COG0317: Guanosine polyphosphate pyrophosphohydrolases/synthetases [Cytophaga hutchinsonii] hypothetical protein LIC11281 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_712912.1 hypothetical protein LA2731 [Leptospira interrogans serovar Lai str. 56601] gb AAN49930.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AAS69886.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] aminopeptidase Y [Clostridium tetani E88] gb AAO34970.1 aminopeptidase Y [Clostridium tetani E88]		2.7.6.5	
4811, 4812 4813, 4814	45657163 28210089	57 25	3.00E-30 5.00E-09	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130 Clostridium tetani E88	two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj BAC48127.1 two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110]		2.7.3.-	
4815, 4816	27377973	49	2.00E-59	Bradyrhizobium japonicum USDA 110	two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj BAC48127.1 two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110]		2.7.3.-	
4817, 4818	27377973	46	3.00E-52	Bradyrhizobium japonicum USDA 110	phage terminase-like protein large subunit [Bacillus clausii KSM-K16] dbj BAD63867.1 phage terminase-like protein large subunit [Bacillus clausii KSM-K16]		2.7.3.-	
4819, 4820	56963101	25	2.00E-11	Bacillus clausii KSM-K16	COG3033: Tryptophanase [Nostoc punctiforme PCC 73102] COG1127: ABC-type transport system involved in resistance to organic solvents, ATPase component [Cytophaga hutchinsonii]	C.freundii tpl gene for tyrosine phenol- lyase	86 3.00E-18 4.1.99.2	
4821, 4822 4823, 4824	23127778 48853579	70 53	1.00E-107 8.00E-30	Nostoc punctiforme PCC 73102 Cytophaga hutchinsonii			1.8.-.-	

4825, 4826	46198917	28	3.00E-17	Thermus thermophilus HB27	transcriptional regulator, tatR family [Thermus thermophilus HB27] gb AA80957.1 transcriptional regulator, tatR family [Thermus thermophilus HB27]				
4827, 4828	45521476	85	2.00E-65	Methylobacillus flagellatus KT	COG0499: S-adenosylhomocysteine hydrolase [Methylobacillus flagellatus KT]	Bordetella pertussis strain Tohama I, complete genome; segment 10/12	87	2.00E-57	3.3.1.1
4829, 4830	48830870	40	1.00E-11	Magnetococcus sp. MC-1	COG0460: Homoserine dehydrogenase [Magnetococcus sp. MC-1]				1.1.1.3
483, 484	20808896	37	7.00E-39	Thermoanaerobact er tengcongensis MB4	UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4] gb AAM2567.1.1 UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4]				6.3.2.15
4833, 4834	23128506	47	2.00E-56	Nostoc punctiforme PCC 73102	COG0010: Arginase/agmatinase/formimionoglutamate hydrolase, arginase family [Nostoc punctiforme PCC 73102]				3.5.3.11
4835, 4836	48853912	30	1.00E-25	Cytophaga hutchinsonii	COG1166: Arginine decarboxylase (spermidine biosynthesis) [Cytophaga hutchinsonii]				4.1.1.20
4837, 4838	32474556	33	2.00E-21	Rhodopirellula ballica SH 1	hypothetical protein RB6958 [Rhodopirellula ballica SH 1] emb CAD75097.1 conserved hypothetical protein [Pirellula sp.]				
4839, 4840	32474556	33	2.00E-21	Rhodopirellula ballica SH 1	hypothetical protein RB6958 [Rhodopirellula ballica SH 1] emb CAD75097.1 conserved hypothetical protein [Pirellula sp.]				
4847, 4848	48855210	24	3.00E-10	Cytophaga hutchinsonii	COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii]				
4849, 4850	48853964	44	3.00E-47	Cytophaga hutchinsonii	COG0111: Phosphoglycerate dehydrogenase and related dehydrogenases [Cytophaga hutchinsonii]				1.1.1.95
485, 486	20808896	39	2.00E-35	Thermoanaerobact er tengcongensis MB4	UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4] gb AAM2567.1.1 UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4]				6.3.2.15
4853, 4854	21673003	59	2.00E-28	Chlorobium tepidum TLS	alpha oxoglutarate ferredoxin oxidoreductase, beta subunit [Chlorobium tepidum TLS] gb AAM71410.1 alpha oxoglutarate ferredoxin oxidoreductase, beta subunit [Chlorobium tepidum TLS]				1.2.7.3
4855, 4856	16124371	32	1.00E-09	Caulobacter crescentus CB15	hypothetical protein CC0116 [Caulobacter crescentus CB15] gb AAK22103.1 hypothetical protein [Caulobacter crescentus CB15] pir C87263 hypothetical protein CC0116 [imported] - Caulobacter crescentus				
4861, 4862	53713899	39	2.00E-16	Bacteroides fragilis YCH46	hypothetical protein BF2607 [Bacteroides fragilis YCH46] dbj BAD49357.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				

[illegible]

4931, 4932	48854681	34	2.00E-09	Cytophaga hutchinsonii	hypothetical protein Chut02002347 [Cytophaga hutchinsonii]				
4933, 4934	48853375	48	2.00E-10	Cytophaga hutchinsonii	COG4430: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
4935, 4936	15895033	40	3.00E-10	Clostridium acetobutylicum ATCC 824	Predicted nucleic acid binding protein, containing KH domain [Clostridium acetobutylicum ATCC 824] gb AAK79722.1 Predicted nucleic acid binding protein, containing KH domain [Clostridium acetobutylicum ATCC 824] pir G97116 probable nucleic acid binding protein, containing KH domain [imported] - Clostridium acetobutylicum sp Q97196 YH56_CLOAB Hypothetical UPF0109 protein CAC1756				
4941, 4942	20090716	30	1.00E-29	Methanosarcina acetivorans C2A	hypothetical protein MA1866 [Methanosarcina acetivorans C2A] gb AAM0527.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A]				
4943, 4944	30249879	44	2.00E-42	Nitrosomonas europaea ATCC 19718	Sulfate transporter [Nitrosomonas europaea ATCC 19718] emb CAD85838.1 Sulfate transporter [Nitrosomonas europaea ATCC 19718]				
4945, 4946	53714523	27	5.00E-28	Bacteroides fragilis YCH46	hypothetical protein BF3236 [Bacteroides fragilis YCH46] db BAD49981.1 hypothetical protein [Bacteroides fragilis YCH46]				
4949, 4950	48856903	38	1.00E-55	Cytophaga hutchinsonii	COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii]				
495, 496	5777601	44	1.00E-41	Lampetra fluviatilis	polymerase polypeptide [Lampetra fluviatilis]				3.4.23.-
4951, 4952	48895505	42	5.00E-18	Trichodesmium erythraeum IMS101	COG3222: Uncharacterized protein conserved in bacteria [Trichodesmium erythraeum IMS101]				
4953, 4954	48854204	43	3.00E-46	Cytophaga hutchinsonii	COG0297: Glycogen synthase [Cytophaga hutchinsonii]				2.4.1.21
4957, 4958	20094865	37	6.00E-45	Methanopyrus kandleri AV19	Fe-S oxidoreductase [Methanopyrus kandleri AV19] gb AAM02642.1 Fe-S oxidoreductase [Methanopyrus kandleri AV19]				
4959, 4960	28854417	33	1.00E-13	Pseudomonas syringae pv. tomato str. DC3000	ferredoxin--NADP reductase [Pseudomonas syringae pv. tomato str. DC3000] ref NP_793786.1 ferredoxin--NADP reductase [Pseudomonas syringae pv. tomato str. DC3000]				1.18.1.2
4963, 4964	9948447	28	2.00E-15	Pseudomonas aeruginosa PAO1	hypothetical protein PA2403 [Pseudomonas aeruginosa PAO1] ref ZP_00140125.1 COG3182: Uncharacterized iron-regulated membrane protein [Pseudomonas aeruginosa UCBP-PA14] pir A83344 hypothetical protein PA2403 [imported] - Pseudomonas aeruginosa (strain PAO1)				
4967, 4968	53760034	52	2.00E-38	Methylobacillus flagellatus KT	ref NP_251093.1 hypothetical protein PA2403 [Pseudomonas aeruginosa PAO1] COG2870: ADP-heptose synthase, bifunctional sugar kinase/adenylyltransferase [Methylobacillus flagellatus KT]				2.7.7.39

4979, 4980	48846050	34	6.00E-23	Geobacter metallireducens GS-15	hypothetical protein Gmet02001503 [Geobacter metallireducens GS-15]				
4983, 4984	29349593	57	3.00E-66	Bacteroides thetaiotaomicron VPI-5482	xylosidase/arabinosidase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79290.1 xylosidase/arabinosidase [Bacteroides thetaiotaomicron VPI-5482]				3.2.1.37
4987, 4988	28262873	55	3.00E-91	Rickettsia sibirica 246	preprotein translocase secA subunit [Rickettsia sibirica 246] ref ZP_00142968.1 preprotein translocase secA subunit [Rickettsia sibirica 246]	Uncultured marine gamma proteobacterium EB000-45B06 fosmid clone	91	2.00E-10	
4989, 4990	32307865	43	6.00E-53	Rickettsia rickettsii	preprotein translocase SecA subunit [Rickettsia rickettsii] ref ZP_00153869.2 COG0653: Preprotein translocase subunit SecA (ATPase, RNA helicase) [Rickettsia rickettsii]				
499, 500	15893497	34	7.00E-10	Clostridium acetobutylicum ATCC 824	Sortase (surface protein transpeptidase), YHCS B subtilis ortholog [Clostridium acetobutylicum ATCC 824] gb AAK78186.1 Sortase (surface protein transpeptidase), YHCS B subtilis ortholog [Clostridium acetobutylicum ATCC 824] pir G96924 sortase (surface protein transpeptidase), YHCS B. subtilis ortholog [imported] - Clostridium acetobutylicum				
4991, 4992	29348249	51	9.00E-39	Bacteroides thetaiotaomicron VPI-5482	O-methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77946.1 O-methyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.1.1.-
4993, 4994	50085810	42	2.00E-51	Acinetobacter sp. ADP1	hypothetical protein ACIAD2753 [Acinetobacter sp. ADP1] emb CAG69498.1 hypothetical protein [Acinetobacter sp. ADP1]				
4995, 4996	48856863	39	2.00E-27	Cytophaga hutchinsonii	COG1073: Hydrolases of the alpha/beta superfamily [Cytophaga hutchinsonii]				
4997, 4998	53711739	29	9.00E-25	Bacteroides fragilis YCH46	hypothetical protein BF0448 [Bacteroides fragilis YCH46] db BAD47197.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
4999, 5000	ABP2662 0	31	4.00E-08		Desc:Streptococcus polypeptide SEQ ID NO 2416. Org:Streptococcus agalactiae				
5, 6	48855182	30	8.00E-13	Cytophaga hutchinsonii	COG2911: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
5005, 5006	26991423	63	3.00E-87	Pseudomonas putida KT2440	type I restriction-modification system, R subunit [Pseudomonas putida KT2440] gb AAN70312.1 type I restriction-modification system, R subunit [Pseudomonas putida KT2440]				3.1.21.3
5007, 5008	48855480	60	7.00E-91	Cytophaga hutchinsonii	COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Cytophaga hutchinsonii]				1.8.-

501, 502	20808329	47	1.00E-38	Thermoanaerobacter tengcongensis MB4	hypothetical protein TTE1925 [Thermoanaerobacter tengcongensis MB4] gb AA025104.1 conserved hypothetical protein [Thermoanaerobacter tengcongensis MB4]			
5011, 5012	50086533	40	6.00E-10	Acinetobacter sp. ADP1	hypothetical protein ACIAD3581 [Acinetobacter sp. ADP1] emb CAG70221.1 conserved hypothetical protein [Acinetobacter sp. ADP1] hypothetical protein CC3273 [Caulobacter crescentus CB15] gb AAK25235.1 hypothetical protein [Caulobacter crescentus CB15] pir G87654 hypothetical protein CC3273 [imported] - Caulobacter crescentus			2.3.1.-
5015, 5016	16127503	47	8.00E-73	Caulobacter crescentus CB15	COG0072: Phenylalanyl-tRNA synthetase beta subunit [Cytophaga hutchinsonii]			6.1.1.20
5017, 5018	48854667	43	4.00E-42	Cytophaga hutchinsonii	hypothetical protein Chut020071868 [Cytophaga hutchinsonii]			
5021, 5022	48855525	39	1.00E-13	Cytophaga hutchinsonii	Methyl-accepting chemotaxis protein [Methanosarcina mazei Go1] gb AAM30029.1 Methyl-accepting chemotaxis protein [Methanosarcina mazei Go1]			
5023, 5024	21226435	57	3.00E-56	Methanosarcina mazei Go1	Desc:Lactococcus lactis protein murG. Org:Lactococcus lactis IL1403 dioxigenase [Bacteroides fragilis YCH46] db BAD48225.1 dioxigenase [Bacteroides fragilis YCH46]			2.4.1.-
5029, 5030	ABB5493	49	2.00E-34	Bacteroides fragilis YCH46	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA precursor [Buchnera aphidicola str. Sg (Schizaphis graminum)] gb AAM68057.1 FKBP-type peptidyl-prolyl cis-trans isomerase [Buchnera aphidicola str. Sg (Schizaphis graminum)] sp Q8K943 FKBA_BUCAP FKBP-type peptidyl-prolyl cis-trans isomerase fkpA (PIase) (Rotamase)			1.3.1.9
5039, 5040	21672779	44	7.00E-16	Buchnera aphidicola str. Sg (Schizaphis graminum)	putative bi-domain oxidoreductase [Streptomyces sp. 139] hypothetical protein Smb20696 [Sinorhizobium meliloti 1021] pir C96017 hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid pSymB emb CAC49803.1 HYPOTHETICAL PROTEIN [Sinorhizobium meliloti 1021]			5.2.1.8
5041, 5042	22657439	38	5.00E-14	Streptomyces sp. 139	similar to hypothetical protein [Rattus norvegicus]			1.1.1.-
5043, 5044	16265151	30	4.00E-07	Sinorhizobium meliloti 1021	hemagglutinin [Bacteroides thetaiotaomicron VPI-5482] gb AAO76645.1 hemagglutinin [Bacteroides thetaiotaomicron VPI-5482]			
5045, 5046	34860755	21	5.00E-21	Rattus norvegicus	protease [Nostoc sp. PCC 7120] pir AI1930 proteinase [imported] - Nostoc sp. (strain PCC 7120) db BAB72953.1 protease [Nostoc sp. PCC 7120]			3.1.11.-
505, 506	29346948	29	5.00E-07	Bacteroides thetaiotaomicron VPI-5482				
5051, 5052	17228491	73	9.00E-17	Nostoc sp. PCC 7120				3.4.21.4 8

5055, 5056	16081128	34	5.00E-26	168	Bacillus subtilis subsp. subtilis str.	hypothetical protein BSU40760 [Bacillus subtilis subsp. subtilis str. 168] emb[CAB16113.1] yyaP [Bacillus subtilis subsp. subtilis str. 168] pir[S66001 conserved hypothetical protein yyaP - Bacillus subtilis sp P37508 YYAP_BACSU Hypothetical protein yyaP dbj BAA05207.1 unknown [Bacillus subtilis]			3.4.24.-
5059, 5060	48854514	44	7.00E-52	hutchinsonii	Cytophaga hutchinsonii	COG1216: Predicted glycosyltransferases [Cytophaga hutchinsonii]			2.4.1.-
5061, 5062	7592812	45	1.00E-17	itans	Actinobacillus actinomycetemcomitans	mannosyl transferase [Actinobacillus actinomycetemcomitans]			2.4.1.-
5063, 5064	48856118	50	2.00E-47	hutchinsonii	Cytophaga hutchinsonii	COG0242: N-formylmethionyl-tRNA deformylase [Cytophaga hutchinsonii]			3.5.1.88
5067, 5068	48854286	35	2.00E-25	hutchinsonii	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]			
507, 508	48855576	27	2.00E-21	hutchinsonii	Cytophaga hutchinsonii	COG4591: ABC-type transport system, involved in lipoprotein release, permease component [Cytophaga hutchinsonii]			
5071, 5072	53795729	44	7.00E-72	aurantiacus	Chloroflexus aurantiacus	COG0827: Adenine-specific DNA methylase [Chloroflexus aurantiacus]			2.1.1.72
5073, 5074	53795729	43	7.00E-24	aurantiacus	Chloroflexus aurantiacus	COG0827: Adenine-specific DNA methylase [Chloroflexus aurantiacus]			
5075, 5076	53713856	31	3.00E-39	YCH46	Bacteroides fragilis YCH46	phenylalanyl-tRNA synthetase beta chain [Bacteroides fragilis YCH46] dbj BAD49314.1 phenylalanyl-tRNA synthetase beta chain [Bacteroides fragilis YCH46]			6.1.1.20
5077, 5078	ABP2564 0	35	5.00E-08			Desc:Streptococcus polypeptide SEQ ID NO 456. Org:Streptococcus pyogenes			2.7.3.-
5079, 5080	34396630	56	1.00E-43	gingivalis W83	Porphyromonas gingivalis W83	SsrA-binding protein [Porphyromonas gingivalis W83] ref NP_904797.1 SsrA-binding protein [Porphyromonas gingivalis W83] sp Q7MWT5 SSRP_PORGI SsrA-binding protein			
5081, 5082	52006884	44	2.00E-26	25259	Thiobacillus denitrificans ATCC 25259	COG0543: 2-polyphenylphenol hydroxylase and related flavodoxin oxidoreductases [Thiobacillus denitrificans ATCC 25259]			
5083, 5084	16127932	51	3.00E-70	rescensu CB15	Caulobacter rescensu CB15	peptidyl-dipeptidase Dcp [Caulobacter crescentus CB15] gb AAK25864.1 peptidyl-dipeptidase Dcp [Caulobacter crescentus CB15] pir D87708 peptidyl-dipeptidase Dcp [Imported] - Caulobacter crescentus putative two-component system response regulator, no kinase domain [Bacteroides thetaiotaomicron VPI-5482] gb AAO79223.1 putative two-component system response regulator, no kinase domain [Bacteroides thetaiotaomicron VPI-5482]			3.4.15.5
5089, 5090	29349526	44	4.00E-21	VPI-5482	Bacteroides thetaitaomicron VPI-5482				

5091,	57159416	33	1.00E-15	Thermococcus kodakaraensis	CDC48VCP homolog, AAA superfamily [Thermococcus kodakaraensis] ref YP_183570.1 CDC48VCP homolog, AAA superfamily [Thermococcus kodakaraensis]			3.6.1.3
5092								
5093,	58460817	41	1.00E-46	Idiomarina loihiensis L2TR	Predicted amidohydrolase [Idiomarina loihiensis L2TR] gb AAV82549.1			
5094					Predicted amidohydrolase [Idiomarina loihiensis L2TR]			
5095,								
5096	15669515	37	4.00E-09	Methanocaldococcus jannaschii DSM 2661	cadmium resistance protein [Methanocaldococcus jannaschii DSM 2661] gb AAB99335.1 cadmium resistance protein [Methanocaldococcus jannaschii DSM 2661] sp Q58721 YD25_METJA Putative HTH-type transcriptional regulator MJ1325 pir D64465 hypothetical protein MJ1325 - Methanococcus jannaschii			
5097,								
5098	29349346	29	1.00E-09	Bacteroides thetaiotaomicron VPI-5482	ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gb AAO79043.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]			
5099,								
5100	20089535	27	1.00E-10	Methanosarcina acetivorans C2A	DNA primase [Methanosarcina acetivorans C2A] gb AAM04090.1 DNA primase [Methanosarcina acetivorans str. C2A] sp Q8TSZ5 PRIS_METAC Probable DNA primase small subunit			2.7.7.-
5101,								
5102	15678984	35	6.00E-28	Methanothermobacter thermautotrophicus str. Delta H	hypothetical protein MTH966 [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85462.1 conserved protein [Methanothermobacter thermautotrophicus str. Delta H] pir C69229 conserved hypothetical protein MTH966 - Methanobacterium thermoautotrophicum (strain Delta H)			
5105,								
5106	29348099	50	9.00E-57	Bacteroides thetaiotaomicron VPI-5482	histidine ammonia-lyase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77796.1 histidine ammonia-lyase [Bacteroides thetaiotaomicron VPI-5482]			4.3.1.3
5107,								
5108	53715428	59	3.00E-79	Bacteroides fragilis YCH46	histidine ammonia-lyase [Bacteroides fragilis YCH46] dbj BAD50886.1 histidine ammonia-lyase [Bacteroides fragilis YCH46]			4.3.1.3
511,								
512	15606650	30	9.00E-09	Aquifex aeolicus VF5	DNA primase [Aquifex aeolicus VF5] gb AAC07430.1 DNA primase [Aquifex aeolicus VF5] pir G70429 DNA primase - Aquifex aeolicus sp Q67465 PRIM_AQUAE DNA primase			2.7.7.-
5111,								
5112	53713534	47	1.00E-68	Bacteroides fragilis YCH46	probable oxidoreductase [Bacteroides fragilis YCH46] dbj BAD48992.1 probable oxidoreductase [Bacteroides fragilis YCH46]			1.-.-.-
5115,								
5116	48863265	34	5.00E-09	Microbulifer degradans 2-40	COG0402: Cytosine deaminase and related metal-dependent hydrolases [Microbulifer degradans 2-40]			
5121,								
5122	34397903	46	2.00E-17	Porphyromonas gingivalis W83	exonuclease ABC, C subunit [Porphyromonas gingivalis W83] ref NP_906065.1 exonuclease ABC, C subunit [Porphyromonas gingivalis W83]			
5123,								
5124	56460818	30	9.00E-29	Idiomarina loihiensis L2TR	Secreted enzyme, contains two amidohydrolase related domains [Idiomarina loihiensis L2TR] gb AAV82550.1 Secreted enzyme, contains two amidohydrolase related domains [Idiomarina loihiensis L2TR]			

5125, 5126	57234544	27	1.00E-08	Dehalococcoides ethenogenes 195	D-ala D-ala ligase [Dehalococcoides ethenogenes 195] gblAAW40049.1 D-ala D-ala ligase [Dehalococcoides ethenogenes 195]			6.3.2.4
5129, 5130	51598166	39	4.00E-19	Yersinia pseudotuberculosis IP 32953	possible restriction modification enzyme [Yersinia pseudotuberculosis IP 32953] embjCAH23119.1 possible restriction modification enzyme [Yersinia pseudotuberculosis IP 32953]			3.1.21.3
5131, 5132	46323894	23	1.00E-09	Burkholderia cepacia R1808	COG2856: Predicted Zn peptidase [Burkholderia cepacia R1808]			
5133, 5134	48856037	45	9.00E-11	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]			
5135, 5136	15794814	64	1.00E-51	Neisseria meningitidis Z2491	DNA-3-methyladenine glycosylase I [Neisseria meningitidis Z2491] embjCAB85151.1 DNA-3-methyladenine glycosylase I [Neisseria meningitidis Z2491] pir A81821 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) NMA1931 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)			3.2.2.20
5137, 5138	29349471	48	2.00E-37	Bacteroides thetaiotaomicron VPI-5482	NADH dehydrogenase I, chain I [Bacteroides thetaiotaomicron VPI-5482] gblAAO79168.1 NADH dehydrogenase I, chain I [Bacteroides thetaiotaomicron VPI-5482]			1.6.5.3
5139, 5140	17227393	65	9.00E-35	Nostoc sp. PCC 7120	hypothetical protein alr8019 [Nostoc sp. PCC 7120] pir AD2553 hypothetical protein alr8019 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120gamma dbj BAB77349.1 ORF_ID:alr8019-transposase-unknown protein [Nostoc sp. PCC 7120]			
5141, 5142	15669248	34	2.00E-28	Methanocaldococcus jannaschii DSM 2661	capsular polysaccharide biosynthesis protein M [Methanocaldococcus jannaschii DSM 2661] gblAAB99063.1 capsular polysaccharide biosynthesis protein M [Methanocaldococcus jannaschii DSM 2661] pir B64432 capsular polysaccharide biosynthesis protein M homolog - Methanocaldococcus jannaschii sp Q58459 YA59_METJA Hypothetical glycosyl transferase MJ1059			2.4.1.-
5145, 5146	48855659	37	6.00E-31	Cytophaga hutchinsonii	COG4251: Bacteriophytochrome (light-regulated signal transduction histidine kinase) [Cytophaga hutchinsonii]			2.7.3.-
5151, 5152	53730535	28	2.00E-18	Dechloromonas aromatica RCB	COG3385: FOG: Transposase and inactivated derivatives [Dechloromonas aromatica RCB]			
5153, 5154	42524381	41	3.00E-45	Bdellovibrio bacteriovorus HD100	DNA-directed RNA polymerase beta chain [Bdellovibrio bacteriovorus HD100] embjCAE80754.1 DNA-directed RNA polymerase beta chain [Bdellovibrio bacteriovorus HD100]	Pseudomonas syringae pv. tomato str. DC3000 section 3 of 21 of the complete genome	87	3.00E-12 2.7.7.6

5157,	21674733	33	3.00E-16	Chlorobium tepidum TLS	cysteine synthase/cystathionine beta-synthase family protein [Chlorobium tepidum TLS]				4.2.1.22
5158	48856049	45	1.00E-31	Cytophaga hutchinsonii	hypothetical protein Chut02001282 [Cytophaga hutchinsonii]				
5159,				Thermoanaerobact	DNA primase (bacterial type) [Thermoanaerobacter tengcongensis MB4]				
5160				er tengcongensis	gb AA024950.1 DNA primase (bacterial type) [Thermoanaerobacter tengcongensis MB4]				2.7.7.-
5161,	20808175	38	6.00E-49	MB4	transcriptional regulator, AraC family [Bacteroides thetaiotaomicron VPI-5482]				
5162				Bacteroides	thetataoomicron VPI-5482				
5163,	29347766	33	1.00E-13	VPI-5482	putative transcriptional regulator [Bacteroides fragilis YCH46]				
5164				Bacteroides fragilis	dbj BAD50718.1 putative transcriptional regulator [Bacteroides fragilis YCH46]				
5165,	53715260	46	2.00E-32	YCH46	COG0495: Leucyl-tRNA synthetase [Cytophaga hutchinsonii]				6.1.1.4
5166				Cytophaga	cytochrome c family protein [Geobacter sulfurreducens PCA]				
5167,	48855120	59	2.00E-76	hutchinsonii	gb AAR36650.1 cytochrome c family protein [Geobacter sulfurreducens PCA]				
5168				Geobacter	putative alpha/beta hydrolase [uncultured crenarchaeote]				3.1.1.1
5169,	39998349	47	1.00E-44	sulfurreducens	COG1033: Predicted exporters of the RND superfamily [Cytophaga hutchinsonii]				
5170				PCA					
517,				uncultured					
518	22797876	42	3.00E-29	crenarchaeote					
5175,				Cytophaga					
5176	48854362	43	1.00E-67	hutchinsonii					
				Legionella					
5177,				pneumophila str.					
5178	54295031	58	7.00E-99	Lens	hypothetical protein lp1211 [Legionella pneumophila str. Lens]			88	2.00E-10 2.3.1.85
				Oryza sativa	emb CAH16351.1 hypothetical protein [Legionella pneumophila str. Lens]				
5179,				(japonica cultivar-	ketose-bisphosphate aldolase class-II family-like [Oryza sativa (japonica cultivar-group)]				
5180	52077151	53	1.00E-26	group)					
				Geobacter					
5181,				metallireducens GS	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]				2.7.3.-
5182	48845444	46	5.00E-52	15					
				Lactobacillus					
5183,				plantarum	orf143 [Lactobacillus plantarum bacteriophage LP65] gb AAV35963.1				
5184	56693191	62	5.00E-10	LP65	orf143 [Lactobacillus plantarum bacteriophage LP65]				

5185,	53711742	55	2.00E-74	Bacteroides fragilis YCH46	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacteroides fragilis YCH46]			6.3.2.15
5186								
519,	48853904	52	6.00E-32	Cytophaga hutchinsonii	COG1843: Flagellar hook capping protein [Cytophaga hutchinsonii]			
520					integrase, site-specific recombinase [Bacteroides thetaiotaomicron VPI-5482] gblAAO77848.1 [integrase, site-specific recombinase [Bacteroides thetaiotaomicron VPI-5482]			
5191,	29348151	34	5.00E-38	Cytophaga hutchinsonii	COG1544: Ribosome-associated protein Y (PSrp-1) [Cytophaga hutchinsonii]			
5192								
5193,	48853519	42	3.00E-12	Chloroflexus aurantiacus	COG0438: Glycosyltransferase [Chloroflexus aurantiacus]			2.4.1.-
5195,	53797263	30	6.00E-39	Cytophaga hutchinsonii	COG0463: Glycosyltransferases involved in cell wall biogenesis [Cytophaga hutchinsonii]			2.-.-.-
5203,	48856035	40	2.00E-20	Cytophaga hutchinsonii				
5204								
5207,	48854843	46	2.00E-22	Magnetococcus sp. MC-1	COG0196: FAD synthase [Cytophaga hutchinsonii]			2.7.1.26
5208								
5209,	48831856	50	1.00E-48	Leptospira interrogans serovar Copenhagen str. Flocruz L1-130	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			2.7.3.-
5210								
521,	45656027	40	6.00E-50	Saccharopolyspora spinosa	hypothetical protein LIC10117 [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130] gblAAS68750.1 [conserved hypothetical protein [Leptospira interrogans serovar Copenhagen str. Flocruz L1-130]			
5211,	41350162	29	5.00E-15	Bacteroides fragilis YCH46	multi-domain regulatory protein, LuxR family [Saccharopolyspora spinosa]			
5212					UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacteroides fragilis YCH46]			6.3.2.15
5213,	53711742	33	4.00E-11	Cytophaga hutchinsonii	COG1251: NAD(P)H-nitrite reductase [Cytophaga hutchinsonii]			1.6.6.4
5214								
5217,	48855076	58	3.00E-65	Cytophaga hutchinsonii	hypothetical protein Chut02002697 [Cytophaga hutchinsonii]			
5218								
5219,	48854498	55	7.00E-96					
5220								

5221, 5222	12517826	57	3.00E-48	Escherichia coli O157:H7	putative peptidoglycan enzyme [Escherichia coli O157:H7 ref NP_289782.1 putative peptidoglycan enzyme [Escherichia coli O157:H7 EDL933] ref NP_312114.1 putative peptidoglycan enzyme [Escherichia coli O157:H7] pir B85985 probable peptidoglycan enzyme mtgA [imported] - Escherichia coli (strain O157:H7, substrain EDL933) dbj B837510.1 putative peptidoglycan enzyme [Escherichia coli O157:H7] pir G91139 probable peptidoglycan enzyme [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050952) sp Q8X911 MTGA_ECO57 Monofunctional biosynthetic peptidoglycan transglycosylase [Monofunctional TGase]	2.4.2.-
5223, 5224	30250418	31	2.00E-21	Nitrosomonas europaea ATCC 19718	DEAD/DEAH box helicase [Nitrosomonas europaea ATCC 19718] emb CAD8641.1 DEAD/DEAH box helicase [Nitrosomonas europaea ATCC 19718]	3.1.21.3
5229, 5230						3.4.24.-
523, 524	28262674	47	2.00E-48	Rickettsia sibirica 246	DNA ligase [Rickettsia sibirica 246] ref ZP_00142769.1 DNA ligase [Rickettsia sibirica 246]	6.5.1.2
5237, 5238	42523059	54	5.00E-58	Bdellovibrio bacteriovorus HD100	probable zinc proteinase [Bdellovibrio bacteriovorus HD100] emb CAE79432.1 probable zinc proteinase [Bdellovibrio bacteriovorus HD100]	3.4.99.-
5245, 5246	53711500	53	3.00E-37	Bacteroides fragilis YCH46	two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD46958.1 two-component system response regulator [Bacteroides fragilis YCH46]	2.7.3.-
5247, 5248	48891723	32	7.00E-16	Trichodesmium enrythraeum IMS101	COG0515: Serine/threonine protein kinase [Trichodesmium enrythraeum IMS101]	2.7.1.-
5251, 5252	48854312	36	3.00E-41	Cytophaga hutchinsonii	COG0370: Fe2+ transport system protein B [Cytophaga hutchinsonii]	
5253, 5254	29347685	61	2.00E-61	Bacteroides thetaiotaomicron VPI-5482	thymidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77382.1 thymidine kinase [Bacteroides thetaiotaomicron VPI-5482]	2.7.1.21
5259, 5260	23613218	25	7.00E-13	Plasmodium falciparum 3D7	hypothetical protein [Plasmodium falciparum 3D7] emb CAD51560.1 hypothetical protein [Plasmodium falciparum 3D7]	3.1.11.-
5263, 5264	23128321	33	4.00E-21	Nostoc punctiforme PCC 73102	COG4886: Leucine-rich repeat (LRR) protein [Nostoc punctiforme PCC 73102]	4.6.1.1
5265, 5266	20807353	31	7.00E-21	Thermoanaerobact er tengcongensis MB4	DNA-directed RNA polymerase specialized sigma subunits, sigma24 homologs [Thermoanaerobacter tengcongensis MB4] gb AAM24128.1 DNA- directed RNA polymerase specialized sigma subunits, sigma24 homologs [Thermoanaerobacter tengcongensis MB4]	

5267, 5268	21674062	51	2.00E-57	Chlorobium tepidum TLS	preprotein translocase SecA subunit [Chlorobium tepidum TLS] gb AAM72469.1 preprotein translocase SecA subunit [Chlorobium tepidum TLS]			
5269, 5270	6460190	30	1.00E-13	Deinococcus radiodurans	transcriptional regulator, TetR family [Deinococcus radiodurans] pir F75261 transcription regulator, TetR family - Deinococcus radiodurans (strain R1) ref NP_296097.1 transcriptional regulator, TetR family [Deinococcus radiodurans R1]			
5271, 5272	56476406	51	5.00E-57	Azoarcus sp. EbN1	hypothetical protein eba1785 [Azoarcus sp. EbN1] emb CAI07094.1 conserved hypothetical protein [Azoarcus sp. EbN1]			
5273, 5274	48854227	51	4.00E-13	Cytophaga hutchinsonii	COG2908: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
5275, 5276	17229012	67	3.00E-40	Nostoc sp. PCC 7120	hypothetical protein air1520 [Nostoc sp. PCC 7120] pir AB1996 hypothetical protein air1520 [imported] - Nostoc sp. (strain PCC 7120) db BAB77886.1 air1520 [Nostoc sp. PCC 7120]			
5277, 5278	15893463	59	2.00E-54	Clostridium acetobutylicum ATCC 824	ABC transporter (ATP-binding protein) [Clostridium acetobutylicum ATCC 824] gb AAK78152.1 ABC transporter (ATP-binding protein) [Clostridium acetobutylicum ATCC 824] pir E96920 ABC transporter (ATP-binding protein) CAC0169 [imported] - Clostridium acetobutylicum		1.8--	
5281, 5282	37528152	71	1.00E-103	Photobacterium luminescens subsp. laumondii TTO1	Type I site-specific deoxyribonuclease HsdR [Photobacterium luminescens subsp. laumondii TTO1] emb CAE16694.1 Type I site-specific deoxyribonuclease HsdR [Photobacterium luminescens subsp. laumondii TTO1]		81	3.00E-18
5287, 5288	48855091	36	2.00E-22	Cytophaga hutchinsonii	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Cytophaga hutchinsonii]			
5291, 5292	53713908	65	2.00E-29	Bacteroides fragilis YCH46	hypothetical protein BF2616 [Bacteroides fragilis YCH46] db BAD49366.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
5293, 5294	48862321	26	1.00E-16	Microbulbifer degradans 2-40	hypothetical protein Mdeg02002532 [Microbulbifer degradans 2-40] putative ABC transporter permease [Bacteroides fragilis YCH46]			
5295, 5296	53712889	30	4.00E-09	Bacteroides fragilis YCH46	db BAD48347.1 putative ABC transporter permease [Bacteroides fragilis YCH46]			
53, 54	AAW9886	7	4.00E-13		Desc.H. pylori GHPO 1695 protein. Org:Helicobacter pylori			2.1.1.72

5301,	18311381	46	4.00E-20	Clostridium perfringens str. 13	30S ribosomal protein S3 [Clostridium perfringens str. 13] dbj BAB82105.1]			
5302				Cytophaga hutchinsonii	30S ribosomal protein S3 [Clostridium perfringens str. 13] sp Q8XHS9 RS3_CLOPE 30S ribosomal protein S3			
5305,	48853434	67	2.00E-40	Rhodopirellula baltica SH 1	COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii]			2.7.7.24
5306				Bacillus thuringiensis serovar konkukian str. 97-27	arsenate reductase [Rhodopirellula baltica SH 1] emb CAD77194.1]			
5309,	32476822	53	2.00E-24	Cytophaga hutchinsonii	arsenate reductase [Pirellula sp.]			1.97.1.5
5310				Thermotoga maritima MSB8	hypothetical protein BT9727_1747 [Bacillus thuringiensis serovar konkukian str. 97-27] gb AA62754.1] hypothetical protein BT9727_1747 [Bacillus thuringiensis serovar konkukian str. 97-27]			
531,	49480552	32	4.00E-16	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-
5311,	48855191	48	6.00E-53	Bacteroides fragilis YCH46	putative two-component system sensor protein without kinase domain [Bacteroides fragilis YCH46] dbj BAD48617.1] putative two-component system sensor protein without kinase domain [Bacteroides fragilis YCH46]			2.7.3.-
5312	53713159	37	6.00E-25	Thermotoga maritima MSB8	hypothetical protein TM1631 [Thermotoga maritima MSB8] gb AAD36698.1]			
5321,				Cytophaga hutchinsonii	conserved hypothetical protein [Thermotoga maritima MSB8] pir G72229			
5322	15644379	38	1.00E-09	Cytophaga hutchinsonii	conserved hypothetical protein - Thermotoga maritima (strain MSB8)			
5323,	48856042	56	4.00E-39	Cytophaga hutchinsonii	COG0465: ATP-dependent Zn proteases [Cytophaga hutchinsonii]			3.4.24.-
5324				Cytophaga hutchinsonii	COG0465: ATP-dependent Zn proteases [Cytophaga hutchinsonii]			3.4.24.-
5325,	48856042	58	3.00E-55	Clostridium tetani E88	putative carbamoyl-phosphate synthase large chain [Clostridium tetani E88]			
5326				Mesorhizobium loti MAFF303099	gb AAO36241.1] putative carbamoyl-phosphate synthase large chain [Clostridium tetani E88]			6.3.4.13
5327,	28211360	38	4.00E-26	Ralstonia eutropha JMP134	hypothetical protein mli7009 [Mesorhizobium loti MAFF303099]			
5328				Microbulifer degradans 2-40	dbj BAB53194.1] mli7009 [Mesorhizobium loti MAFF303099]			
5333,	13475838	35	1.00E-26		COG1112: Superfamily I DNA and RNA helicases and helicase subunits			2.7.7.-
5334	53761281	35	8.00E-18		COG0577: ABC-type antimicrobial peptide transport system, permease component [Microbulifer degradans 2-40]			
5335,								
5336								
5341,								
5342								
5345,								
5346								

5347,	20808572	49	3.00E-62	Thermoanaerobacter tengcongensis MB4	Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains [Thermoanaerobacter tengcongensis MB4] gb AAM25347.1 Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains [Thermoanaerobacter tengcongensis MB4] sp Q8R841 GLMS_THETN				2.6.1.16
5348					Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase)				
5349,	48856843	50	5.00E-73	Cytophaga hutchinsonii	COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases				6.2.1.1
5350									
5351,	48732838	46	1.00E-20	Pseudomonas fluorescens PfO-1	COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Pseudomonas fluorescens PfO-1]				
5352					hypothetical protein MJ0570 [Methanocaldococcus jannaschii DSM 2661] gb AAB98564.1 conserved hypothetical protein [Methanocaldococcus jannaschii DSM 2661] pir B64371 hypothetical protein MJ0570 - Methanococcus jannaschii sp Q57990 Y570_METJA Hypothetical protein MJ0570				
5355,	15668750	34	6.00E-26	Methanocaldococcus jannaschii DSM 2661					
5356									
5357,				Chromobacterium violaceum ATCC 12472	conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_900582.1 hypothetical protein CV0912 [Chromobacterium violaceum ATCC 12472]				1.14.13.-
5358	34102220	36	6.00E-29		succinoglycan biosynthesis protein exoA [Clostridium tetani E88] gb AAO36740.1 succinoglycan biosynthesis protein exoA [Clostridium tetani E88]				
5359,				Clostridium tetani E88					
5360	28211859	41	9.00E-27	Bacteriophage RM 378	putative glycosyltransferases [Bacteriophage RM 378]				2.4.1.-
5365,									
5366	30044003	25	2.00E-12	Chloroflexus aurantiacus	COG0438: Glycosyltransferase [Chloroflexus aurantiacus]				
5367,	53794669	25	7.00E-10						
5368									
5369,					At5g28460/F21B23_120 [Arabidopsis thaliana] gb AAK97697.1 AT5g28460/F21B23_120 [Arabidopsis thaliana] ref NP_680234.1 pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] gb AAF88002.1 contains similarity to PPR family PFO1535 (Domain of unknown function), score=340.5, E=1.9e-98, N=2 [Arabidopsis thaliana]				
5370	27363272	26	1.00E-15	Arabidopsis thaliana					
537,				Psychrobacter sp. 273-4	COG2352: Phosphoenolpyruvate carboxylase [Psychrobacter sp. 273-4]				4.1.1.31
538	52853863	37	6.00E-25	Microbulifer degradans 2-40	COG2755: Lysophospholipase L1 and related esterases [Microbulifer degradans 2-40]				
5371,									
5372	48863713	61	8.00E-22	Bacteroides fragilis YCH46	peptide deformylase [Bacteroides fragilis YCH46] dbj BAD48431.1 peptide deformylase [Bacteroides fragilis YCH46]				3.5.1.88
5373,									
5374	53712973	42	1.00E-27						

5375,	53714080	36	5.00E-32	Bacteroides fragilis YCH46	tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]			
5376					dbj BAD49538.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]			
5377,	48854369	38	1.00E-28	Cytophaga hutchinsonii	COG0608: Single-stranded DNA-specific exonuclease [Cytophaga hutchinsonii]			3.1.-
5378					hypothetical protein MA1679 [Methanosarcina acetivorans C2A]			
5379,					gb AAM05086.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A]			
5380	20090531	42	2.00E-20	Microbulbifer degradans 2-40	COG0577: ABC-type antimicrobial peptide transport system, permease component [Microbulbifer degradans 2-40]			
5383,	48864231	31	1.00E-22	Wolinella succinogenes DSM 1740	ADP-HEPTOSE-LPS HEPTOSYLTRANSFERASE II (RFAF) [Wolinella succinogenes DSM 1740]			
5384					HEPTOSYLTRANSFERASE II (RFAF) [Wolinella succinogenes]			
5389,	34557794	31	1.00E-14					
5390								
539,								
540	48855609	77	2.00E-63	Cytophaga hutchinsonii	COG0178: Excinuclease ATPase subunit [Cytophaga hutchinsonii]	Bacteroides fragilis YCH46 DNA, complete genome	93 4.00E-07	
5395,					hypothetical protein aq_1006 [Aquifex aeolicus VF5] gb AAC07092.1			
5396	15606308	22	1.00E-08	Aquifex aeolicus VF5	hypothetical protein [Aquifex aeolicus VF5] pir A70387 conserved hypothetical protein aq_1006 - Aquifex aeolicus sp O67124 RA50_AQUAE Probable DNA double-strand break repair rad50 ATPase			
5399,								
5400	48856125	37	2.00E-28	Cytophaga hutchinsonii	COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii]			
5401,					MutT/NUDIX family protein [Burkholderia pseudomallei K96243]			
5402	53717978	30	3.00E-10	Burkholderia pseudomallei K96243	emb CAH34326.1 MutT/NUDIX family protein [Burkholderia pseudomallei K96243]			3.6.1.-
5405,								
5406	48854499	55	5.00E-39	Cytophaga hutchinsonii	COG0325: Predicted enzyme with a TIM-barrel fold [Cytophaga hutchinsonii]			2.7.3.-
5413,								
5414	15384032	32	4.00E-12	uncultured crenarchaeote 74A4	xanthine-guanine phosphoribosyltransferase [uncultured crenarchaeote 74A4]			2.4.2.-
5415,								
5416	48854158	52	2.00E-31	Cytophaga hutchinsonii	COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii]			1.11.1.1
5419,								
5420	48855100	55	1.00E-27	Cytophaga hutchinsonii	COG0424: Nucleotide-binding protein implicated in inhibition of septum formation [Cytophaga hutchinsonii]			
5421,								
5422	48855348	26	4.00E-09	Cytophaga hutchinsonii	hypothetical protein Chut02001679 [Cytophaga hutchinsonii]			
5427,					deoxyribonuclease, TatD family [Geobacter sulfurreducens PCA]			
5428	39997584	43	3.00E-57	Geobacter sulfurreducens PCA	gb AAR35862.1 deoxyribonuclease, TatD family [Geobacter sulfurreducens PCA]			3.1.21.-

543, 544	29346396	32	5.00E-23	Bacteroides thetaiotaomicron VPI-5482	conserved hypothetical protein, putative DNA-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO76093.1 conserved hypothetical protein, putative DNA-binding protein [Bacteroides thetaiotaomicron VPI-5482]			
5437, 5438	53715101	35	2.00E-31	Bacteroides fragilis YCH46	hypothetical protein BF3817 [Bacteroides fragilis YCH46] dbj BAD50559.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
5439, 5440	48853176	35	5.00E-38	Ferroplasma acidarmanus	COG0624: Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase and related deacylases [Ferroplasma acidarmanus]			3.5.1.16
5441, 5442	52550513	36	2.00E-08	uncultured archaeon GZfos9D8	conserved hypothetical protein [uncultured archaeon GZfos9D8]			
5443, 5444	48855541	79	2.00E-62	Cytophaga hutchinsonii	COG1875: Predicted ATPase related to phosphate starvation-inducible protein PhoH [Cytophaga hutchinsonii]	Chlamydia muridarum section 27 of 85 of the complete genome	93 1.00E-06	
545, 546	48853731	41	2.00E-22	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-
5453, 5454	17231921	40	3.00E-53	Nostoc sp. PCC 7120	hypothetical protein al4429 [Nostoc sp. PCC 7120] dbj BAB76128.1 hlpA (Nostoc sp. PCC 7120) pir AE2359 hypothetical protein hlpA [imported] - Nostoc sp. (strain PCC 7120)			
5455, 5456	23016842	40	8.00E-47	Magnetospirillum magnetotacticum MS-1	COG0367: Asparagine synthase (glutamine-hydrolyzing) [Magnetospirillum magnetotacticum MS-1]			6.3.5.4
5457, 5458	48855191	48	2.00E-53	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Cytophaga hutchinsonii]			2.7.3.-

5459,	37528266	28	3.00E-11	Photothabdus luminescens subsp. laumondii TTO1	Transposase, IS630 family [Photothabdus luminescens subsp. laumondii TTO1] ref[NP_930575.1] Transposase, IS630 family [Photothabdus luminescens subsp. laumondii TTO1] ref[NP_930493.1] Transposase, IS630 family [Photothabdus luminescens subsp. laumondii TTO1] ref[NP_930331.1] Transposase, IS630 family [Photothabdus luminescens subsp. laumondii TTO1] ref[NP_928792.1] Transposase, IS630 family [Photothabdus luminescens subsp. laumondii TTO1] ref[NP_928083.1] Transposase, IS630 family [Photothabdus luminescens subsp. laumondii TTO1] ref[NP_927821.1] Transposase, IS630 family [Photothabdus luminescens subsp. laumondii TTO1] emb[CAE16814.1] Transposase, IS630 family [Photothabdus luminescens subsp. laumondii TTO1] emb[CAE15731.1] Transposase, IS630 family [Photothabdus luminescens subsp. laumondii TTO1] emb[CAE15643.1] Transposase, IS630 family [Photothabdus luminescens subsp. laumondii TTO1] emb[CAE15473.1] Transposase, IS630 family [Photothabdus luminescens subsp. laumondii TTO1] emb[CAE13790.1] Transposase, IS630 family [Photothabdus luminescens subsp. laumondii TTO1] emb[CAE13033.1] Transposase, IS630 COG2171: Tetrahydrodipicolinate N-succinyltransferase [Cytophaga hutchinsonii]				2.3.1.11 7
5460,	48858605	67	4.00E-69	Cytophaga hutchinsonii	COG3124: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
5461,	48853925	39	3.00E-25	Cytophaga hutchinsonii	COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii]				2.7.7.24
5462,	48853434	69	1.00E-85	Cytophaga hutchinsonii	glyoxylase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] ref[YP_123011.1] hypothetical protein lpp0673 [Legionella pneumophila str. Paris] gb AAU26708.1 glyoxylase [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] emb[CAH11821.1] hypothetical protein [Legionella pneumophila str. Paris]				
5463,	52840856	50	3.00E-31	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	ABC transporter, ATP-binding/permease protein [Brucella suis 1330] gb AAN29385.1 ABC transporter, ATP-binding/permease protein [Brucella suis 1330]				
5464,	23501343	31	2.00E-29	Brucella suis 1330	COG0026: Phosphoribosylaminoimidazole carboxylase (NCAIR synthetase) [Cytophaga hutchinsonii]				4.1.1.21
5465,	48854305	44	2.00E-27	Cytophaga hutchinsonii	methionyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD51240.1 methionyl-tRNA synthetase [Bacteroides fragilis YCH46]	Mus musculus cDNA clone IMAGE:30025832	81	1.00E-41	6.1.1.10
5466,	53715782	62	1.00E-79	Bacteroides fragilis YCH46	COG3391: Uncharacterized conserved protein [Nostoc punctiforme PCC 73102]				
5467,	23126366	51	3.00E-61	Nostoc punctiforme PCC 73102					

5481,	48860370	41	2.00E-30	Clostridium thermocellum ATCC 27405	COG2197: Response regulator containing a CheY-like receiver domain and an HTH DNA-binding domain [Clostridium thermocellum ATCC 27405]			2.7.3.-
5482				Thermoanaerobacter tengcongensis MB4	hypothetical protein TTE0217 [Thermoanaerobacter tengcongensis MB4]			
5485,	20806743	43	4.00E-60	MB4	gb AAAM23518.1 conserved hypothetical protein [Thermoanaerobacter tengcongensis MB4]			
5486				Shewanella oneidensis MR-1	peptidase, M16 family [Shewanella oneidensis MR-1]			3.4.-.-
5487,	24375064	40	6.00E-48	Shewanella oneidensis MR-1	peptidase, M16 family [Shewanella oneidensis MR-1]			
5489,	45526941	53	4.00E-36	Crocospaera watsonii WH 8501	COG0058: Glucan phosphorylase [Crocospaera watsonii WH 8501]			2.4.1.1
5490				Cytophaga hutchinsonii	COG1530: Ribonucleases G and E [Cytophaga hutchinsonii]			3.1.4.-
5493,	48854348	46	1.00E-32	Cytophaga hutchinsonii				
5494				Cytophaga hutchinsonii	COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii]			
5499,	48853518	38	2.00E-41	Ralstonia solanacearum GMI1000	hypothetical protein RS02260 [Ralstonia solanacearum GMI1000]			
5500				Ralstonia solanacearum GMI1000	emb CAD13614.1 CONSERVED HYPOTHETICAL PROTEIN [Ralstonia solanacearum]			
5503,	17544805	58	1.00E-18	Clostridium tetani E88	DNA mismatch repair protein mutS [Clostridium tetani E88] gb AAO35868.1			
5504				Clostridium tetani E88	DNA mismatch repair protein mutS [Clostridium tetani E88]			
551,	28210987	47	3.00E-42	Clostridium thermocellum ATCC 27405	sp Q895H2 MUTS_CLOTE DNA mismatch repair protein mutS			
552				Clostridium thermocellum ATCC 27405	COG0417: DNA polymerase elongation subunit (family B) [Clostridium thermocellum ATCC 27405]			
5511,	48860541	25	2.00E-12	Cytophaga hutchinsonii	COG1796: DNA polymerase IV (family X) [Cytophaga hutchinsonii]			2.7.7.7
5512				Cytophaga hutchinsonii	hypothetical protein CE0259 [Corynebacterium efficiens YS-314]			
5515,	48853823	39	4.00E-36	Corynebacterium efficiens YS-314	dbj BAC17069.1 conserved hypothetical protein [Corynebacterium efficiens YS-314]			3.1.21.3
5517,	25026815	38	1.00E-23	Pyrococcus furiosus DSM 3638	transcription initiation factor TFIIE [Pyrococcus furiosus DSM 3638]			
5518				Pyrococcus furiosus DSM 3638	gb AAL80615.1 transcription initiation factor TFIIE [Pyrococcus furiosus DSM 3638]			
5519,	18976863	40	5.00E-30	Pyrococcus furiosus DSM 3638	transcription initiation factor TFIIE [Pyrococcus furiosus DSM 3638]			
5520				Pyrococcus furiosus DSM 3638	gb AAL80615.1 transcription initiation factor TFIIE [Pyrococcus furiosus DSM 3638]			
5521,	18976863	40	5.00E-30	Pyrococcus furiosus DSM 3638	transcription initiation factor TFIIE [Pyrococcus furiosus DSM 3638]			
5522				Methanothermobacter thermautotrophicus str. Delta H	phytoene dehydrogenase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB86273.1 phytoene dehydrogenase [Methanothermobacter thermautotrophicus str. Delta H] pir E59108 phytoene dehydrogenase - Methanobacterium thermoautotrophicum (strain Delta H)			
5525,	15679795	42	2.00E-55	str. Delta H				
5526								

5527, 5528	29348887	39	8.00E-33	Bacteroides thetataotamicon VPI-5482	integrase [Bacteroides thetataotamicon VPI-5482] gb AAO78584.1 Integrase [Bacteroides thetataotamicon VPI-5482]				
5529, 5530	48854354	47	7.00E-26	Cytophaga hutchinsonii	hypothetical protein Chut02003027 [Cytophaga hutchinsonii]				
5531, 5532	34556501	42	1.00E-47	Wolinella succinogenes DSM 1740	GALACTOSYL TRANSFERASE, GDP-MANNOSE PYROPHOSPHORYLASE,PHOSPHOMANNOMUTASE, UDP-GALACTOSE 4-EPIMERASE, GALACTOSYL TRANSFERASE,NUCLEOTIDE SUGAR DEHYDROGENASE, NUCLEOTIDE SUGAR EPIMERASE, ANDPUTATIVE EPIMERASE/DEHYDRATASE GENES; AND UNKNOWN GENES [Wolinella succinogenes DSM 1740] emb CAE09216.1 GALACTOSYL TRANSFERASE, GDP-MANNOSE PYROPHOSPHORYLASE,PHOSPHOMANNOMUTASE, UDP-GALACTOSE 4-EPIMERASE, GALACTOSYL TRANSFERASE,NUCLEOTIDE SUGAR DEHYDROGENASE, NUCLEOTIDE SUGAR EPIMERASE, ANDPUTATIVE EPIMERASE/DEHYDRATASE GENES; AND UNKNOWN GENES [Wolinella succinogenes]			6.3.5.4	
5533, 5534	42523194	41	3.00E-45	Bdellovibrio bacteriovorus HD100	UDP-N-acetyl-D-quinovosamine 4-epimerase [Bdellovibrio bacteriovorus HD100] emb CAE79567.1 UDP-N-acetyl-D-quinovosamine 4-epimerase [Bdellovibrio bacteriovorus HD100]			5.1.3.-	
5535, 5536	15894081	34	6.00E-29	Clostridium acetobutylicum ATCC 824	Nucleoside-diphosphate-sugar epimerase (UDP-glucose 4-epimerase) [Clostridium acetobutylicum ATCC 824] gb AAK78770.1 Nucleoside- diphosphate-sugar epimerase (UDP-glucose 4-epimerase) [Clostridium acetobutylicum ATCC 824] pir [G96997 nucleoside-diphosphate-sugar epimerase (UDP-glucose 4-epimerase) [imported] - Clostridium acetobutylicum]			5.1.3.2	
5541, 5542	32476822	53	2.00E-24	Rhodopirella baltica SH 1	arsenate reductase [Rhodopirella baltica SH 1] emb CAD77194.1 arsenate reductase [Pirella sp.]			1.97.1.5	
5545, 5546	53713337	66	2.00E-39	Bacteroides fragilis YCH46	putative GTP-binding protein [Bacteroides fragilis YCH46] dbj BAD48795.1 putative GTP-binding protein [Bacteroides fragilis YCH46]				
5547, 5548	48854755	56	7.00E-65	Cytophaga hutchinsonii	COG0774: UDP-3-O-acyl-N-acetylglucosamine deacetylase [Cytophaga hutchinsonii]			3.5.1.-	
5551, 5552	52856886	49	4.00E-19	Xylella fastidiosa Ann-1	COG5368: Uncharacterized protein conserved in bacteria [Xylella fastidiosa Ann-1]				
5553, 5554	53712076	32	1.00E-15	Bacteroides fragilis YCH46	hypothetical protein BF0783 [Bacteroides fragilis YCH46] dbj BAD47534.1 hypothetical protein [Bacteroides fragilis YCH46]				
5555, 5556	48853808	36	6.00E-11	Cytophaga hutchinsonii	COG0594: RNase P protein component [Cytophaga hutchinsonii]				

5559, 5560	25026974	42	2.00E-24	Corynebacterium efficiens YS-314	hypothetical protein CE0418 [Corynebacterium efficiens YS-314] dbj BAC17228.1 hypothetical protein [Corynebacterium efficiens YS-314]				
5561, 5562	53712631	55	4.00E-40	Bacteroides fragilis YCH46	tyrosine type site-specific recombinase [Bacteroides fragilis dbj BAD48089.1 tyrosine type site-specific recombinase [Bacteroides fragilis YCH46]				
5569, 5570	54296325	30	3.00E-19	Legionella pneumophila str. Paris	hypothetical protein lpp0354 [Legionella pneumophila str. Paris] emb CAH11502.1 hypothetical protein [Legionella pneumophila str. Paris]				
557, 558	48853718	37	1.00E-19	Cytophaga hutchinsonii	COG2120: Uncharacterized proteins, LmbE homologs [Cytophaga hutchinsonii]				
5577, 5578	48855087	32	6.00E-18	Cytophaga hutchinsonii	COG1773: Rubredoxin [Cytophaga hutchinsonii]				
5583, 5584	48855659	40	2.00E-47	Cytophaga hutchinsonii	COG4251: Bacteriophytochrome (light-regulated signal transduction histidine kinase) [Cytophaga hutchinsonii]				2.7.3.-
5585, 5586	22996431	29	5.00E-16	Xylella fastidiosa Ann-1	COG4924: Uncharacterized protein conserved in bacteria [Xylella fastidiosa Ann-1]				
5589, 5590	48846049	41	2.00E-38	Geobacter metallireducens GS-15	COG0587: DNA polymerase III, alpha subunit [Geobacter metallireducens GS-15]				2.7.7.7
5591, 5592	32471828	52	1.00E-44	Rhodopirellula baltica SH 1	glutathione peroxidase [Rhodopirellula baltica SH 1] emb CAD72506.1 glutathione peroxidase [Pirellula sp.]				1.11.1.9
5595, 5596	9715733	36	9.00E-13	Anabaena sp. 90	peptide synthetase [Anabaena sp. 90]				
5597, 5598	52842392	37	8.00E-41	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	peptide synthetase, non-ribosomal [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] peptide synthetase, non- ribosomal [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]				2.1.2.9
5599, 5600	55379401	28	1.00E-19	Haloarcula marismortui ATCC 43049	N(2)N(2)-dimethylguanosine tRNA methyltransferase [Haloarcula marismortui ATCC 43049] gb AAV47545.1 N(2)N(2)-dimethylguanosine tRNA methyltransferase [Haloarcula marismortui ATCC 43049]				2.1.1.32
5601, 5602	15644050	38	3.00E-15	Thermotoga maritima MSB8	hypothetical protein TM1295 [Thermotoga maritima MSB8] gb AAD36369.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir J72272 conserved hypothetical protein - Thermotoga maritima (strain MSB8)				
5603, 5604	48855841	52	1.00E-62	Cytophaga hutchinsonii	COG0380: Trehalose-6-phosphate synthase [Cytophaga hutchinsonii]				2.4.1.15
5605, 5606	48856924	29	4.00E-25	Cytophaga hutchinsonii	COG1538: Outer membrane protein [Cytophaga hutchinsonii]				

5609, 5610	48477477	41	2.00E-41	Picrophilus torridus DSM 9790	protein translation initiation factor 2 subunit alpha [Picrophilus torridus DSM 9790]			
5615, 5616	37222112	54	2.00E-83	uncultured bacterium	Uvs063 [uncultured bacterium]			
5617, 5618	1711282	39	9.00E-21	Bacillus circulans	chitinase C [Bacillus circulans]			3.2.1.14
5619, 5620	46019862	33	2.00E-23	Streptococcus thermophilus	putative endonuclease [Streptococcus thermophilus] UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Thermosynechococcus elongatus BP-1] dbj BAC09361.1 UDP-N- acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl- undecaprenol N-acetylglucosamine transferase [Thermosynechococcus elongatus BP-1] sp Q8DHY4 MURG_SYNEL UDP-N-acetylglucosamine-N- acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N- acetylglucosamine transferase (Undecaprenyl-PP-MurNAc-pentapeptide- UDP-GlcNAc GlcNAc transferase)			2.4.1.-
5621, 5622	22299352	31	5.00E-10	Thermosynechococ cus elongatus BP-1	COG5000: Signal transduction histidine kinase involved in nitrogen fixation and metabolism regulation [Cytophaga hutchinsonii]			
5623, 5624	48855461	26	2.00E-08	Cytophaga hutchinsonii	COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii]			2.7.3.-
5627, 5628	48855703	33	2.00E-25	Cytophaga hutchinsonii	COG0261: Ribosomal protein L21 [Cytophaga hutchinsonii]			
563, 564	48855887	57	4.00E-24	Cytophaga hutchinsonii	beta-hexosaminidase precursor [Bacteroides thetaiotaomicron VPI-5482] gb AAO75566.1 beta-hexosaminidase precursor [Bacteroides thetaitaomicron VPI-5482]			3.2.1.52
5633, 5634	29345869	31	6.00E-27	Bacteroides thetaitaomicron VPI-5482	COG0178: Exonuclease ATPase subunit [Cytophaga hutchinsonii]			
5637, 5638	48854339	55	4.00E-86	Cytophaga hutchinsonii	septum formation protein Maf [Bacteroides fragilis YCH46] dbj BAD50025.1 septum formation protein Maf [Bacteroides fragilis YCH46] putative xanthosine triphosphate pyrophosphatase [Bacteroides thetaitaomicron VPI-5482] gb AAO78234.1 putative xanthosine triphosphate pyrophosphatase [Bacteroides thetaiotaomicron VPI-5482] sensory transduction histidine kinase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85400.1 sensory transduction histidine kinase [Methanothermobacter thermautotrophicus str. Delta H] pir [G69220 sensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain Delta H)]			2.7.7.56
5639, 5640	53714567	46	4.00E-43	Bacteroides fragilis YCH46				
5649, 5650				Bacteroides thetaitaomicron VPI-5482				
5649, 5650	29348537	55	9.00E-36					
5651, 5652	15678922	37	7.00E-34	Methanothermobac ter thermautotrophicus str. Delta H				2.7.3.-

5653, 5654	55978296	32	3.00E-10	Thermus thermophilus HB8	hypothetical protein TTHB113 [Thermus thermophilus HB8] dbj[BAD71909.1] conserved hypothetical protein [Thermus thermophilus HB8]				
5655, 5656	23124336	48	2.00E-56	Nostoc punctiforme PCC 73102	COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102]				2.7.3.-
5657, 5658	48854565	42	2.00E-26	Cytophaga hutchinsonii	COG0431: Predicted flavoprotein [Cytophaga hutchinsonii]				
5659, 5660	56962495	38	9.00E-25	Bacillus clausii KSM-K16	two-component response regulator of nitrate reduction [Bacillus clausii KSM-K16] dbj[BAD63260.1] two-component response regulator of nitrate reduction [Bacillus clausii KSM-K16]				
5661, 5662	29349422	56	4.00E-45	Bacteroides thetaiotaomicron VPI-5482	putative type II restriction endonuclease [Bacteroides thetaiotaomicron VPI-5482] gb AAO79119.1 putative type II restriction endonuclease [Bacteroides thetaiotaomicron VPI-5482]				3.1.21.4
5669, 5670	52550550	37	4.00E-35	uncultured archaeon GZfos9E5	two-component hybrid sensor and regulator [uncultured archaeon GZfos9E5]				2.7.3.-
5671, 5672	53714385	42	5.00E-18	Bacteroides fragilis YCH46	putative glycosylhydrolase [Bacteroides fragilis YCH46] dbj[BAD49843.1] putative glycosylhydrolase [Bacteroides fragilis YCH46]				3.2.1.17
5673, 5674	9837394	40	1.00E-07	Flavobacterium johnsoniae	Flo10 [Flavobacterium johnsoniae]				3.6.3.4
5675, 5676	9837394	40	1.00E-07	Flavobacterium johnsoniae	Flo10 [Flavobacterium johnsoniae]				3.6.3.4
5685, 5686	33595845	50	3.00E-28	Bordetella parapertussis	hypothetical protein BPP1172 [Bordetella parapertussis 12822] ref NP_887934.1 hypothetical protein BB1388 [Bordetella bronchiseptica RB50] emb CAE36473.1 conserved hypothetical protein [Bordetella parapertussis] emb CAE31886.1 conserved hypothetical protein [Bordetella bronchiseptica RB50]				
5687, 5688	ABB8477 1	46	9.00E-57		Desc:DNA polymerase III holoenzyme delta subunit related protein SEQ ID:144. Org: Cytophaga hutchinsonii				2.7.7.7
5689, 5690	15383990	60	2.00E-59	uncultured crenarchaeote 74A4	cysteinyI-tRNA synthetase [uncultured crenarchaeote 74A4]				6.1.1.16
5691, 5692	48855366	69	2.00E-23	Cytophaga hutchinsonii	COG3209: Rhs family protein [Cytophaga hutchinsonii]				
5695, 5696	29349387	50	1.00E-28	Bacteroides thetaiotaomicron VPI-5482	putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79084.1 putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.1.1.-
5697, 5698	48853518	40	7.00E-31	Cytophaga hutchinsonii	COG4974: Site-specific recombinase XerD [Cytophaga hutchinsonii]				

57, 58	2281663	54	3.00E-60	Flavobacterium johnsoniae	gliding motility protein [Flavobacterium johnsoniae] pir T44443 gliding motility protein [imported] - Flavobacterium johnsoniae				1.8.-.-
5701,				Cytophaga	COG4867: Uncharacterized protein with a von Willebrand factor type A (VWA) domain [Cytophaga hutchinsonii]				
5702	48854298	58	4.00E-87	hutchinsonii	COG1083: CMP-N-acetylneuraminic acid synthetase [Cytophaga hutchinsonii]				2.7.7.43
5705,	48854593	51	2.00E-58	Cytophaga hutchinsonii	COG1875: Predicted ATPase related to phosphate starvation-inducible protein PhoH [Cytophaga hutchinsonii]				
5706	48854593	51	2.00E-58	Cytophaga hutchinsonii	putative helicase [Acinetobacter sp. ADP1] emb CAG68837.1 putative helicase [Acinetobacter sp. ADP1]				
5707	48855541	73	1.00E-115	hutchinsonii	COG0196: FAD synthase [Cytophaga hutchinsonii]				2.7.1.26
5708	48855541	73	1.00E-115	hutchinsonii	COG2166: SufE protein probably involved in Fe-S center assembly [Cytophaga hutchinsonii]				
571,	50085149	41	1.00E-27	ADP1	hypothetical protein ST2175 [Sulfolobus tokodaii str. 7] dbj BAB67280.1 245aa long conserved hypothetical protein [Sulfolobus tokodaii str. 7]				2.1.1.79
5711,	48854843	44	4.00E-47	Cytophaga hutchinsonii	COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii]				1.8.-.-
5712	48854843	44	4.00E-47	Cytophaga hutchinsonii	COG1109: Phosphomannomutase [Cytophaga hutchinsonii]				5.4.2.8
5713,	48854817	57	3.00E-42	Cytophaga hutchinsonii	hypothetical protein Bd0790 [Bdellovibrio bacteriovorus HD100] emb CAE78740.1 conserved hypothetical protein [Bdellovibrio bacteriovorus HD100]				
5714	48854817	57	3.00E-42	Cytophaga hutchinsonii	sensory transduction histidine kinase [Methanosarcina acetivorans C2A] gbj AAM03996.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A]				2.7.3.-
5715,				Sulfolobus tokodaii str. 7	hypothetical protein Meth02003909 [Methanosarcina barkeri str. fusaro]				
5716	15922502	27	1.00E-13	str. 7	hypothetical protein SSO3050 [Sulfolobus solfataricus P2] gbj AAK43150.1				
5719,	48856329	54	1.00E-51	Cytophaga hutchinsonii	Hypothetical protein SSO3050 [Sulfolobus solfataricus P2] pir G90486				
5720	48856329	54	1.00E-51	Cytophaga hutchinsonii	hypothetical protein SSO3050 [imported] - Sulfolobus solfataricus				
5725,	48854793	56	2.00E-97	Cytophaga hutchinsonii	probable pilin biogenesis protein [Clostridium perfringens str. 13] dbj BAB81991.1 probable pilin biogenesis protein [Clostridium perfringens str. 13]				
5726	48854793	56	2.00E-97	Cytophaga hutchinsonii	COG0789: Predicted transcriptional regulators [Cytophaga hutchinsonii]				
573,				Bdellovibrio bacteriovorus	transcription-repair coupling factor [Chlorobium tepidum TLS] gbj AAM71892.1 transcription-repair coupling factor [Chlorobium tepidum TLS]				
574	42522367	53	2.00E-20	HD100					
5731,				Methanosarcina acetivorans C2A					
5732	20089441	35	2.00E-29	acetivorans C2A					
5733,	48838133	34	7.00E-26	Methanosarcina barkeri str. fusaro					
5734	48838133	34	7.00E-26	Methanosarcina barkeri str. fusaro					
5735,				Sulfolobus solfataricus P2					
5736	15899755	34	6.00E-26	Sulfolobus solfataricus P2					
5741,				Clostridium perfringens str. 13					
5742	18311267	34	5.00E-24	perfringens str. 13					
5743,	48854732	25	8.00E-18	Cytophaga hutchinsonii					
5744	48854732	25	8.00E-18	Cytophaga hutchinsonii					
5745,				Chlorobium tepidum TLS					
5746	21673485	25	1.00E-20	tepidum TLS					

5751, 5752	53715815	31	2.00E-42	Bacteroides fragilis YCH46	two-component system sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46] dbj BAD51273.1 two-component system sensor histidine kinase/response regulator hybrid [Bacteroides fragilis YCH46]	2.7.3.-
5753, 5754	29347164	37	3.00E-42	Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase/response regulator, hybrid (one component system) [Bacteroides thetaiotaomicron VPI-5482] gb AAO76861.1 two-component system sensor histidine kinase/response regulator, hybrid (one component system) [Bacteroides thetaiotaomicron VPI-5482]	
5757, 5758	48856549	66	1.00E-104	Cytophaga hutchinsonii	COG2204: Response regulator containing CheY-like receiver, AAA-type ATPase, and DNA-binding domains [Cytophaga hutchinsonii]	
5759, 5760	48856079	62	1.00E-66	Cytophaga hutchinsonii	COG0621: 2-methylthioadenine synthetase [Cytophaga hutchinsonii]	1.8.-
5761, 5762	48891723	32	6.00E-16	Trichodesmium erythraeum IMS101	COG0515: Serine/threonine protein kinase [Trichodesmium erythraeum IMS101]	2.7.1.-
5767, 5768	48855464	38	8.00E-25	Cytophaga hutchinsonii	COG1999: Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems [Cytophaga hutchinsonii]	
5769, 5770	16802005	37	2.00E-35	Listeria innocua Clip11262	hypothetical protein lin2946 [Listeria innocua Clip11262] emb CAC98171.1 lin2946 [Listeria innocua] pir AC1800 hypothetical protein lin2946 [imported] [Listeria innocua (strain Clip11262)]	
577, 578	53715867	51	4.00E-37	Bacteroides fragilis YCH46	putative xanthosine triphosphate pyrophosphatase [Bacteroides fragilis YCH46] dbj BAD51325.1 putative xanthosine triphosphate pyrophosphatase [Bacteroides fragilis YCH46]	2.7.7.56
5777, 5778	2995399	36	3.00E-17	Bacillus megaterium	regulatory protein [Bacillus megaterium] gb AA83973.1 mercury resistance operon negative regulator MerR1 [Bacillus sp. RC607]	
5781, 5782	53797309	45	1.00E-60	Chloroflexus aurantiacus	sp P22853 MERR_BACCE Mercuric resistance operon regulatory protein pir T44501 merR1 protein [imported] - Clostridium butyricum dbj BAB62429.1 mercury-responsive transcriptional regulator protein [Bacillus cereus] dbj BAA86113.1 MerR1 [Clostridium butyricum]	6.1.1.16
5783, 5784	15605808	37	3.00E-18	Aquifex aeolicus VF5	hypothetical protein aq_268 [Aquifex aeolicus VF5] gb AAC06590.1 hypothetical protein [Aquifex aeolicus VF5] pir E70324 conserved hypothetical protein aq_268 - Aquifex aeolicus	
5787, 5788	53711500	51	1.00E-53	Bacteroides fragilis YCH46	two-component system response regulator [Bacteroides fragilis YCH46] dbj BAD46958.1 two-component system response regulator [Bacteroides fragilis YCH46]	2.7.3.-

5789,	48895439	31	9.00E-16	Trichodesmium erythraeum IMS101	COG0431: Predicted flavoprotein [Trichodesmium erythraeum IMS101]				
5790				Cytophaga	COG1748: Saccharophane dehydrogenase and related proteins [Cytophaga hutchinsonii]				1.5.1.10
579,	48854542	45	4.00E-23	hutchinsonii					
580									
5791,				Streptomyces	hypothetical protein [Streptomyces avermitilis MA-4680] ref[NP_824022.1]				
5792	29606495	47	1.00E-43	avermitilis MA-4680	hypothetical protein SAV2846 [Streptomyces avermitilis MA-4680]				
5793,				Streptomyces	hypothetical protein [Streptomyces avermitilis MA-4680] ref[NP_824022.1]				
5794	29606495	43	1.00E-24	avermitilis MA-4680	hypothetical protein SAV2846 [Streptomyces avermitilis MA-4680]				
5799,				Bacteroides	DNA helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79209.1]				
5800	29349512	28	9.00E-24	thetaitaomicron VPI-5482	DNA helicase [Bacteroides thetaiotaomicron VPI-5482]				
5805,				Bdellovibrio	Redox-sensitive transcriptional activator [Bdellovibrio bacteriovorus HD100]				
5806	42523943	38	9.00E-35	bacteriovorus HD100	emb CAE80316.1] Redox-sensitive transcriptional activator [Bdellovibrio bacteriovorus HD100]				
5807,				Bacteroides fragilis	putative helicase [Bacteroides fragilis YCH46]				
5808	53713469	50	9.00E-72	YCH46	helicase [Bacteroides fragilis YCH46]				
581,				Nostoc punctiforme	COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102]				2.7.3.-
582	23129412	31	1.00E-14	PCC 73102	two-component response regulator [Synechococcus elongatus PCC 6301]				
5813,				Synechococcus	dbj BAD78390.1] two-component response regulator [Synechococcus elongatus PCC 6301] ref ZP_00202158.1] COG2200: FOG: EAL domain				2.7.3.-
5814	56750209	40	2.00E-34	6301	[Synechococcus elongatus PCC 7942]				
5815,				Clostridium	COG0124: Histidyl-tRNA synthetase [Clostridium thermocellum ATCC 27405]				6.1.1.21
5816	48860303	42	3.00E-53	thermocellum ATCC 27405	histidine-tRNA ligase [Clostridium perfringens str. 13] dbj BAB81640.1]				
5817,				Clostridium	histidine-tRNA ligase [Clostridium perfringens str. 13]				
5818	18310916	50	6.00E-34	perfringens str. 13	sp Q8XJ27 SYH_CLOPE Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HisRS)				6.1.1.21
5821,				Bacteroides	DNA replication and repair protein RecF, ABC family ATPase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79360.1] DNA replication and repair				
5822	29349663	39	5.00E-20	thetaitaomicron VPI-5482	protein RecF, ABC family ATPase [Bacteroides thetaiotaomicron VPI-5482] sp Q89ZW6 REC_F_BACTN DNA replication and repair protein recF				

5829,								hypothetical protein PA2403 [Pseudomonas aeruginosa PAO1] ref ZP_00140125.1 COG3182: Uncharacterized iron-regulated membrane protein [Pseudomonas aeruginosa UCAPP-PA14] pir A83344 hypothetical protein PA2403 [Imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_251093.1 hypothetical protein PA2403 [Pseudomonas aeruginosa PAO1]				1.8.1.2
5830,	9948447	28	5.00E-17	Pseudomonas								
5831,	ABP0492			aeruginosa PAO1								
5832,	1	63	4.00E-43									
5833,												
5834,	17228866	50	2.00E-51	Nostoc sp. PCC								2.7.1.63
5835,				7120								
5836,	48856692	50	3.00E-23	Cytophaga								
5837,				hutchinsonii								
5838,												
5839,												
5840,	53715815	33	4.00E-38	Bacteroides fragilis								2.7.3.-
5841,				YCH46								
5842,	48857007	53	4.00E-67	Cytophaga								2.7.3.-
5843,				hutchinsonii								
5844,	48857007	47	6.00E-75	Cytophaga								2.7.3.-
5845,				hutchinsonii								
5846,												
5847,												
5848,												
5849,												
5850,	29348618	41	9.00E-54	Bacteroides								
5851,				thetataoamicron								
5852,				VPI-5482								
5853,												
5854,	29346596	74	4.00E-36	Bacteroides								
5855,				thetataoamicron								
5856,				VPI-5482								
5857,												
5858,	41407758	36	8.00E-39	Clostridium								
5859,				thermocellum								
5860,	48859986	31	3.00E-25	ATCC 27405								
5861,												
5862,												
5863,	41407758	36	8.00E-39	Mycobacterium								2.1.1.-
5864,				avium subsp.								
5865,				paratuberculosis								
5866,	41407758	36	8.00E-39	str. k10								
5867,												
5868,												
5869,	28199718	33	2.00E-25	Xylella fastidiosa								3.4.17.2
5870,				Temecula1								1
5871,												
5872,	28199718	33	2.00E-25	4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 14579]								1.13.11.
5873,												27
5874,	30018489	52	1.00E-41	ATCC 14579								

5865, 5866	48853959	46	8.00E-27	Cytophaga hutchinsonii	COG0416: Fatty acid/phospholipid biosynthesis enzyme [Cytophaga hutchinsonii]			
5867, 5868	53715112	28	2.00E-21	Bacteroides fragilis YCH46	4-alpha-glucanotransferase [Bacteroides fragilis YCH46] dbj BAD50570.1 4- alpha-glucanotransferase [Bacteroides fragilis YCH46]			
5869, 5870	ABB8477	44	1.00E-56		Desc:DNA polymerase III holoenzyme delta subunit related protein SEQ ID:144. Org: Cytophaga hutchinsonii			
587, 588	17231112	69	1.00E-51	Nostoc sp. PCC 7120	type I restriction modification enzyme M subunit [Nostoc sp. PCC 7120] dbj BAB75319.1 type I restriction modification enzyme M subunit [Nostoc sp. PCC 7120] pir AE2258 type I restriction modification enzyme M chain [Imported] - Nostoc sp. (strain PCC 7120)	Nostoc sp. PCC 7120 DNA, complete genome	87	7.00E-12 2.1.1.72
5873, 5874	13508372	39	4.00E-27	Mycoplasma pneumoniae M129	hypothetical protein MPN633 [Mycoplasma pneumoniae M129] gb AAB95857.1 conserved hypothetical protein, see: MPN635 [Mycoplasma pneumoniae M129] pir S73535 hypothetical protein C12_orf247 - Mycoplasma pneumoniae (strain ATCC 29342) sp P75164 YG33_MYCPN Hypothetical protein MPN633 (C12_orf247)			
5875, 5876	48856042	52	4.00E-32	Cytophaga hutchinsonii	COG0465: ATP-dependent Zn proteases [Cytophaga hutchinsonii]			3.4.24.-
5879, 5880	17231112	68	4.00E-42	Nostoc sp. PCC 7120	type I restriction modification enzyme M subunit [Nostoc sp. PCC 7120] dbj BAB75319.1 type I restriction modification enzyme M subunit [Nostoc sp. PCC 7120] pir AE2258 type I restriction modification enzyme M chain [Imported] - Nostoc sp. (strain PCC 7120)	Nostoc sp. PCC 7120 DNA, complete genome	87	5.00E-12 2.1.1.72
5881, 5882	15606196	33	3.00E-08	Aquifex aeolicus VF5	(p)ppGpp 3-pyrophosphohydrolase [Aquifex aeolicus VF5] gb AAC06975.1 (p)ppGpp 3-pyrophosphohydrolase [Aquifex aeolicus VF5] pir A70373 (p)ppGpp 3-pyrophosphohydrolase - Aquifex aeolicus sp O67012 SPOT_AQUAE Guanosine-3',5'-bis(diphosphate) 3'- pyrophosphohydrolase ((ppGpp)ase) (Penta-phosphate guanosine-3'- pyrophosphohydrolase)			3.1.7.2
5883, 5884	57160028	30	5.00E-09	Thermococcus kodakaraensis	predicted transcription regulator, DUF118 helix-turn-helix family [Thermococcus kodakaraensis] ref YP_184182.1 predicted transcription regulator, DUF118 helix-turn-helix family [Thermococcus kodakaraensis]			
5885, 5886	23125101	35	1.00E-12	Nostoc punctiforme PCC 73102	COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Nostoc punctiforme PCC 73102]			
5887, 5888	23474779	24	7.00E-07	Desulfovibrio desulfuricans G20	COG4564: Signal transduction histidine kinase [Desulfovibrio desulfuricans G20]			2.7.3.-
5889, 5890	48854298	60	1.00E-71	Cytophaga hutchinsonii	COG4867: Uncharacterized protein with a von Willebrand factor type A (vWA) domain [Cytophaga hutchinsonii]			

589,	48854139	59	5.00E-44	Cytophaga hutchinsonii	COG1066: Predicted ATP-dependent serine protease [Cytophaga hutchinsonii]			3.4.21.-
590				Geobacillus kaustophilus	hypothetical protein GK0592 [Geobacillus kaustophilus HTA426]			
5891,					dbj BAD74877.1 hypothetical conserved protein [Geobacillus kaustophilus HTA426]			2.1.1.-
5892	56419127	62	4.00E-60	HTA426				
5893,				Cytophaga hutchinsonii	hypothetical protein Chut02001715 [Cytophaga hutchinsonii]			
5894	48855383	61	5.00E-55	hutchinsonii	hypothetical protein CTC00544 [Clostridium tetani E88] gb AAO35164.1			
5895,				Clostridium tetani	conserved protein [Clostridium tetani E88]			
5896	28210283	28	2.00E-17	E88				
5897,				Leptospira interrogans serovar	hypothetical protein LA3317 [Leptospira interrogans serovar Lai str. 56601]			
5898	24216016	69	1.00E-61	Lai str. 56601	gb AAN50515.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601]		88	7.00E-21
5899,				Anopheles gambiae				
5900	31195995	54	3.00E-41	gambiae	ENSANGP00000000470 [Anopheles gambiae]			2.3.1.-
				Bacteroides thetaiotaomicron	ABC transporter, ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO75801.1 ABC transporter, ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482]			1.8.-
59, 60	29346104	48	2.00E-33	VPI-5482				
5903,				Cytophaga hutchinsonii	COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii]			2.7.7.24
5904	48853434	68	1.00E-50	hutchinsonii				
5907,				Microbulbifer degradans 2-40	COG0784: FOG: CheY-like receiver [Microbulbifer degradans 2-40]			2.7.3.-
5908	48864299	41	4.00E-12	degradans 2-40	hypothetical protein TTC1430 [Thermus thermophilus HB27]			
5909,				Thermus thermophilus HB27	gb AAS81772.1 hypothetical protein TTC1430 [Thermus thermophilus HB27]			
5910	46199732	48	4.00E-71	thermophilus HB27				
591,					glutamate synthase, small subunit [Azoarcus sp. EbN1] emb CAI07366.1			1.4.1.13
592	56476678	64	5.00E-84	Azoarcus sp. EbN1	Glutamate synthase, small subunit [Azoarcus sp. EbN1]			
				Rhodopirellula baetica SH 1	conserved hypothetical protein-putative sodium:solute symporter [Rhodopirellula baetica SH 1] emb CAD73139.1 conserved hypothetical protein-putative sodium:solute symporter [Pirellula sp.]			
5911,				baetica SH 1	putative RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79825.1 putative RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482]			
5912	32472461	32	2.00E-18	Bacteroides thetaiotaomicron	type sigma factor [Bacteroides thetaiotaomicron VPI-5482]			
5915,					COG1181: D-alanine-D-alanine ligase and related ATP-grasp enzymes [Cytophaga hutchinsonii]			6.3.2.4
5916	29350128	36	6.00E-25	VPI-5482				
5919,				Cytophaga hutchinsonii				
5920	48854866	49	2.00E-74	hutchinsonii				

5921,	48855764	39	7.00E-25	Cytophaga hutchinsonii	COG5316: Uncharacterized conserved protein [Cytophaga hutchinsonii]				
5922				Tetraodon	uncharacterized conserved protein [Tetraodon nigroviridis]				
5929,	47212116	56	3.00E-17	nigroviridis	uncharacterized conserved protein [Tetraodon nigroviridis]				
5930				Pyrococcus	hypothetical acylaminoacyl-peptidase [Pyrococcus furiosus DSM 3638]				
593,	18976690	30	7.00E-07	Pyrococcus furiosus DSM 3638	hypothetical acylaminoacyl-peptidase [Pyrococcus furiosus DSM 3638]				
594				Pyrococcus furiosus DSM 3638	hypothetical acylaminoacyl-peptidase [Pyrococcus furiosus DSM 3638]				
5931,	34397422	40	7.00E-09	Porphyromonas gingivalis W83	DNA-binding response regulator, LuxR family [Porphyromonas gingivalis W83]				
5932				Porphyromonas gingivalis W83	DNA-binding response regulator, LuxR family [Porphyromonas gingivalis W83]				
5933,	48855192	43	2.00E-52	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]				
5934				Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]				
5939,	34397422	40	7.00E-09	Porphyromonas gingivalis W83	exonuclease ABC, C subunit [Porphyromonas gingivalis W83]				
5940	34397903	44	2.00E-62	Porphyromonas gingivalis W83	ref[NP_906085.1] exonuclease ABC, C subunit [Porphyromonas gingivalis W83]				2.7.7.7
5941,				Clostridium thermocellum	COG0587: DNA polymerase III, alpha subunit [Clostridium thermocellum ATCC 27405]				2.7.7.7
5942	48860373	52	8.00E-86	ATCC 27405	COG0587: DNA polymerase III, alpha subunit [Clostridium thermocellum ATCC 27405]				
5945,	48854708	24	5.00E-19	Cytophaga hutchinsonii	hypothetical protein Chut0202377 [Cytophaga hutchinsonii]				
5946				Cytophaga hutchinsonii	hypothetical protein Chut0202377 [Cytophaga hutchinsonii]				
5949,				Moorella thermoacetica	COG0598: Mg2+ and Co2+ transporters [Moorella thermoacetica ATCC 39073]				
5950	49236276	22	3.00E-17	ATCC 39073	COG0598: Mg2+ and Co2+ transporters [Moorella thermoacetica ATCC 39073]				
595,				Geobacter metallireducens GS-15	COG3189: Uncharacterized conserved protein [Geobacter metallireducens GS-15]				2.1.1.10
596	48846288	51	1.00E-26	Geobacter metallireducens GS-15	COG3189: Uncharacterized conserved protein [Geobacter metallireducens GS-15]				7
5951,				Bacteroides fragilis YCH46	putative outer membrane protein OmpH [Bacteroides fragilis YCH46]				
5952	53711793	27	5.00E-08	YCH46	dbj[BAD47251.1] putative outer membrane protein OmpH [Bacteroides fragilis YCH46]				
5955,				uncultured	hypothetical protein [uncultured crenarchaeote]				
5956	22797891	32	2.00E-15	crenarchaeote	hypothetical protein [uncultured crenarchaeote]				
5959,				Thermotoga maritima MSB8	hypothetical protein TM1636 [Thermotoga maritima MSB8]				
5960	15644384	25	8.00E-14	maritima MSB8	conserved hypothetical protein [Thermotoga maritima MSB8]				
5961,				Bacteroides thetaiotaomicron VPI-5482	conserved hypothetical protein - Thermotoga maritima (strain MSB8) sp[Q9X1X1]RA50 THEME Probable DNA double-strand break repair rad50 ATPase				3.1.11.-
5962	29348148	45	2.00E-22	VPI-5482	transcription anti-termination protein [Bacteroides thetaiotaomicron VPI-5482]				

5963, 5964	29349252	53	1.00E-98	Bacteroides thetaiotaomicron VPI-5482	ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gb AAO78949.1 ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]			3.6.1.-
5967, 5968	24214475	32	1.00E-11	Leptospira interrogans serovar Lai str. 56601	hypothetical protein LA1775 [Leptospira interrogans serovar Lai str. 56601] gb AAN48974.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601]			
5969, 5970	22797889	36	3.00E-19	uncultured crenarchaeote	putative histidine kinase [uncultured crenarchaeote]			2.7.3.-
5971, 5972	41205694	41	8.00E-56	Geobacillus stearothermophilus	putative rhamnosyltransferase [Geobacillus stearothermophilus]			2.4.-
5973, 5974	48855182	29	2.00E-22	Cytophaga hutchinsonii	COG2911: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
5977, 5978	16802005	38	3.00E-24	Listeria innocua Clp11262	hypothetical protein lin2946 [Listeria innocua Clp11262] emb CAC98171.1 lin2946 [Listeria innocua] pir AC1800 hypothetical protein lin2946 [Imported] Listeria innocua (strain Clp11262)			
5979, 5980	48839666	78	2.00E-80	Methanosarcina barkeri str. fusaro	COG4742: Predicted transcriptional regulator [Methanosarcina barkeri str. fusaro]	Methanosarcina acetivorans str. C2A, section 503 of 534 of the complete genome	83 1.00E-47	
5981, 5982	20091607	36	5.00E-44	Methanosarcina acetivorans C2A	sensory transduction histidine kinase [Methanosarcina acetivorans C2A] gb AAM06162.1 sensory transduction histidine kinase [Methanosarcina acetivorans str. C2A]			2.7.3.-
5983, 5984	53715101	33	2.00E-26	Bacteroides fragilis YCH46	hypothetical protein BF3817 [Bacteroides fragilis YCH46] db BAD50559.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
5987, 5988	10956006	53	1.00E-77	Coxiella burnetii	hypothetical protein [Coxiella burnetii] emb CAA63678.1 orf 410 [Coxiella burnetii] emb CAA53126.1 unnamed protein product [Coxiella burnetii] pir S38238 hypothetical protein - Coxiella burnetii			
5989, 5990	48838087	27	1.00E-08	Methanosarcina barkeri str. fusaro	COG0608: Single-stranded DNA-specific exonuclease [Methanosarcina barkeri str. fusaro]			3.1.-
599, 600	34398083	48	4.00E-47	Porphyromonas gingivalis W83	polypeptide deformylase [Porphyromonas gingivalis W83] ref NP_906244.1 polypeptide deformylase [Porphyromonas gingivalis W83] sp Q7MT07 DEF_PORGI Peptide deformylase (PDF) (Polypeptide deformylase)			3.5.1.88
5993, 5994	48833949	48	4.00E-66	Magnetococcus sp. MC-1	COG0463: Glycosyltransferases involved in cell wall biogenesis [Magnetococcus sp. MC-1]			2.4.1.-
5995, 5996	48854977	61	6.00E-87	Cytophaga hutchinsonii	COG0685: 5,10-methylenetetrahydrofolate reductase [Cytophaga hutchinsonii]			1.5.1.20

6003, 6004	48839274	56	3.00E-79	Methanosarcina barkeri str. fusaro	COG4096: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Methanosarcina barkeri str. fusaro]			3.1.21.3
6005, 6006	37519843	56	6.00E-66	Gloeobacter violaceus PCC 7421	hypothetical protein gl0274 [Gloeobacter violaceus PCC 7421] dbj BAC88215.1 gl0274 [Gloeobacter violaceus PCC 7421] UDP-N-acetylmuramate dehydrogenase [Thermoanaerobacter tengcongensis MB4] gb AAM25027.1 UDP-N-acetylmuramate dehydrogenase [Thermoanaerobacter tengcongensis MB4] sp Q8R8Z6 MURB_THETN UDP-N-acetylenolpyruvoylglucosamine reductase (UDP-N-acetylmuramate dehydrogenase)			3.4.19.1
6011, 6012	20808252	26	2.00E-12	Thermoanaerobact er tengcongensis MB4	signal-transducing histidine kinase [Archaeoglobus fulgidus DSM 4304] gb AAB90464.1 signal-transducing histidine kinase [Archaeoglobus fulgidus DSM 4304] pir B69346 signal-transducing histidine kinase homolog - Archaeoglobus fulgidus			1.1.1.15 8
6013, 6014	11498376	32	1.00E-32	Archaeoglobus fulgidus DSM 4304	hypothetical protein ABC4087 [Bacillus clausii KSM-K16] dbj BAD66618.1 conserved hypothetical protein [Bacillus clausii KSM-K16] hypothetical protein aII4429 [Nostoc sp. PCC 7120] dbj BAB76128.1 hlpA [Nostoc sp. PCC 7120] pir AE2359 hypothetical protein hlpA [imported] - Nostoc sp. (strain PCC 7120)			2.7.3.-
6017, 6018	56955845	37	5.00E-27	Bacillus clausii KSM-K16	hypothetical protein STH2259 [Symbiobacterium thermophilum IAM 14863] dbj BAD41244.1 hypothetical protein [Symbiobacterium thermophilum IAM 14863]			
6019, 6020	17231921	42	2.00E-54	Nostoc sp. PCC 7120	hypothetical protein TTC1428 [Thermus thermophilus HB27] gb AAS81770.1 hypothetical protein TTC1428 [Thermus thermophilus HB27]			
6021, 6022	51893397	25	4.00E-11	Symbiobacterium thermophilum IAM 14863	putative glycosylhydrolase [Bacteroides fragilis YCH46] dbj BAD49843.1 putative glycosylhydrolase [Bacteroides fragilis YCH46]			3.2.1.17
6023, 6024	46199730	37	5.00E-12	Thermus thermophilus HB27	COG0845: Membrane-fusion protein [Cytophaga hutchinsonii] transcriptional regulator, Crp family [Porphyromonas gingivalis W83] ref NP_905705.1 transcriptional regulator, Crp family [Porphyromonas gingivalis W83]			
6025, 6026	53714385	34	2.00E-20	Bacteroides fragilis YCH46	COG2202: FOG: PAS/PAC domain [Nostoc punctiforme PCC 73102]			2.7.3.-
6027, 6028	48855612	42	4.00E-47	Cytophaga hutchinsonii				
6029, 6030	34397542	33	1.00E-31	Porphyromonas gingivalis W83				
6033, 6034	23128539	39	3.00E-16	Nostoc punctiforme PCC 73102				

6035,	24214122	31	4.00E-29	Leptospira interrogans serovar Lai str. 56601	Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gb AAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601]			
6036					hybrid sensor [Myxococcus xanthus]			
6037,	13516917	28	5.00E-16	Myxococcus xanthus				
6038					dipeptidyl peptidase IV [Prevotella intermedia]			3.4.14.-
6039,	47826745	27	6.00E-17	Prevotella intermedia				
6040					endonuclease [Xanthomonas axonopodis pv. citri str. 306] gb AAM35495.1			3.2.-
6045,	21241377	58	4.00E-44	Xanthomonas axonopodis pv. citri str. 306	endonuclease [Xanthomonas axonopodis pv. citri str. 306]			
6046					Desc:Arabidopsis thaliana protein fragment SEQ ID NO: 65409.			1.17.4.1
6047,	AAG5152	50	5.00E-44		Org:Arabidopsis thaliana			
6048					Desc:isoprenoid related protein sequence SEQ ID No 28.			4.1.3.37
6049,	AAO2185	7	2.00E-60		Org:Synechococcus sp			6.3.4.2
6050					COG0504: CTP synthase (UTP-ammonia lyase) [Cytophaga hutchinsonii]			
605,	48856944	63	3.00E-60	Cytophaga hutchinsonii	hypothetical protein SO2930 [Shewanella oneidensis MR-1] gb AAN55944.1			
606					hypothetical protein [Shewanella oneidensis MR-1]			
6051,	24374457	42	5.00E-60	Shewanella oneidensis MR-1				
6052					COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii]			2.7.3.-
6053,	48854564	53	5.00E-67	Cytophaga hutchinsonii	sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_714399.1 CysC; CysN [Leptospira interrogans serovar Lai str. 56601] gb AAN51417.1 CysN; CysC [Leptospira interrogans serovar lai str. 56601] gb AAS71912.1 sulfate adenylyltransferase subunit 1 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			2.7.7.4
6054					hypothetical protein Chut02003091 [Cytophaga hutchinsonii]			
6055,	45659189	52	8.00E-89	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	DNA polymerase [Podovirus SOG]			
6056					hypothetical protein Reut02003175 [Ralstonia metallidurans CH34]			
6063,	48854003	28	1.00E-25	Cytophaga hutchinsonii				
6064								
6065,	32442287	28	2.00E-11	Podovirus SOG				2.7.7.7
6066								
6067,	48769633	33	9.00E-11	Ralstonia metallidurans CH34				
6068								

6069,	16264609	29	5.00E-07	Sinorhizobium meliloti 1021	putative oligopeptide uptake ABC transporter periplasmic solute-binding protein precursor [Sinorhizobium meliloti 1021] emb CAC33589.1			
6070					oligopeptide ABC transporter [Sinorhizobium meliloti] pir E95949 probable oligopeptide uptake ABC transporter periplasmic solute-binding protein precursor oppA; [imported] - Sinorhizobium meliloti (strain 1021)			
607,	53795203	44	6.00E-25	Chloroflexus aurantiacus	magaplasmid pSymB emb CAC49261.1 putative oligopeptide uptake ABC transporter periplasmic solute-binding protein precursor [Sinorhizobium meliloti 1021]			3.5.2.6
6071,	27262180	57	1.00E-27	Hellobacillus	COG1680: Beta-lactamase class C and other penicillin binding proteins [Chloroflexus aurantiacus]			2.7.7.7
6072	AA78012	29	2.00E-17		exonuclease ABC subunit C [Hellobacillus mobilis]			
6073,					Desc:Sphaerotilus natans SnaBI endonuclease protein SEQ ID NO:4.			
6074	53717831	48	2.00E-48	Burkholderia pseudomallei K96243	Org:Sphaerotilus natans			
6075,					glutamyl-tRNA amidotransferase subunit B [Burkholderia pseudomallei K96243] emb CAH34176.1 glutamyl-tRNA amidotransferase subunit B			6.3.5.-
6076	24374986	44	5.00E-46	Shewanella oneidensis MR-1	[Burkholderia pseudomallei K96243]			
6077,					hypothetical protein phosphatase [Shewanella oneidensis MR-1]			
6078	27377973	48	5.00E-25	Bradyrhizobium japonicum USDA 110	gb AAN56473.1 conserved hypothetical protein [Shewanella oneidensis MR- 1]			2.7.3.-
6079,					two-component hybrid sensor and regulator [Bradyrhizobium japonicum USDA 110] dbj BAC48127.1 two-component hybrid sensor and regulator			
6080	48853721	33	3.00E-13	Cytophaga hutchinsonii	[Bradyrhizobium japonicum USDA 110]			
6081,					hypothetical protein Chut02003580 [Cytophaga hutchinsonii]			
6082	56477873	32	9.00E-24	Azoarcus sp. EbN1	glycosyl transferase, family 2 [Azoarcus sp. EbN1] emb CAI08561.1			2.4.1.-
6085,					Glycosyl transferase, family 2 [Azoarcus sp. EbN1]			
6086	20808429	38	2.00E-16	Thermoanaerobact er tengcongensis MB4	antirestriction protein [Thermoanaerobacter tengcongensis MB4]			
6087,					gb AAM25204.1 antirestriction protein [Thermoanaerobacter tengcongensis MB4]			
6088	48855433	62	8.00E-42	Cytophaga hutchinsonii	COG0458: Carbamoylphosphate synthase large subunit (split gene in Mj)			6.3.5.5
609,	48854120	58	1.00E-56	Cytophaga hutchinsonii	[Cytophaga hutchinsonii]			6.2.1.3
6091,					COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii]			
6092	48856607	48	3.00E-16	Cytophaga hutchinsonii	COG1321: Mn-dependent transcriptional regulator [Cytophaga hutchinsonii]			
6093,					TonB [Bacteroides thetaiotaomicron VPI-5482] gb AAO77166.1 TonB			
6094	29347469	34	1.00E-13	Bacteroides thetaitaomicron VPI-5482	[Bacteroides thetaiotaomicron VPI-5482]			
6099,					COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii]			2.7.3.-
6100	48853766	35	8.00E-41	Cytophaga hutchinsonii				
6103,								
6104								

6105, 6106	48839924	57	6.00E-45	Methanosarcina barkeri str. fusaro	COG5316: Uncharacterized conserved protein [Methanosarcina barkeri str. fusaro]			
6107, 6108 6109, 6110	48891840	33	3.00E-29	Trichodesmium erythraeum IMS101	COG1232: Protoporphyrinogen oxidase [Trichodesmium erythraeum IMS101]			1.3.3.4
	53797309	45	1.00E-60	Chloroflexus aurantiacus	COG0215: Cysteinyl-tRNA synthetase [Chloroflexus aurantiacus]			6.1.1.16
611, 612	29350148	34	2.00E-23	Bacteroides thetaiotaomicron VPI-5482	transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_812706.1 transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_811980.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] ref NP_810669.1 transposase, invertase [Bacteroides thetaiotaomicron VPI- 5482] ref NP_809398.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO79845.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78900.1 transposase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78174.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76863.1 transposase, invertase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76710.1 transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75592.1 transposase [Bacteroides thetaiotaomicron VPI-5482]			
6111, 6112	29349387	41	6.00E-17	Bacteroides thetaiotaomicron VPI-5482	putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79084.1 putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482]			
6113, 6114 6115, 6116 6119, 6120 6121, 6122 6123, 6124	13508087	33	2.00E-14	Mycoplasma pneumoniae M129	5-formyl tetrahydrofolate cyclo-ligase (H10858) homolog [Mycoplasma pneumoniae M129] gb AAB96136.1 5-formyl tetrahydrofolate cyclo-ligase (H10858) homolog; similar to GenBank Accession Number D64160, from H. Influenzae [Mycoplasma pneumoniae M129] pir S73814 probable 5-formyl tetrahydrofolate cyclo-ligase H10858 - Mycoplasma pneumoniae (strain ATCC 29342) sp P75430 Y245_MYCPN Hypothetical protein MG245 homolog (H91_orf164)			6.3.3.2
	48856028	47	1.00E-39	Cytophaga hutchinsonii	COG1057: Nicotinic acid mononucleotide adenylyltransferase [Cytophaga hutchinsonii]			2.7.7.18
	48855616	26	5.00E-24	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]			
				Strongylocentrotus purpuratus	egg bindin receptor 1 [Strongylocentrotus purpuratus] gb AAR03494.1 egg bindin receptor 1 precursor [Strongylocentrotus purpuratus]			2.7.3.-

6127,	34397354	69	6.00E-19	Porphyrromonas gingivalis W83	orotate phosphoribosyltransferase [Porphyrromonas gingivalis W83] ref NP_905518.1 orotate phosphoribosyltransferase [Porphyrromonas gingivalis W83] sp Q7MUX4 PYRE_PORGI Orotate phosphoribosyltransferase (OPRT) (OPRTase)			2.4.2.10
6128,	48854506	39	9.00E-15	Cytophaga hutchinsonii	hypothetical protein Chut02002705 [Cytophaga hutchinsonii]			3.6.1.-
6129,				Symbiobacterium thermophilum IAM	RNA polymerase ECF-type sigma factor [Symbiobacterium thermophilum IAM 14863] dbj BAD39830.1 RNA polymerase ECF-type sigma factor [Symbiobacterium thermophilum IAM 14863]			
613,	51891983	36	4.00E-15	Thermosynechococcus elongatus BP-1	phosphoenolpyruvate synthase [Thermosynechococcus elongatus BP-1] dbj BAC08316.1 phosphoenolpyruvate synthase [Thermosynechococcus elongatus BP-1]			2.7.9.2
6135,	22298307	62	3.00E-90	Helicobacter pylori	hypothetical protein jhp0094 [Helicobacter pylori J99] gb AAD05675.1 putative [Helicobacter pylori J99] pir E71975 hypothetical protein [hp0094 - Helicobacter pylori (strain J99)]			2.4.-
6136,	15611164	44	3.00E-39	Desulfotalea psychrophila Lsv54	hypothetical protein DP2762 [Desulfotalea psychrophila Lsv54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila Lsv54]			2.1.1.14 4
6141,	51246614	29	3.00E-19	Desulfotalea psychrophila Lsv54	hypothetical protein DP2762 [Desulfotalea psychrophila Lsv54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila Lsv54]			2.1.1.14 4
6143,	51246614	29	1.00E-21	Bacillus halodurans C-125	cardiolipin synthetase [Bacillus halodurans C-125] dbj BAB06577.1 cardiolipin synthetase [Bacillus halodurans C-125] pir B84007 cardiolipin synthetase BH2858 [imported] - Bacillus halodurans (strain C-125) sp Q9K8Z4 CLS_BACHD Cardiolipin synthetase (Cardiolipin synthase) (CL synthase)			2.7.8.-
6145,	15615421	36	1.00E-33	Mannheimia succiniciproducens	CarB protein [Mannheimia succiniciproducens MBEL55E] gb AAU38098.1 CarB protein [Mannheimia succiniciproducens MBEL55E]			6.3.5.5
6147,	52425546	26	2.00E-13	Mycobacterium tuberculosis H37Rv	hypothetical protein Rv0329c [Mycobacterium tuberculosis H37Rv] ref NP_334753.1 MitM-related protein [Mycobacterium tuberculosis CDC1551] gb AAK44567.1 MitM-related protein [Mycobacterium tuberculosis CDC1551] pir B70527 hypothetical protein Rv0329c - Mycobacterium tuberculosis (strain H37Rv) emb CAB09577.1 CONSERVED HYPOTHETICAL PROTEIN [Mycobacterium tuberculosis H37Rv]			
615,	15607470	27	4.00E-07	uncultured archaeon	alpha-mannosidase [uncultured archaeon GZfos3D4]			3.2.1.24
6153,	52550389	39	3.00E-47	GZfos3D4	putative translation elongation factor EF Tu-like protein [uncultured crenarchaeote]			
6154,	42557720	44	7.00E-23	crenarchaeote				

6157, 6158	48855337	63	5.00E-93	Cytophaga hutchinsonii	COG1508: DNA-directed RNA polymerase specialized sigma subunit, sigma54 homolog [Cytophaga hutchinsonii]	:		
6159, 6160	1185191	57	4.00E-64	Odontella sinensis	ORF 644 [Odontella sinensis] pir S78301 hypothetical protein 644 - Odontella sinensis chloroplast ref NP_043642.1 ORF 844 [Odontella sinensis] sp P49825 FTSH_ODOSI Cell division protein ftsH homolog ATP phosphoribosyltransferase [Bacteroides fragilis YCH46] dbj BAD49935.1 ATP phosphoribosyltransferase [Bacteroides fragilis YCH46]	Odontella sinensis complete chloroplast genome 89	1.00E-07	3.4.24.-
6161, 6162	53714477	58	4.00E-66	Bacteroides fragilis YCH46				2.4.2.17
6165, 6166	48853743	67	1.00E-118	Cytophaga hutchinsonii	COG0188: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit [Cytophaga hutchinsonii]			5.99.1.-
6167, 6168	48893692	30	2.00E-35	Trichodesmium erythraeum IMS101	COG2317: Zn-dependent carboxypeptidase [Trichodesmium erythraeum IMS101]			3.4.17.1 9
6169, 6170	48854510	56	5.00E-51	Cytophaga hutchinsonii	COG0622: Predicted phosphoesterase [Cytophaga hutchinsonii]			
6173, 6174	54032283	33	3.00E-10	Polaromonas sp. JS666	COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Polaromonas sp. JS666]			
6177, 6178	42525886	44	1.00E-27	Treponema denticola ATCC 35405	UDP-N-acetylmuramoylalanine-D-glutamate ligase [Treponema denticola ATCC 35405] gb AAS10865.1 UDP-N-acetylmuramoylalanine-D-glutamate ligase [Treponema denticola ATCC 35405]			6.3.2.9
6179, 6180	48851974	31	5.00E-12	Ferroplasma acidarmanus	hypothetical protein Faci02001417 [Ferroplasma acidarmanus]			
6181, 6182	48864233	35	6.00E-22	Microbulbifer degradans 2-40	COG0845: Membrane-fusion protein [Microbulbifer degradans 2-40]			
6183, 6184	48853832	60	2.00E-45	Cytophaga hutchinsonii	COG0484: DnaJ-class molecular chaperone with C-terminal Zn finger domain [Cytophaga hutchinsonii]			
6187, 6188	48853636	33	1.00E-24	Cytophaga hutchinsonii	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii]			2.7.3.-
619, 620	29346219	29	1.00E-07	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT0809 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75916.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482]			
6195, 6196	39995659	23	2.00E-14	Geobacter sulfurreducens PCA	hypothetical protein GSU0552 [Geobacter sulfurreducens PCA] gb AAR33883.1 conserved domain protein [Geobacter sulfurreducens PCA]			
6201, 6202	46120990	38	1.00E-33	Methylobacillus flagellatus KT	COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Methylobacillus flagellatus KT]			2.7.3.-
6203, 6204	48855896	41	4.00E-50	Cytophaga hutchinsonii	COG0557: Exoribonuclease R [Cytophaga hutchinsonii]			3.1.-

6209, 6210	53713098	64	1.00E-39	Bacteroides fragilis YCH46	GAF domain-containing protein involved in signal transduction [Bacteroides fragilis YCH46] dbj BAD48556.1 GAF domain-containing protein involved in signal transduction [Bacteroides fragilis YCH46]				
6213, 6214	29349346	30	6.00E-13	Bacteroides thetataoamicron VPI-5482	ATP-dependent DNA helicase recQ [Bacteroides thetataoamicron VPI-5482] gb AAO79043.1 ATP-dependent DNA helicase recQ [Bacteroides thetataoamicron VPI-5482]				3.6.1.-
6215, 6216	56808880	31	4.00E-17	Streptococcus pyogenes M49 591	hypothetical protein SpyOM01000106 [Streptococcus pyogenes M49 591]				
6217, 6218	48853520	66	1.00E-118	Cytophaga hutchinsonii	COG0192: S-adenosylmethionine synthetase [Cytophaga hutchinsonii]	Bacteroides thetataoamicron VPI-5482, section 14 of 21 of the complete genome	83	6.00E-20	2.5.1.6
6219, 6220	53711352	64	2.00E-91	Bacteroides fragilis YCH46	S-adenosylmethionine synthetase [Bacteroides fragilis YCH46] dbj BAD46810.1 S-adenosylmethionine synthetase [Bacteroides fragilis YCH46]	Bacteroides thetataoamicron VPI-5482, section 14 of 21 of the complete genome	83	4.00E-20	2.5.1.6
6221, 6222	29347668	42	2.00E-19	Bacteroides thetataoamicron VPI-5482	GTP-binding protein [Bacteroides thetataoamicron VPI-5482] gb AAO77365.1 GTP-binding protein [Bacteroides thetataoamicron VPI-5482]				
6225, 6226	31195773	45	6.00E-22	Anopheles gambiae	ENSANGP00000000136 [Anopheles gambiae]				2.3.1.-
623, 624	53721095	35	7.00E-10	Burkholderia pseudomallei K96243	hypothetical protein BPSS0056 [Burkholderia pseudomallei K96243] emb CAH37499.1 conserved hypothetical protein [Burkholderia pseudomallei K96243]				
6231, 6232	21672859	38	8.00E-16	Chlorobium tepidum TLS	ATP synthase F1, delta subunit [Chlorobium tepidum TLS] gb AAM71266.1 ATP synthase F1, delta subunit [Chlorobium tepidum TLS]				3.6.3.15
6237, 6238	23501247	37	1.00E-29	Brucella suis 1330 Nitrosomonas europaea ATCC	DNA-binding response regulator, LuxR family [Brucella suis 1330] ref NP_540499.1 TRANSCRIPTIONAL REGULATORY PROTEIN DEGU [Brucella melitensis 16M] gb AAN29289.1 DNA-binding response regulator, LuxR family [Brucella suis 1330] gb AAL52763.1 two-component response regulator [Brucella melitensis 16M] pir AH3449 transcription regulatory protein degU [imported] - Brucella melitensis (strain 16M)				
6243, 6244	30249879	39	4.00E-27	19718	Sulfate transporter [Nitrosomonas europaea ATCC 19718] emb CAD85838.1 Sulfate transporter [Nitrosomonas europaea ATCC 19718]				

6251,	48854662	24	5.00E-15	Cytophaga hutchinsonii	COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Cytophaga hutchinsonii]			
6252,					COG0071: Molecular chaperone (small heat shock protein) [Cytophaga hutchinsonii]			
6253,	48855680	58	2.00E-35	Cytophaga hutchinsonii				
6254,				Anopheles gambiae				3.1.-
6255,	31194811	47	2.00E-33	Wolfinella succinogenes DSM 1740	ENSANGP00000002016 [Anopheles gambiae]			
6256					ADP-HEPTOSE-LPS HEPTOSYLTRANSFERASE II (RFAF) [Wolfinella succinogenes DSM 1740] emb[CAE10509.1] ADP-HEPTOSE-LPS HEPTOSYLTRANSFERASE II (RFAF) [Wolfinella succinogenes]			
6257,	34557794	31	3.00E-15	Shewanella oneidensis MR-1	peptidase, M13 family [Shewanella oneidensis MR-1] gb AAN56820.1			3.4.24.7
6258					peptidase, M13 family [Shewanella oneidensis MR-1]			1
6259,	24375333	34	1.00E-20	Methanosarcina mazei Go1				
6260					Ferredoxin [Methanosarcina mazei Go1] gb AAM32910.1 Ferredoxin [Methanosarcina mazei Go1]		84 1.00E-11	1.6.4.-
6265,	21229316	67	1.00E-108	Microbulifer degradans 2-40	COG0577: ABC-type antimicrobial peptide transport system, permease component [Microbulifer degradans 2-40]			
6266								
6269,	48864231	29	1.00E-12	Cytophaga hutchinsonii	COG2373: Large extracellular alpha-helical protein [Cytophaga hutchinsonii]			
627,								
627,	48855210	27	4.00E-15	Cytophaga hutchinsonii	COG1209: dTDP-glucose pyrophosphorylase [Cytophaga hutchinsonii]			2.7.7.24
6273,								
6274,	48853434	68	1.00E-50	Cytophaga hutchinsonii	COG1250: 3-hydroxyacyl-CoA dehydrogenase [Cytophaga hutchinsonii]			1.1.1.35
6277,								
6278	48854116	65	1.00E-108	Anabaena variabilis ATCC 29413	COG2942: N-acyl-D-glucosamine 2-epimerase [Anabaena variabilis ATCC 29413]			5.1.3.8
6279,								
6280	46135554	32	6.00E-09	Desulfovibrio vulgaris subsp. vulgaris str.	type I restriction-modification system, M subunit [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96186.1 type I restriction-modification system, M subunit [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			2.1.1.72
6281,								
6282	46580119	50	3.00E-68	uncultured bacterium	Uvs062 [uncultured bacterium]			
6283,								
6284	37222111	48	2.00E-74	Pasteurella multocida subsp. multocida str. Pm70	RecQ [Pasteurella multocida subsp. multocida str. Pm70] gb AAK03511.1			
6285,								
6286	15603292	42	5.00E-17	Cytophaga hutchinsonii	RecQ [Pasteurella multocida subsp. multocida str. Pm70] sp Q9CL21 RECQ_PASMU ATP-dependent DNA helicase recQ			3.6.1.-
6289,								
6290	48856559	36	5.00E-18		COG0526: Thiol-disulfide isomerase and thioredoxins [Cytophaga hutchinsonii]			

6291, 6292	57167915	42	6.00E-21	Campylobacter coli RM2228	para-aminobenzoate synthetase (pabB) [Campylobacter coli RM2228] gb EAL57701.1 para-aminobenzoate synthetase (pabB) [Campylobacter coli RM2228]	Haemophilus ducreyi strain 35000HP section 5 of 6 of the complete genome	89	1.00E-11	4.1.3.-
6293, 6294	42521895	69	1.00E-125	Bdellovibrio bacteriovorus HD100	preprotein translocase SecA subunit [Bdellovibrio bacteriovorus HD100] emb CAE77929.1 preprotein translocase SecA subunit [Bdellovibrio bacteriovorus HD100]				
6295, 6296	42521895	69	1.00E-125	Bdellovibrio bacteriovorus HD100	preprotein translocase SecA subunit [Bdellovibrio bacteriovorus HD100] emb CAE77929.1 preprotein translocase SecA subunit [Bdellovibrio bacteriovorus HD100]	Haemophilus ducreyi strain 35000HP section 5 of 6 of the complete genome	89	1.00E-11	
6297, 6298	48854534	38	7.00E-19	Cytophaga hutchinsonii	COG2834: Outer membrane lipoprotein-sorting protein [Cytophaga hutchinsonii]				
6299, 6300	48854534	38	7.00E-19	Cytophaga hutchinsonii	COG2834: Outer membrane lipoprotein-sorting protein [Cytophaga hutchinsonii]				
63, 64 6301, 6302	15644112 ABB5290 9	35 50	6.00E-07 4.00E-72	Thermotoga maritima MSB8	response regulator [Thermotoga maritima MSB8] gb AAD36430.1 response regulator [Thermotoga maritima MSB8] pir A72263 response regulator - Thermotoga maritima (strain MSB8)				
6303, 6304	ABB5290 9	50	4.00E-72		Desc:Escherichia coli polypeptide SEQ ID NO 1226. Org:Escherichia coli				
6305, 6306	53715355	27	2.00E-20	Bacteroides fragilis YCH46	Desc:Escherichia coli polypeptide SEQ ID NO 1226. Org:Escherichia coli				
631, 632	53711742	45	5.00E-46	Bacteroides fragilis YCH46	hypothetical protein BF4071 [Bacteroides fragilis YCH46] dbj BAD50813.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
6311, 6312	48854498	54	2.00E-60	Cytophaga hutchinsonii	UDP-N-acetylmuramoylalanine-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D- alanyl ligase [Bacteroides fragilis YCH46] dbj BAD47200.1 UDP-N- acetylmuramoylalanine-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacteroides fragilis YCH46]			3.1.3.15	
6313, 6314 6319, 6320	45656929 48855775	50 23	1.00E-58 8.00E-08	Leptospira interrogans serovar Copenhageni str. Ficruz L1-130 Cytophaga hutchinsonii	hypothetical protein Chut02002697 [Cytophaga hutchinsonii] adenylate or guanylate cyclase [Leptospira interrogans serovar Copenhageni str. Ficruz L1-130] ref NP_713221.1 adenylate cyclase [Leptospira interrogans serovar Lai str. 56601] gb AAN50239.1 adenylate cyclase [Leptospira interrogans serovar lai str. 56601] gb AAS69652.1 adenylate or guanylate cyclase [Leptospira interrogans serovar Copenhageni str. Ficruz L1-130] hypothetical protein Chut02000984 [Cytophaga hutchinsonii]				4.6.1.2

6325, 6326	56675038	43	8.00E-19	uncultured bacterium	cellulase [uncultured bacterium]				
6333, 6334	48845443	39	1.00E-47	Geobacter metallireducens GS-15	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]				2.7.3.-
6335, 6336	12515380	43	2.00E-64	Escherichia coli O157:H7	unknown protein encoded within prophage CP-933R [Escherichia coli O157:H7] ref NP_287814.1 unknown protein encoded within prophage CP-933R [Escherichia coli O157:H7 EDL933] ref NP_309982.1 hypothetical protein ECs1955 [Escherichia coli O157:H7] dbj BAB35378.1 hypothetical protein [Escherichia coli O157:H7] pir C90873 hypothetical protein ECs1855 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) pir H85745 unknown protein encoded within prophage CP-933R [imported] - Escherichia coli (strain O157:H7, substrain EDL933)				
6337, 6338	15678563	60	8.00E-51	Methanothermobacter thermautotrophicus str. Delta H	peptide methionine sulfoxide reductase [Methanothermobacter thermotrophicus str. Delta H] gb AAB8504.1.1 peptide methionine sulfoxide reductase [Methanothermobacter thermotrophicus str. Delta H] pir F69170 peptide methionine sulfoxide reductase - Methanobacterium thermoautotrophicum (strain Delta H) sp Q26635 MSRA_METTH Peptide methionine sulfoxide reductase msrA (Protein-methionine-S-oxide reductase) (Peptide Met(O) reductase)	Methanosarcina acetivorans str. C2A, section 349 of 534 of the complete genome	83	6.00E-66	2.6.1.16
6339, 6340	48838915	75	1.00E-125	Methanosarcina barkeri str. fusaro	COG0449: Glucosamine 6-phosphate synthetase, contains amidotransferase and phosphosugar isomerase domains [Methanosarcina barkeri str. fusaro]				
6341, 6342	48853602	60	7.00E-98	Cytophaga hutchinsonii	COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii]				
6343, 6344	18309430	22	5.00E-07	Clostridium perfringens str. 13	probable transcriptional regulator [Clostridium perfringens str. 13] dbj BAB80154.1 probable transcriptional regulator [Clostridium perfringens str. 13]				
6345, 6346	48860240	35	3.00E-15	Clostridium thermocellum ATCC 27405	COG2207: AraC-type DNA-binding domain-containing proteins [Clostridium thermocellum ATCC 27405]	Cytophaga sp. KUC-1 alcdh gene for alcohol dehydrogenase, complete cds	85	1.00E-15	2.1.1.63
6347, 6348	11345445	34	1.00E-07	Acinetobacter baumannii	unknown [Acinetobacter baumannii]				

6353, 6354, 6357, 6358	48859423 48853385	30 45	6.00E-09 2.00E-18	Clostridium thermocellum ATCC 27405 Cytophaga hutchinsonii	hypothetical protein Cht02001311 [Clostridium thermocellum ATCC 27405] hypothetical protein Cht02003884 [Cytophaga hutchinsonii]				
6359, 6360					Eremothecium gossypii ATCC 10895 chromosome VI, complete sequence	##	5.00E-30		
6361, 6362					Eremothecium gossypii ATCC 10895 chromosome VI, complete sequence	##	5.00E-30		
6365, 6366	29605540	49	1.00E-13	Streptomyces avermitilis MA-4680	putative arginase [Streptomyces avermitilis MA-4680] ref NP_823071.1 putative arginase [Streptomyces avermitilis MA-4680]			3.5.3.1	
6369, 6370	34397003	44	1.00E-74	Porphyromonas gingivalis W83	translation elongation factor G, putative [Porphyromonas gingivalis W83] ref NP_905168.1 translation elongation factor G, putative [Porphyromonas gingivalis W83]			3.6.1.48	
637, 638	46201417	36	2.00E-18	Magnetospirillum magnetotacticum MS-1	COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1]			2.7.3.-	
6375, 6376	48854533	66	2.00E-84	Cytophaga hutchinsonii	COG0284: Ornithine-5'-phosphate decarboxylase [Cytophaga hutchinsonii] conserved hypothetical protein [Chromobacterium violaceum ATCC 12472] ref NP_902156.1 hypothetical protein CV2486 [Chromobacterium violaceum ATCC 12472]			4.1.1.23	
6377, 6378	34103796	30	6.00E-07	Chromobacterium violaceum ATCC 12472	DNA polymerase I [Vibrio vulnificus CMCP6] gbl AAO09403.1 DNA polymerase I [Vibrio vulnificus CMCP6]				
6381, 6382	27364348	25	2.00E-11	Vibrio vulnificus CMCP6	response regulator [Porphyromonas gingivalis W83] ref NP_905164.1 response regulator [Porphyromonas gingivalis W83]			2.7.7.7	
6383, 6384	34396999	57	7.00E-63	Porphyromonas gingivalis W83					
6385, 6386	48854752	50	5.00E-90	Cytophaga hutchinsonii	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Cytophaga hutchinsonii]			2.7.3.-	

6387, 6388, 6393, 6394	28854897	37	1.00E-23	Pseudomonas syringae pv. tomato str. DC3000	ISPsy11, transposase OrfB [Pseudomonas syringae pv. tomato str. DC3000] ref[NP_794264.1] ISPsy11, transposase OrfB [Pseudomonas syringae pv. tomato str. DC3000]				
6395, 6396	18481484	36	1.00E-06	Tetrahymena thermophila	endonuclease [Tetrahymena thermophila]				
6397, 6398	29347576	37	3.00E-40	Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77273.1 two-component system sensor histidine kinase [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-
6401, 6402	29346363	33	5.00E-16	Bacteroides thetaiotaomicron VPI-5482	Integrase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76060.1 Integrase [Bacteroides thetaiotaomicron VPI-5482]				
6403, 6404	48855725	29	2.00E-16	Cytophaga hutchinsonii	hypothetical protein Chut02000929 [Cytophaga hutchinsonii]				
6405, 6406	48895816	39	1.00E-16	Trichodesmium erythraeum IMS101	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Trichodesmium erythraeum IMS101]				2.7.3.-
6407, 6408	20090869	29	1.00E-08	Methanosarcina acetivorans C2A	hypothetical protein MA2021 [Methanosarcina acetivorans C2A] gb AAM05424.1 hypothetical protein [Methanosarcina acetivorans str. C2A]				
	48858046	40	7.00E-51	Clostridium thermocellum ATCC 27405	COG0178: Excinuclease ATPase subunit [Clostridium thermocellum ATCC 27405]				

6409,	20808983	32	6.00E-16	Thermoanaerobacter tengcongensis MB4	transposase [Thermoanaerobacter tengcongensis MB4] ref NP_623590.1				
6410					transposase [Thermoanaerobacter tengcongensis MB4] ref NP_622797.1				
641,	48854524	63	2.00E-67	Cytophaga hutchinsonii	transposase [Thermoanaerobacter tengcongensis MB4] ref NP_622779.1				
642					transposase [Thermoanaerobacter tengcongensis MB4] ref NP_622700.1				
					transposase [Thermoanaerobacter tengcongensis MB4] ref NP_622094.1				
					transposase [Thermoanaerobacter tengcongensis MB4] ref NP_622043.1				
					transposase [Thermoanaerobacter tengcongensis MB4] ref NP_622035.1				
					transposase [Thermoanaerobacter tengcongensis MB4] ref NP_621726.1				
					transposase [Thermoanaerobacter tengcongensis MB4] gbl AAM25194.1				
					transposase [Thermoanaerobacter tengcongensis MB4] gbl AAM23647.1				
					transposase [Thermoanaerobacter tengcongensis MB4] gbl AAM25758.1				
					transposase [Thermoanaerobacter tengcongensis MB4] gbl AAM24401.1				
					transposase [Thermoanaerobacter tengcongensis MB4] gbl AAM24383.1				
					transposase [Thermoanaerobacter tengcongensis MB4] gbl AAM24304.1				
					transposase [Thermoanaerobacter tengcongensis MB4] gbl AAM23698.1				
					transposase [Thermoanaerobacter tengcongensis MB4] gbl AAM23639.1				
6409,					transposase [Thermoanaerobacter tengcongensis MB4] gbl AAM23330.1				
6410					COG1217: Predicted membrane GTPase involved in stress response				3.6.1.48
641,					[Cytophaga hutchinsonii]				
642					ADP-heptose:LPS heptosyltransferase II [Bdellovibrio bacteriovorus HD100]				
6411,					emb CAE79384.1 ADP-heptose:LPS heptosyltransferase II [Bdellovibrio bacteriovorus HD100]				
6412	42523011	35	7.00E-20	Bdellovibrio bacteriovorus HD100					
					histidyl-tRNA synthetase [Clostridium tetani E88] gbl AAO36465.1 histidyl-tRNA synthetase [Clostridium tetani E88] sp Q892X7 SYH_CLOTE Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HisRS)				6.1.1.21
6415,	28211584	38	4.00E-19	Clostridium tetani E88	branched-chain amino acid binding protein [Pyrobaculum aerophilum str. IM2] gbl AAL63934.1 branched-chain amino acid binding protein				
6417,					Pyrobaculum aerophilum str. IM2				
6418	18313085	33	2.00E-37	Pyrobaculum aerophilum str. IM2					
					COG1523: Type II secretory pathway, pullulanase PulA and related glycosidases [Trichodesmium erythraeum IMS101]				
6419,	48894700	44	1.00E-28	Trichodesmium erythraeum IMS101					
6420				Legionella pneumophila str. Paris				92	3.00E-14
6423,					hypothetical protein lpp0323 [Legionella pneumophila str. Paris]				3.2.1.-
6424	54296294	37	7.00E-34	Legionella pneumophila str. Paris	emb CAH11471.1 hypothetical protein [Legionella pneumophila str. Paris]				2.3.1.-

6427,	32469352	50	1.00E-07	Francisella tularensis subsp. novicida	unknown [Francisella tularensis subsp. novicida]				
6428					conserved hypothetical protein [Porphyromonas gingivalis W83]				
6429,	34397310	42	2.00E-30	Porphyromonas gingivalis W83	ref NP_905474.1 hypothetical protein PG1300 [Porphyromonas gingivalis W83]				2.1.1.-
6431,					tRNA delta(2)-isopentenylpyrophosphate transferase [Treponema denticola ATCC 35405]				
6432	42526955	40	2.00E-16	Treponema denticola ATCC 35405	transferase [Treponema denticola ATCC 35405]				2.5.1.8
6435,					putative restriction enzyme modulator protein [Staphylococcus aureus subsp. aureus MRSA252]				
6436	49482330	39	1.00E-24	Staphylococcus aureus subsp. aureus MRSA252	modulator protein [Staphylococcus aureus subsp. aureus MRSA252]				
6437,					histidyl-tRNA synthetase [Clostridium tetani E88]				
6438	28211584	31	4.00E-22	Clostridium tetani E88	tRNA synthetase [Clostridium tetani E88]				6.1.1.21
6439,	51573655	56	2.00E-25	Borrelia garinii PBI	tRNA synthetase [Borrelia garinii PBI]				
6440					isoleucyl-tRNA synthetase [Borrelia garinii PBI]				6.1.1.5
6441,					tRNA synthetase [Borrelia garinii PBI]				
6442	48854681	34	8.00E-13	Cytophaga hutchinsonii	hypothetical protein Chut02002347 [Cytophaga hutchinsonii]				
6443,					hypothetical protein Chut02002840 [Cytophaga hutchinsonii]				
6444	48854173	28	1.00E-25	Cytophaga hutchinsonii	hypothetical protein Chut02002840 [Cytophaga hutchinsonii]				
6449,					hypothetical protein Chte02000708 [Clostridium thermocellum ATCC 27405]				
6450	48859986	31	3.00E-25	Clostridium thermocellum ATCC 27405	hypothetical protein Chte02000708 [Clostridium thermocellum ATCC 27405]				
645,					COG2202: FOG: PAS/PAC domain [Anabaena variabilis ATCC 29413]				2.7.3.-
646	53765108	32	4.00E-25	Anabaena variabilis ATCC 29413	hypothetical protein LIC13227 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_714224.1 hypothetical protein LA4044				
					[Leptospira interrogans serovar Lai str. 56601] gb AA51242.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601]				
6453,					gb AA571772.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				
6454	45659049	37	2.00E-21	Fiocruz L1-130	serovar Copenhageni str. Fiocruz L1-130]				
6455,					COG1309: Transcriptional regulator [Thiobacillus denitrificans ATCC 25259]				
6456	52006061	35	9.00E-28	Thiobacillus denitrificans ATCC 25259	COG0774: UDP-3-O-acetyl-N-acetylglucosamine deacetylase [Cytophaga hutchinsonii]				
6457,									
6458	48854755	59	1.00E-74	Cytophaga hutchinsonii					4.2.1.-

6459,	53797309	45	1.00E-60	Chloroflexus aurantiacus	COG0215: CysteinyI-tRNA synthetase [Chloroflexus aurantiacus]				6.1.1.16
6460				Globobacter violaceus PCC 7421	hypothetical protein glr2879 [Globobacter violaceus PCC 7421] dbj BAC90820.1 glr2879 [Globobacter violaceus PCC 7421]				
6461,	37522448	28	3.00E-08						
6462				Desulfotalea psychrophila LSv54	hypothetical protein DP2762 [Desulfotalea psychrophila LSv54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila LSv54]				2.1.1.14 4
6463,	51246614	30	3.00E-21	Desulfotalea psychrophila LSv54	hypothetical protein DP2762 [Desulfotalea psychrophila LSv54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila LSv54]				2.1.1.14 4
6464				Cytophaga hutchinsonii	COG0337: 3-dehydroquinase synthetase [Cytophaga hutchinsonii] signal transduction histidine kinase [Vibrio vulnificus YJ016] dbj BAC94870.1 signal transduction histidine kinase [Vibrio vulnificus YJ016]				4.2.3.4
6465,	51246614	30	9.00E-21	Desulfotalea psychrophila LSv54	hypothetical protein DP2762 [Desulfotalea psychrophila LSv54] emb CAG37491.1 hypothetical protein [Desulfotalea psychrophila LSv54]				2.1.1.14 4
6466				Vibrio vulnificus YJ016					2.7.3.-
6467,	48856143	37	2.00E-18						
6468									
647,	37680290	40	2.00E-13						
6471,									2.4.1.-
6472									
6473,				Geobacillus stearothermophilus	endo-1,4-beta-xylanase (EC 3.2.1.8) - Bacillus stearothermophilus sp P45703 XYN2_BACST Endo-1,4-beta-xylanase precursor (Xylanase) (1,4-beta-D-xylan xylanohydrolase) dbj BAA05668.1 xylanase [Geobacillus stearothermophilus]				3.2.1.8
6474	2126856	51	1.00E-48						
6475,				Porphyromonas gingivalis W83	uroporphyrinogen-III synthase HemD, putative [Porphyromonas gingivalis W83] ref NP_904537.1 uroporphyrinogen-III synthase HemD, putative [Porphyromonas gingivalis W83]				
6476	34396369	50	1.00E-38						
6477,				Geobacter sulfurreducens PCA	GTP pyrophosphokinase [Geobacter sulfurreducens PCA] gb AAR35612.1 GTP pyrophosphokinase [Geobacter sulfurreducens PCA]				2.7.6.5
6478	39997334	63	1.00E-125						
6479,				Bdellovibrio bacteriovorus HD100	GTP pyrophosphokinase [Bdellovibrio bacteriovorus HD100] emb CAE79448.1 GTP pyrophosphokinase [Bdellovibrio bacteriovorus HD100]				2.7.6.5
6480	42523075	51	1.00E-90						
6481,				Methanosarcina mazei Go1	Methyl-accepting chemotaxis protein [Methanosarcina mazei Go1] gb AAM30029.1 Methyl-accepting chemotaxis protein [Methanosarcina mazei Go1]				
6482	21226435	56	4.00E-35						
6483,				Deinococcus radiodurans	conserved hypothetical protein [Deinococcus radiodurans] pir H75297 conserved hypothetical protein - Deinococcus radiodurans (strain R1) ref NP_295956.1 hypothetical protein DR2234 [Deinococcus radiodurans R1]				
6484	6460039	32	5.00E-21						
6485,				Symbiobacterium thermophilum IAM 14863	two-component sensor histidine kinase [Symbiobacterium thermophilum IAM 14863] dbj BAD40025.1 two-component sensor histidine kinase [Symbiobacterium thermophilum IAM 14863]				2.7.3.-
6486	51892178	29	1.00E-14						

649,	48856580	48	2.00E-31	Cytophaga hutchinsonii	hypothetical protein Chut02000314 [Cytophaga hutchinsonii]				
650				Geobacter sulfurreducens PCA	trehalose-phosphatase [Geobacter sulfurreducens PCA] gb AAR35711.1				3.1.3.12
6491,	39997433	37	3.00E-21		trehalose-phosphatase [Geobacter sulfurreducens PCA]				
6492					putative histidine ammonia-lyase [Staphylococcus aureus subsp. aureus MRSA252] emb CAG39036.1 putative histidine ammonia-lyase [Staphylococcus aureus subsp. aureus MRSA252] sp Q6GKT7 HUTH_STAAR Histidine ammonia-lyase (Histidase)				4.3.1.3
6495,	49482281	40	2.00E-20	Staphylococcus aureus subsp. aureus MRSA252	thiamine biosynthesis protein [Pyrococcus horikoshii OT3] dbj BAA30255.1				
6496					446aa long hypothetical thiamine biosynthesis protein [Pyrococcus horikoshii OT3] pir E71057 probable thiamin biosynthesis protein - Pyrococcus horikoshii				2.7.4.7
6503,	14590982	43	7.00E-35	Pyrococcus horikoshii OT3					
6504									
651,	48856481	69	3.00E-55	Cytophaga hutchinsonii	COG1225: Peroxiredoxin [Cytophaga hutchinsonii]				1.6.4.-
652					hypothetical protein mir4723 [Mesorhizobium loti MAFF303099] dbj BAB51313.1 mir4723 [Mesorhizobium loti MAFF303099]				
6511,	13473959	37	5.00E-15	Mesorhizobium loti MAFF303099					
6512									
6513,	48854274	41	7.00E-47	Cytophaga hutchinsonii	COG3239: Fatty acid desaturase [Cytophaga hutchinsonii]				1.14.99.
6514									25
6515,	56675038	43	2.00E-15	uncultured bacterium	cellulase [uncultured bacterium]				
6516									
6521,	50287657	44	1.00E-18	Candida glabrata	unnamed protein product [Candida glabrata] emb CAG59182.1 unnamed protein product [Candida glabrata CBS138]				
6522									
6527,	52698490	45	5.00E-14	Rickettsia akari str. Hartford	COG0080: Ribosomal protein L11 [Rickettsia akari str. Hartford]				
6528									
6529,				Wolbachia endosymbiont of Drosophila	ferrochelatase [Wolbachia endosymbiont of Drosophila melanogaster] gb AAS14832.1 ferrochelatase [Wolbachia endosymbiont of Drosophila melanogaster]				4.99.1.1
6530	42520983	57	3.00E-73	melanogaster					
653,									
654	53759377	34	7.00E-14	Methylobacillus flagellatus KT	COG2010: Cytochrome c, mono- and di-heme variants [Methylobacillus flagellatus KT]				1.7.99.3
6533,									
6534	53714870	42	6.00E-14	Bacteroides fragilis YCH46	RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46] dbj BAD50328.1 RNA polymerase ECF-type sigma factor [Bacteroides fragilis YCH46]				
6535,									
6536	34396896	61	4.00E-48	Porphyromonas gingivalis W83	polyA polymerase family protein [Porphyromonas gingivalis W83] ref NP_905062.1 polyA polymerase family protein [Porphyromonas gingivalis W83]				2.7.7.19
6537,									
6538	53712197	32	5.00E-13	Bacteroides fragilis YCH46	hypothetical protein BF0904 [Bacteroides fragilis YCH46] dbj BAD47655.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				

6539, 6540	32477219	38	2.00E-18	Rhodopirellula baltica SH 1	hypothetical acetyltransferase [Rhodopirellula baltica SH 1] emb CAD77288.1 hypothetical acetyltransferase [Pirellula sp.]			
6541, 6542	56750395	35	2.00E-07	Synechococcus elongatus PCC 6301	hypothetical protein syc0386_c [Synechococcus elongatus PCC 6301] dbj BAD76576.1 unknown protein [Synechococcus elongatus PCC 6301]			
6543, 6544	17547951	31	1.00E-14	Ralstonia solanacearum GM1000	PUTATIVE BACTERIOPHAGE-RELATED PROTEIN [Ralstonia solanacearum GM1000] emb CAD17020.1 PUTATIVE BACTERIOPHAGE- RELATED PROTEIN [Ralstonia solanacearum]			
6549, 6550	34396235	53	1.00E-64	Porphyromonas gingivalis W83	sensor histidine kinase [Porphyromonas gingivalis W83] ref NP_904403.1			2.7.3.-
6551, 6552	48862211	47	5.00E-33	Microbulbifer degradans 2-40	sensor histidine kinase [Porphyromonas gingivalis W83] COG2989: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40]			
6553, 6554	53758638	37	2.00E-31	Methylococcus capsulatus str. Bath	conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_113480.1 hypothetical protein MCA1003 [Methylococcus capsulatus str. Bath]			
6555, 6556	48854335	41	8.00E-28	Cytophaga hutchinsonii	COG3762: Predicted membrane protein [Cytophaga hutchinsonii] hypothetical protein MA4122 [Methanosarcina acetivorans C2A] ref NP_616740.1 hypothetical protein MA1814 [Methanosarcina acetivorans C2A] ref NP_615925.1 hypothetical protein MA0973 [Methanosarcina acetivorans C2A] gb AAM07470.1 predicted protein [Methanosarcina acetivorans str. C2A] gb AAM05220.1 predicted protein [Methanosarcina acetivorans str. C2A] gb AAM04405.1 predicted protein [Methanosarcina acetivorans str. C2A]	Methanosarcina acetivorans str. C2A, section 319 of 534 of the complete genome	85 4.00E-57	
6565, 6566	20094987	34	1.00E-07	Methanopyrus kandleri AV19 uncultured	19 kDa subunit of the signal recognition particle [Methanopyrus kandleri AV19] gb AAM02764.1 19 kDa subunit of the signal recognition particle [Methanopyrus kandleri AV19] sp Q8TV49 SR19_METKA Signal recognition particle 19 kDa protein (SRP19)			
6567, 6568	52550522	45	9.00E-54	GZfos9D8 archaeon	Bpml endonuclease-methyltransferase fusion protein type IIg [uncultured archaeon GZfos9D8]			
6569, 6570	31194811	45	1.00E-33	Anopheles gambiae	ENSANGP00000002016 [Anopheles gambiae] glucose-inhibited division protein B [Porphyromonas gingivalis W83] ref NP_905481.1 glucose-inhibited division protein B [Porphyromonas gingivalis W83] sp Q7MV10 GIDB_PORGI Methyltransferase gldB (Glucose inhibited division protein B)			3.1.-
657, 658	34397317	41	2.00E-18	Porphyromonas gingivalis W83				

6571,	29349974	42	4.00E-38	Bacteroides thetataoamicon	two-component system response regulator protein [Bacteroides thetataoamicon VPI-5482] gb AAO79671.1 two-component system response regulator protein [Bacteroides thetataoamicon VPI-5482]				
6572									
6575,				Bacillus halodurans	two-component response regulator [Bacillus halodurans C-125]				
6576	15616404	42	7.00E-10	C-125	dbj BAB07561.1 two-component response regulator [Bacillus halodurans C-125] pir B84130 two-component response regulator BH3842 [imported] - Bacillus halodurans (strain C-125)				
6581,				Cytophaga					1.3.3.1
6582	48854536	55	5.00E-64	hutchinsonii	COG0167: Dihydroorotate dehydrogenase [Cytophaga hutchinsonii]				
6589,				Cytophaga					2.3.1.51
6590	48853682	29	9.00E-20	hutchinsonii	COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Cytophaga hutchinsonii]				
659,				Clostridium					2.7.3.-
660	48860418	43	1.00E-28	thermocellum	COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405]				
6591,				Chlorobium	ATP-dependent Clp protease, ATP-binding subunit ClpC [Chlorobium tepidum TLS] gb AAM71439.1 ATP-dependent Clp protease, ATP-binding subunit ClpC [Chlorobium tepidum TLS]				
6592	21673032	67	2.00E-17	tepidum TLS					
6593,				Nostoc sp. PCC	two-component sensor histidine kinase [Nostoc sp. PCC 7120] pir AG1909				2.7.3.-
6594	17228320	34	8.00E-18	7120	two-component sensor histidine kinase all0825 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB72782.1 two-component sensor histidine kinase [Nostoc sp. PCC 7120]				
6595,	ABP0398				Desc: Human ORFX protein sequence SEQ ID NO:7944. Org: Homo sapiens				
6596	1	36	8.00E-11	Geobacter					
6601,				metallireducens GS	COG2804: Type II secretory pathway, ATPase PulE/Tfp pilus assembly pathway, ATPase PilB [Geobacter metallireducens GS-15]				
6602	48846577	55	3.00E-79	15					
6603,				Cytophaga					2.7.3.-
6604	48856489	45	4.00E-61	hutchinsonii	COG2202: FOG: PAS/PAC domain [Cytophaga hutchinsonii]				
6605,				Leptospira					
6606	24212810	38	3.00E-17	interrogans serovar Lai str. 56601	Para-aminobenzoate synthetase [Leptospira interrogans serovar Lai str. 56601] gb AAN47309.1 Para-aminobenzoate synthetase [Leptospira interrogans serovar lai str. 56601]				4.1.3.-
6609,				Idiomarina					
6610	56460818	49	1.00E-61	lohiensis L2TR	Secreted enzyme, contains two amidohydrolase related domains [Idiomarina lohiensis L2TR] gb AAV82550.1 Secreted enzyme, contains two amidohydrolase related domains [Idiomarina lohiensis L2TR]				
6613,				Idiomarina	Predicted hydrolase of the alpha/beta superfamily [Idiomarina lohiensis L2TR] gb AAV83358.1 Predicted hydrolase of the alpha/beta superfamily				3.2.1.41
6614	56461626	36	7.00E-28	lohiensis L2TR					
6615,				Burkholderia	COG0604: NADPH:quinone reductase and related Zn-dependent oxidoreductases [Burkholderia cepacia R18194]				1.6.5.5
6616	46311319	50	2.00E-18	cepacia R18194					

6617, 6618	28211857	26	2.00E-16	Clostridium tetani E88	glycosyl transferase [Clostridium tetani E88]				2.4.1.-
6619, 6620	53765041	28	1.00E-17	Anabaena variabilis ATCC 29413	COG0463: Glycosyltransferases involved in cell wall biogenesis [Anabaena variabilis ATCC 29413]				2.-.-
6623, 6624	48855616	67	1.00E-112	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]				
6629, 6630	48854463	52	5.00E-49	Cytophaga hutchinsonii	COG0193: Peptidyl-RNA hydrolase [Cytophaga hutchinsonii]				3.1.1.29
6631, 6632	53796261	74	5.00E-45	Chloroflexus aurantiacus	COG4898: Uncharacterized protein conserved in bacteria [Chloroflexus aurantiacus]				
6637, 6638	21672859	38	8.00E-16	Chlorobium tepidum TLS	ATP synthase F1, delta subunit [Chlorobium tepidum TLS] gb AAM71266.1 ATP synthase F1, delta subunit [Chlorobium tepidum TLS]				3.6.3.15
6643, 6644	48855342	39	7.00E-18	Cytophaga hutchinsonii	COG0612: Predicted Zn-dependent peptidases [Cytophaga hutchinsonii]				3.4.99.-
6645, 6646	48854662	24	2.00E-19	Cytophaga hutchinsonii	COG0589: Universal stress protein UspA and related nucleotide-binding proteins [Cytophaga hutchinsonii]				
6647, 6648	48854272	43	2.00E-40	Cytophaga hutchinsonii	COG0564: Pseudouridylylase synthases, 23S RNA-specific [Cytophaga hutchinsonii]				4.2.1.70
6649, 6650	47569655	58	1.00E-10	Bacillus cereus G9241	prophage LambdaSa2, HNH endonuclease family protein [Bacillus cereus G9241] gb EAL12072.1 prophage LambdaSa2, HNH endonuclease family protein [Bacillus cereus G9241]				
665, 666	17547951	31	1.00E-14	Ralstonia solanacearum GMI1000	PUTATIVE BACTERIOPHAGE-RELATED PROTEIN [Ralstonia solanacearum GMI1000] emb CAD17020.1 PUTATIVE BACTERIOPHAGE-RELATED PROTEIN [Ralstonia solanacearum]				
6651, 6652	31194343	51	9.00E-38	Anopheles gambiae	ENSANGP00000000181 [Anopheles gambiae]				
6653, 6654	30020326	47	1.00E-40	Bacillus cereus ATCC 14579	Dihydrofolate reductase [Bacillus cereus ATCC 14579] gb AAP09158.1 Dihydrofolate reductase [Bacillus cereus ATCC 14579]				1.5.1.3
6655, 6656	53715360	48	1.00E-60	Bacteroides fragilis YCH46	ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46] dbj BAD50818.1 ATP-dependent DNA helicase RecQ [Bacteroides fragilis YCH46]				3.6.1.-
6657, 6658	48856124	44	3.00E-22	Cytophaga hutchinsonii	COG0770: UDP-N-acetylmuramyl pentapeptide synthase [Cytophaga hutchinsonii]				6.3.2.15
6659, 6660	27382562	24	2.00E-18	Bradyrhizobium japonicum USDA 110	hypothetical protein bfr7451 [Bradyrhizobium japonicum USDA 110] dbj BACS2716.1 bfr7451 [Bradyrhizobium japonicum USDA 110]				6.3.2.4
6665, 6666	52006523	55	3.00E-40	Thiobacillus denitrificans ATCC 25259	COG0532: Translation initiation factor 2 (IF-2; GTPase) [Thiobacillus denitrificans ATCC 25259]				

6667,	23123559	30	7.00E-14	Nostoc punctiforme PCC 73102	COG5485: Predicted ester cyclase [Nostoc punctiforme PCC 73102]				
6668				Cytophaga hutchinsonii					1.5.3.-
6677,	48856145	42	3.00E-37		COG0506: Proline dehydrogenase [Cytophaga hutchinsonii]				
6679,				Pyrococcus furiosus DSM 3638	glycosyl transferase [Pyrococcus furiosus DSM 3638] gb AAL81483.1				
6680	18977731	34	4.00E-30	Francisella tularensis subsp. tularensis Schu 4	glycosyl transferase [Pyrococcus furiosus DSM 3638]				
6681,				Francisella tularensis subsp. tularensis Schu 4	hypothetical protein FTT0522 [Francisella tularensis subsp. tularensis Schu 4] emb CAG45155.1 conserved hypothetical protein [Francisella tularensis subsp. tularensis]				2.1.1.72
6682	56707657	52	1.00E-28	tularensis Schu 4					
6683,				synthetic construct	hypothetical protein FTT0520 [synthetic construct]				
6684	57339644	49	9.00E-50	Bdellovibrio bacteriovorus HD100	putative potassium/proton antiporter [Bdellovibrio bacteriovorus HD100]				
6687,				bacteriovorus HD100	emb CAE80097.1 putative potassium/proton antiporter [Bdellovibrio bacteriovorus HD100]				
6688	42523724	44	4.00E-18	Bacteroides thetaiotaomicron VPI-5482	bacteriovorus HD100				
6689,				Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT2008 [Bacteroides thetaiotaomicron VPI-5482]				
6690	29347418	43	1.00E-46	Cytophaga hutchinsonii	gb AAO77115.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
6693,				Cytophaga hutchinsonii	COG0317: Guanosine polyphosphate pyrophosphohydrolases/synthetases [Cytophaga hutchinsonii]				2.7.6.5
6694	48856298	58	1.00E-109	Cytophaga hutchinsonii					
6695,				Cytophaga hutchinsonii	COG1522: Transcriptional regulators [Cytophaga hutchinsonii]				
6696	48856980	50	5.00E-39		Response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain [Thermoanaerobacter tengcongensis MB4]				
6697,				Thermoanaerobacter tengcongensis MB4	gb AAM25604.1 Response regulators consisting of a CheY-like receiver domain and a HTH DNA-binding domain [Thermoanaerobacter tengcongensis MB4]				2.7.3.-
6698	20808829	36	8.00E-11	Clostridium thermocellum ATCC 27405	tengcongensis MB4				
6699,				Clostridium thermocellum ATCC 27405	COG1040: Predicted amidophosphoribosyltransferases [Clostridium thermocellum ATCC 27405]				
6700.	48859351	31	4.00E-19	Legionella pneumophila str. Paris					
67, 68	54295921	38	3.00E-11	Cytophaga hutchinsonii	hypothetical protein plpp0078 [Legionella pneumophila str. Paris] emb CAH17255.1 hypothetical protein [Legionella pneumophila str. Paris]				
6701,				Cytophaga hutchinsonii	hypothetical protein Chut02003551 [Cytophaga hutchinsonii]				
6702	48853695	55	6.00E-65						
6703,				Nostoc punctiforme PCC 73102	hypothetical protein Npun02006402 [Nostoc punctiforme PCC 73102]				
6704	23125186	36	4.00E-22	Cytophaga hutchinsonii	COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Cytophaga hutchinsonii]				6.2.1.3
6707,									
6708	48854120	51	2.00E-74						

6709, 6710	48855792	38	3.00E-25	Cytophaga hutchinsonii	COG2353: Uncharacterized conserved protein [Cytophaga hutchinsonii] PUTATIVE BACTERIOPHAGE-RELATED PROTEIN [Ralstonia solanacearum GM11000] emb CAD17020.1 PUTATIVE BACTERIOPHAGE- RELATED PROTEIN [Ralstonia solanacearum]				
671, 672	17547951	30	2.00E-13	Ralstonia solanacearum GM11000	two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482] gb AAO78783.1 two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482]				
6721, 6722	29349086	24	1.00E-12	Bacteroides thetaitaomicron VPI-5482	putative two-component system sensor protein histidine kinase [Bacteroides fragilis YCH46] dbj BAD50632.1 putative two-component system sensor protein histidine kinase [Bacteroides fragilis YCH46]				2.7.3.-
6723, 6724	53715174	39	3.00E-38	Bacteroides fragilis YCH46	COG2137: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
6727, 6728	48854316	45	4.00E-32	Cytophaga hutchinsonii	methionyl-CoA mutase [Leptospira interrogans serovar Lal str. 56601] gb AAN50154.1 methionyl-CoA mutase [Leptospira interrogans serovar lai str. 56601]				5.4.99.2
6729, 6730	24215655	56	2.00E-93	Leptospira interrogans serovar Lal str. 56601	COG1674: DNA segregation ATPase FtsK/SpoIIIE and related proteins [Cytophaga hutchinsonii]				
673, 674	48854535	73	1.00E-101	Cytophaga hutchinsonii	transcriptional regulator, TetR family [Bacteroides thetaiotaomicron VPI- 5482] gb AAO76513.1 transcriptional regulator, TetR family [Bacteroides thetaitaomicron VPI-5482]				
6731, 6732	29346816	31	3.00E-12	Bacteroides thetaitaomicron VPI-5482	hypothetical protein Atu0403 [Agrobacterium tumefaciens str. C58] gb AAL41424.1 conserved hypothetical protein [Agrobacterium tumefaciens str. C58] gb AAK86218.1 AGR_C_710p [Agrobacterium tumefaciens str. C58] pir AB2626 conserved hypothetical protein Atu0403 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) pir A97408 hypothetical protein AGR_C_710 [imported] - Agrobacterium tumefaciens (strain C58, Cereon) ref NP_353433.1 hypothetical protein AGR_C_710 [Agrobacterium tumefaciens str. C58]				
6735, 6736	17934318	33	8.00E-14	Agrobacterium tumefaciens str. C58	hypothetical protein BF3507 [Bacteroides fragilis YCH46] dbj BAD50250.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
6737, 6738	53714792	43	8.00E-17	Bacteroides fragilis YCH46	COG0188: Type IIA topoisomerase (DNA gyrase/topo II, topoisomerase IV), A subunit [Cytophaga hutchinsonii]				5.99.1.-
6739, 6740	48853743	60	2.00E-91	Cytophaga hutchinsonii	Desc:H3 homologue of prolyl-tripeptidyl peptidase DPP. Org: Porphyromonas gingivalis				
6741, 6742	AAB1851 2	35	2.00E-08						

6749,	53715862	53	2.00E-54	Bacteroides fragilis YCH46	DNA mismatch repair protein mutS [Bacteroides fragilis YCH46]			
6750					dbj BAD51320.1 DNA mismatch repair protein mutS [Bacteroides fragilis YCH46]			
675,	21226234	63	2.00E-38	Methanosarcina mazei Go1	hypothetical protein MM0132 [Methanosarcina mazei Go1] gb AAM29828.1 conserved protein [Methanosarcina mazei Goe1]			
6751,	48854843	38	5.00E-45	Cytophaga hutchinsonii	COG0196: FAD synthase [Cytophaga hutchinsonii]			2.7.1.26
6753,	48855703	33	4.00E-27	Cytophaga hutchinsonii	COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii]			2.7.3.-
6754								
6757,	48853840	32	9.00E-25	Cytophaga hutchinsonii	COG0438: Glycosyltransferase [Cytophaga hutchinsonii]			
6758								
6763,	56477305	34	3.00E-11	Azoarcus sp. EbN1	hypothetical protein ebA3316 [Azoarcus sp. EbN1] emb CAI07993.1 conserved hypothetical protein [Azoarcus sp. EbN1]			
6764				Leuconostoc mesenteroides subsp. mesenteroides				
6765,	23025125	54	1.00E-57	ATCC 8293	COG4974: Site-specific recombinase XerD [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]			
6766							84	1.00E-10
6767,	53760034	52	2.00E-38	Methylobacillus flagellatus KT	COG2870: ADP-heptose synthase, bifunctional sugar kinase/adenylyltransferase [Methylobacillus flagellatus KT]			2.7.7.39
6768				Thermoanaerobacter tengcongensis	UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4]			
6769,	20808896	39	2.00E-35	MB4	tengcongensis MB4] gb AAM25671.1 UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4]			6.3.2.15
6770								
677,	53714426	60	5.00E-50	Bacteroides fragilis YCH46	hypothetical protein BF3139 [Bacteroides fragilis YCH46] dbj BAD49884.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			
678								
6771,				Thermoanaerobacter tengcongensis	UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4]			
6772	20808896	38	4.00E-36	MB4	tengcongensis MB4] gb AAM25671.1 UDP-N-acetylmuramyl pentapeptide synthase [Thermoanaerobacter tengcongensis MB4]			6.3.2.15
6773,				Microbulbifer degradans	COG0216: Protein chain release factor A [Microbulbifer degradans 2-40]			
6774	48863872	52	1.00E-81	degradans 2-40				
6775,	ABB5552	37	1.00E-26		Desc: Lactococcus lactis protein yweC. Org: Lactococcus lactis IL1403			
6776					DNA Pol III Epsilon Chain [Bacteroides thetaiotaomicron VPI-5482]			
6777,	29346773	53	2.00E-54	Bacteroides thetaiotaomicron VPI-5482	gb AAO76470.1 DNA Pol III Epsilon Chain [Bacteroides thetaiotaomicron VPI-5482]			2.7.7.7
6778								
6781,	48855683	53	3.00E-42	Cytophaga hutchinsonii	COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii]			
6782								

6783,									hypothetical protein MTH570 [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85076.1 unknown [Methanothermobacter			
6784	15678598	47	5.00E-29						thermautotrophicus str. Delta H] pir E69175 hypothetical protein MTH570 -			
6785,									Methanothermobacter thermautotrophicum (strain Delta H)			
6786	53714487	56	3.00E-44						SsrA-binding protein [Bacteroides fragilis YCH46] dbj BAD48945.1 SsrA-binding protein [Bacteroides fragilis YCH46]			
679,									peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46]			
680	53712369	24	2.00E-15						dbj BAD47827.1 peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46]			
6791,									two-component system response regulator [Bacteroides fragilis YCH46]			
6792	53714651	40	3.00E-42						dbj BAD50109.1 two-component system response regulator [Bacteroides fragilis YCH46]			
6793,												
6794	48831352	24	5.00E-23						COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			2.7.3.-
6797,									predicted transcription regulator, DUF118 helix-turn-helix family			
6798	57160028	30	3.00E-09						[Thermococcus kodakaraensis] ref YP_184182.1 predicted transcription regulator, DUF118 helix-turn-helix family [Thermococcus kodakaraensis]			
6799,									ABC transporter, ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO77601.1 ABC transporter, ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482]			1.8.-.-
6800	29347904	66	3.00E-77						COG1331: Highly conserved protein containing a thioredoxin domain			
6801,									[Cytophaga hutchinsonii]			
6802	48856612	44	1.00E-32						conserved hypothetical protein [Campylobacter coli RM2228]			
6803,									gb EAL56874.1 conserved hypothetical protein [Campylobacter coli RM2228]			
6804	57168392	38	5.00E-40						PUTATIVE METHYL TRANSFERASE [Molinitella succinogenes DSM 1740]			
6805,									emb CAE09463.1 PUTATIVE METHYL TRANSFERASE [Molinitella succinogenes]			
6806	34556748	32	7.00E-17						COG0642: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405]			2.7.3.-
6807,												
6808	48858932	42	9.00E-36						COG2314: Predicted membrane protein [Trichodesmium erythraeum IMS101]			
6809,									MutS2 family protein [Porphyromonas gingivalis W83] ref NP_904691.1			
6810	48894405	27	4.00E-08						MutS2 family protein [Porphyromonas gingivalis W83]			
681,									hypothetical protein BF1779 [Bacteroides fragilis YCH46] dbj BAD48526.1			
682	34396524	36	2.00E-35						hypothetical protein [Bacteroides fragilis YCH46]			
6813,												
6814	53713068	29	1.00E-09									

6817, 6818	48478030	36	4.00E-16	Picrophilus torridus DSM 9790	hypothetical conserved protein DUF52 [Picrophilus torridus DSM 9790] gb AAT43543.1 hypothetical conserved protein DUF52 [Picrophilus torridus DSM 9790]			
6821, 6822	15896812	43	1.00E-28	acyl-carrier-protein Wolinella succinogenes DSM 1740	3-oxoacyl-[acyl-carrier-protein] synthase III [Clostridium acetobutylicum ATCC 824] gb AAK81501.1 3-oxoacyl-[acyl-carrier-protein] synthase III [Clostridium acetobutylicum ATCC 824] p B97339 3-oxoacyl-[acyl-carrier-protein] synthase III [imported] - Clostridium acetobutylicum sp Q97DA2 FABH_CLOAB 3-oxoacyl-[acyl-carrier-protein] synthase III (Beta-ketoacyl-ACP synthase III) (KAS III)			2.3.1.41
6823, 6824	34557550	38	9.00E-20	Wolinella succinogenes DSM 1740	hypothetical protein WS1180 [Wolinella succinogenes DSM 1740] emb CAE10265.1 hypothetical protein [Wolinella succinogenes]			
6825, 6826	34557550	33	7.00E-26	Wolinella succinogenes DSM 1740	hypothetical protein WS1180 [Wolinella succinogenes DSM 1740] emb CAE10265.1 hypothetical protein [Wolinella succinogenes]			
6827, 6828	7592813	47	6.00E-64	Actinobacillus actinomycetemcomitans	GDP-mannose pyrophosphorylase homolog [Actinobacillus actinomycetemcomitans]			2.7.7.22
6829, 6830	48853833	49	3.00E-41	Cytophaga hutchinsonii	COG0576: Molecular chaperone GrpE (heat shock protein) [Cytophaga hutchinsonii]			
6831, 6832	45358644	54	4.00E-76	Methanococcus maripaludis S2	putative LPS biosynthesis protein WbpG [Methanococcus maripaludis S2] emb CAF30637.1 putative LPS biosynthesis protein WbpG [Methanococcus maripaludis S2]			
6833, 6834	30249085	52	4.00E-57	Nitrosomonas europaea ATCC 19718	Transposase IS4 family [Nitrosomonas europaea ATCC 19718] emb CAD85004.1 Transposase IS4 family [Nitrosomonas europaea ATCC 19718]			
6837, 6838	45547643	30	5.00E-27	Rubrobacter xylanophilus DSM 9941	COG0614: ABC-type Fe3+-hydroxamate transport system, periplasmic component [Rubrobacter xylanophilus DSM 9941]			
6847, 6848	48854546	35	1.00E-15	Cytophaga hutchinsonii	COG1943: Transposase and inactivated derivatives [Cytophaga hutchinsonii]			
6849, 6850	53760393	40	4.00E-48	Methylobacillus flagellatus KT	COG2821: Membrane-bound lytic murein transglycosylase [Methylobacillus flagellatus KT]			3.2.1.-
685, 686	48839466	94	2.00E-63	Methanosarcina barkeri str. fusaro	COG1335: Amidases related to nicotinamidase [Methanosarcina barkeri str. fusaro]			
6851, 6852	14994235	32	2.00E-31	Scyllorhinus torazame	L-gulonolactone oxidase [Scyllorhinus torazame] sp Q90YK3 GGLO_SCYTO L-gulonolactone oxidase (LGO) (L-gulonono-gamma-lactone oxidase) [GLO]			1.1.3.8
6855, 6856	57506273	61	8.00E-45	Campylobacter upsaliensis RM3195	Fic family protein [Campylobacter upsaliensis RM3195] gb EAL52255.1 Fic family protein [Campylobacter upsaliensis RM3195]			

6857, 6858	52006879	36	8.00E-45	Thiobacillus denitrificans ATCC 25259	COG2199: FOG:GGDEF domain [Thiobacillus denitrificans ATCC 25259] phosphopantothenoylcysteine decarboxylase/phosphopantothenate-- cysteine ligase [Campylobacter lari RM2100] gb EAL55505.1 phosphopantothenoylcysteine decarboxylase/phosphopantothenate-- cysteine ligase [Campylobacter lari RM2100]	Clostridium acetobutylicum ATCC 824 section 66 of 356 of the complete genome	89	7.00E-07	2.7.3.-
6859, 6860	57240391	47	6.00E-19	Campylobacter lari RM2100					
6861, 6862	52007207	37	1.00E-50	Thiobacillus denitrificans ATCC 25259	COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Thiobacillus denitrificans ATCC 25259]				3.1.21.3
6865, 6866	53712714	28	5.00E-20	Bacteroides fragilis YCH46	hypothetical protein BF1421 [Bacteroides fragilis YCH46] dbj BAD48172.1 hypothetical protein [Bacteroides fragilis YCH46]				
6869, 6870	48895292	50	2.00E-35	Trichodesmium erythraeum IMS101	COG4123: Predicted O-methyltransferase [Trichodesmium erythraeum IMS101]				2.1.1.-
687, 688	29349986	34	4.00E-21	Bacteroides thetaiotaomicron VPI-5482	transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_812545.1 transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_811586.1 transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_811340.1 transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_811312.1 transposase [Bacteroides thetaiotaomicron VPI-5482] ref NP_810805.1 integrase [Bacteroides thetaiotaomicron VPI-5482] ref NP_809831.1 integrase [Bacteroides thetaiotaomicron VPI-5482] ref NP_809271.1 transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79683.1 transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78739.1 transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77780.1 transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77534.1 transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77506.1 transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76999.1 integrase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76025.1 integrase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75465.1 transposase [Bacteroides thetaiotaomicron VPI-5482]				
6871, 6872	46446869	37	4.00E-38	Parachlamydia sp. UWE25	putative cysteinyl tRNA synthetase [Parachlamydia sp. UWE25] emb CAF23959.1 putative cysteinyl tRNA synthetase [Parachlamydia sp. UWE25]				6.1.1.16
6873, 6874	45657880	54	2.00E-60	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	cysteinyl-tRNA synthetase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70603.1 cysteinyl-tRNA synthetase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				6.1.1.16

6875, 6876	34557269	53	2.00E-75	Wollinella succinogenes DSM 1740	ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes DSM 1740] emb CAE09984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes]			3.6.1.-
6877, 6878	34557269	64	2.00E-65	Wollinella succinogenes DSM 1740	ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes DSM 1740] emb CAE09984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes]			3.6.1.-
6881, 6882	48855504	58	8.00E-46	Cytophaga hutchinsonii	COG0045: Succinyl-CoA synthetase, beta subunit [Cytophaga hutchinsonii]			6.2.1.5
6883, 6884	34558415	47	1.00E-50	Wollinella succinogenes DSM 1740	PUTATIVE HYDROLASE [Wollinella succinogenes DSM 1740] emb CAE1130.1 PUTATIVE HYDROLASE [Wollinella succinogenes]			3.1.3.18
6885, 6886	34557246	43	2.00E-35	Wollinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes]			
6887, 6888	34557873	48	3.00E-48	Wollinella succinogenes DSM 1740	hypothetical protein WS1545 [Wollinella succinogenes DSM 1740] emb CAE10588.1 conserved hypothetical protein [Wollinella succinogenes]			
6889, 6890	558266	62	1.00E-67	Wollinella succinogenes	orf [Wollinella succinogenes] pir S50154 hypothetical protein 2 - Wollinella succinogenes			
689, 690	48855088	60	2.00E-73	Cytophaga hutchinsonii	COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Cytophaga hutchinsonii]			1.6.6.4
6891, 6892	34557291	46	5.00E-22	Wollinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10006.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes]			2.7.3.-
6895, 6896	558266	55	2.00E-43	Wollinella succinogenes	orf [Wollinella succinogenes] pir S50154 hypothetical protein 2 - Wollinella succinogenes			
6897, 6898	558266	61	3.00E-71	Wollinella succinogenes	orf [Wollinella succinogenes] pir S50154 hypothetical protein 2 - Wollinella succinogenes			
69, 70	48783402	23	7.00E-08	Burkholderia fungorum LB400	COG0396: ABC-type transport system involved in Fe-S cluster assembly, ATPase component [Burkholderia fungorum LB400]			
6903, 6904	57241681	71	2.00E-88	Campylobacter lari RM2100	DNA gyrase, B subunit [Campylobacter lari RM2100] gb EAL54351.1 DNA gyrase, B subunit [Campylobacter lari RM2100]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 1/6	85 2.00E-28	5.99.1.3
6905, 6906	34556843	39	6.00E-35	Wollinella succinogenes DSM 1740	hypothetical protein WS0414 [Wollinella succinogenes DSM 1740] emb CAE09558.1 conserved hypothetical protein [Wollinella succinogenes]			2.7.3.-

6907, 6908	34558149	31	1.00E-17	1740	Wolinella succinogenes DSM	SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes DSM 1740] emb[CAE10864.1]			
6909, 6910	57167731	62	1.00E-29	RM2228	Campylobacter coli	SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes] conserved hypothetical protein TIGR00044 [Campylobacter coli RM2228] gb[EA157517.1] conserved hypothetical protein TIGR00044 [Campylobacter coli RM2228]			
6911, 6912	34556508	48	4.00E-27	1740	Wolinella succinogenes DSM	PUTATIVE UDP-GLUCOSE 6-DEHYDROGENASE [Wolinella succinogenes DSM 1740] emb[CAE09223.1] PUTATIVE UDP-GLUCOSE 6- DEHYDROGENASE [Wolinella succinogenes]	1.1.1.-		
6913, 6914	23111511	37	1.00E-14	hafnense DCB-2	Desulfotobacterium	COG0494: NTP pyrophosphohydrolases including oxidative damage repair enzymes [Desulfotobacterium hafnense DCB-2]	3.6.1.-		
6915, 6916	4972799	63	3.00E-29	fennelliae	Helicobacter	DNA-directed RNA polymerase beta and beta' subunits [Helicobacter fennelliae]	2.7.7.6		
6917, 6918	34556481	29	4.00E-44	1740	Wolinella succinogenes DSM	hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb[CAE09196.1] conserved hypothetical protein [Wolinella succinogenes]	2.7.3.-		
6923, 6924	45523345	39	1.00E-12	watsonii WH 8501	Crocospaera	COG1253: Hemolysins and related proteins containing CBS domains [Crocospaera watsonii WH 8501]			
6925, 6926	34557967	45	8.00E-25	1740	Wolinella succinogenes DSM	hypothetical protein WS1651 [Wolinella succinogenes DSM 1740] emb[CAE10682.1] conserved hypothetical protein [Wolinella succinogenes]			
6927, 6928	34558795	25	3.00E-11	6C6	Alvinella pompejana epibiont	TonB-dependent receptor [Alvinella pompejana epibiont 6C6]			
6929, 6930	45523887	46	1.00E-66	watsonii WH 8501	Crocospaera	COG5433: Transposase [Crocospaera watsonii WH 8501]			
693, 694	45187901	29	6.00E-13	syningae B728a	Pseudomonas syningae pv.	COG1943: Transposase and inactivated derivatives [Pseudomonas syringae pv. syringae B728a] ref[ZP_00205512.1] COG1943: Transposase and inactivated derivatives [Pseudomonas syringae pv. syringae B728a]			
6931, 6932	48845760	34	2.00E-09	15	Geobacter metallireducens GS	COG2234: Predicted aminopeptidases [Geobacter metallireducens GS-15]			
6945, 6946	53692806	34	1.00E-16	somnus 129PT	Haemophilus somnus 129PT	hypothetical protein Hsom02000321 [Haemophilus somnus 129PT]			
6947, 6948	21228303	22	6.00E-12	mazei Go1	Methanosarcina	hypothetical protein MM2201 [Methanosarcina mazei Go1] gb[AAM31897.1] hypothetical protein [Methanosarcina mazei Go1]			

6949, 6950	53691562	41	2.00E-55	Desulfovibrio desulfuricans G20	COG3437: Response regulator containing a CheY-like receiver domain and an HD-GYP domain [Desulfovibrio desulfuricans G20]				
695, 696	21674062	52	1.00E-73	Chlorobium tepidum TLS	preprotein translocase SecA subunit [Chlorobium tepidum TLS] gb AAM72469.1 preprotein translocase SecA subunit [Chlorobium tepidum TLS]				
6951, 6952	53711371	40	8.00E-26	Bacteroides fragilis YCH46	putative zinc ABC transporter zinc-binding protein [Bacteroides fragilis YCH46] db BAD46829.1 putative zinc ABC transporter zinc-binding protein [Bacteroides fragilis YCH46]				
6953, 6954	57168109	37	1.00E-21	Campylobacter coli RM2228	signal-transducing protein, histidine kinase, putative [Campylobacter coli RM2228] gb EAL57152.1 signal-transducing protein, histidine kinase, putative [Campylobacter coli RM2228]				2.7.3.-
6955, 6956	16330194	51	5.00E-07	Synechocystis sp. PCC 6803	carboxynorspermidine decarboxylase [Synechocystis sp. PCC 6803] db BAA17602.1 carboxynorspermidine decarboxylase [Synechocystis sp. PCC 6803] pir S77268 carboxynorspermidine decarboxylase - Synechocystis sp. (strain PCC 6803)				4.1.1.-
6957, 6958	57237871	30	5.00E-13	Campylobacter jejuni RM1221	hypothetical protein CJE1127 [Campylobacter jejuni RM1221] gb AAW35454.1 hypothetical protein CJE1127 [Campylobacter jejuni RM1221]				
6959, 6960	48630999	31	2.00E-17	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]				2.7.3.-
6961, 6962	34558379	34	2.00E-08	Wolinella succinogenes DSM 1740	DNA POLYMERASE III SUBUNITS GAMMA AND TAU [Wolinella succinogenes DSM 1740] emb CAE11094.1 DNA POLYMERASE III SUBUNITS GAMMA AND TAU [Wolinella succinogenes]				
6967, 6968	54302166	33	2.00E-32	Photobacterium profundum SS9	hypothetical protein PBPRB0486 [Photobacterium profundum SS9] emb CAG22359.1 hypothetical protein [Photobacterium profundum]				
6969, 6970	6967929	63	6.00E-88	Campylobacter jejuni subsp. jejuni NCTC 11168	hypothetical protein Cj0458c [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281645.1 hypothetical protein Cj0458c [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81390 hypothetical protein Cj0458c [imported] - Campylobacter jejuni (strain NCTC 11168)				1.8.-
697, 698	48854227	50	1.00E-11	Cytophaga hutchinsonii	COG2908: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]				
6971, 6972	57240857	61	1.00E-62	Campylobacter lari RM2100	tRNA-(6)A37 thiotransferase enzyme MiaB [Campylobacter lari RM2100] gb EAL55250.1 tRNA-(6)A37 thiotransferase enzyme MiaB [Campylobacter lari RM2100]				1.8.-
6973, 6974	37520502	24	2.00E-10	Gloeobacter violaceus PCC 7421	potassium channel protein [Gloeobacter violaceus PCC 7421] db BAC88874.1 potassium channel protein [Gloeobacter violaceus PCC 7421]				
6975, 6976	48863979	32	2.00E-36	Microbulbifer degradans 2-40	COG1033: Predicted exporters of the RND superfamily [Microbulbifer degradans 2-40]				

6977, 6978	34556927	60	3.00E-97	Wolonia succinogenes DSM 1740	PUTATIVE GTP-BINDING PROTEIN [Wolonia succinogenes DSM 1740] emb CAE09642.1 PUTATIVE GTP-BINDING PROTEIN [Wolonia succinogenes]				
6979, 6980	23015878	54	5.00E-78	Magnetospirillum magnetotacticum MS-1	COG2703: Hemerythrin [Magnetospirillum magnetotacticum MS-1]				
6981, 6982	52007207	47	7.00E-68	Thiobacillus denitrificans ATCC 25259	COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Thiobacillus denitrificans ATCC 25259]				3.1.21.3
6983, 6984	48839711	46	9.00E-25	Methanosarcina barkeri str. fusaro	COG0732: Restriction endonuclease S subunits [Methanosarcina barkeri str. fusaro]				3.1.21.3
6985, 6986	16272498	44	3.00E-16	Haemophilus Influenzae Rd KW20	hypothetical protein HI0554 [Haemophilus Influenzae Rd KW20] gb AAC22217.1 H. Influenzae predicted coding region HI0554 [Haemophilus influenzae Rd KW20] pir [E64009 hypothetical protein HI0554 - Haemophilus influenzae (strain Rd KW20) sp P44014 Y554_HAEIN Hypothetical protein HI0554]				
6987, 6988	48860427	49	3.00E-63	Clostridium thermocellum ATCC 27405	COG1052: Lactate dehydrogenase and related dehydrogenases [Clostridium thermocellum ATCC 27405]				1.1.1.95
6989, 6990	34558097	46	7.00E-51	Wolonia succinogenes DSM 1740	MULTIDRUG-EFFLUX TRANSPORTER [Wolonia succinogenes DSM 1740] emb CAE10812.1 MULTIDRUG-EFFLUX TRANSPORTER [Wolonia succinogenes]				
699, 700	48854228	54	1.00E-42	Cytophaga hutchinsonii	COG1819: Glycosyl transferases, related to UDP-glucuronosyltransferase [Cytophaga hutchinsonii]				
6991, 6992	53712708	35	3.00E-25	Bacteroides fragilis YCH46	hypothetical protein BF1415 [Bacteroides fragilis YCH46] db BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
6995, 6996	48864065	45	1.00E-30	Microbulbifer degradans 2-40	COG0328: Ribonuclease HI [Microbulbifer degradans 2-40]				
6997, 6998	48864065	43	4.00E-12	Microbulbifer degradans 2-40	COG0328: Ribonuclease HI [Microbulbifer degradans 2-40]				
6999, 7000	49237161	53	7.00E-38	Moorella thermoacetica ATCC 39073	COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Moorella thermoacetica ATCC 39073]				1.2.1.2
7003, 7004	23130700	32	2.00E-25	Nostoc punctiforme PCC 73102	COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Nostoc punctiforme PCC 73102]				1.1.1.10 0
7005, 7006	15612820	58	2.00E-58	Bacillus halodurans C-125	urease accessory protein [Bacillus halodurans C-125] db BAB03976.1 urease accessory protein [Bacillus halodurans C-125] pir [A83682 urease accessory protein ureG [imported] - Bacillus halodurans (strain C-125)]				

7009, 7010	42522153	26	8.00E-07	Bdellovibrio bacteriovorus HD100	hypothetical protein Bd0554 [Bdellovibrio bacteriovorus HD100] emb CAE78526.1 conserved hypothetical protein [Bdellovibrio bacteriovorus HD100]			
7011, 7012	32262806	40	3.00E-53	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860786.1 hypothetical protein HH1255 [Helicobacter hepaticus ATCC 51449]			
7015, 7016	34105120	22	1.00E-09	Chromobacterium violaceum ATCC 12472	probable type II secretion system protein [Chromobacterium violaceum ATCC 12472] ref NP_903484.1 probable type II secretion system protein [Chromobacterium violaceum ATCC 12472]			
7017, 7018	20807566	33	8.00E-31	Thermoanaerobacter tengcongensis MB4	Diguanylate cyclase/phosphodiesterase domain 1 (GGDEF) [Thermoanaerobacter tengcongensis MB4] gb AAM24341.1 Diguanylate cyclase/phosphodiesterase domain 1 (GGDEF) [Thermoanaerobacter tengcongensis MB4]			2.7.3.-
7019, 7020	51245892	25	1.00E-06	Desulfotalea psychrophila LSV54	related to integrase [Desulfotalea psychrophila LSV54] emb CAG36769.1 related to integrase [Desulfotalea psychrophila LSV54]			
7021, 7022	48864587	46	4.00E-21	Microbulbifer degradans 2-40	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Microbulbifer degradans 2-40]			
7023, 7024	48864587	31	2.00E-18	Microbulbifer degradans 2-40	COG0664: cAMP-binding proteins - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinases [Microbulbifer degradans 2-40]			
7027, 7028	34558792	34	5.00E-26	Alvinella pompejana epibiont 6C6	conserved hypothetical protein [Alvinella pompejana epibiont 6C6]			
7035, 7036	48862944	37	3.00E-58	Microbulbifer degradans 2-40	COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Microbulbifer degradans 2-40]			3.4.21.-
7039, 7040	23024040	38	8.00E-48	Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293	COG0442: Poly(I)-RNA synthetase [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]			6.1.1.15
7041, 7042	AAW90018	25	5.00E-12		Desc:Expressed antigen for cluster 43. Org:Helicobacter pylori			3.2.1.-
7045, 7046	4049717	24	2.00E-07	Melanoplus sanguinipes entomopoxvirus	ORF MSV156 hypothetical protein [Melanoplus sanguinipes entomopoxvirus] pir T28317 ORF MSV156 hypothetical protein - Melanoplus sanguinipes entomopoxvirus ref NP_048227.1 ORF MSV156 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]			

7049, 7050	34396413	69	3.00E-66	Porphyromonas gingivalis W83	conserved hypothetical protein [Porphyromonas gingivalis W83] ref NP_904581.1 hypothetical protein PG0257 [Porphyromonas gingivalis W83]			
705, 706	48856969	33	6.00E-22	Cytophaga hutchinsonii	COG1792: Cell shape-determining protein [Cytophaga hutchinsonii]			
7051, 7052	15606924	45	2.00E-20	Aquifex aeolicus VF5	dolichol-phosphate mannosyltransferase [Aquifex aeolicus VF5] gb AAC07699.1 dolichol-phosphate mannosyltransferase [Aquifex aeolicus VF5] pir G70463 dolichol-phosphate mannosyltransferase - Aquifex aeolicus			2.4.1.83
7053, 7054	53685350	25	5.00E-22	Desulfotobacterium hafniense DCB-2	COG0535: Predicted Fe-S oxidoreductases [Desulfotobacterium hafniense DCB-2]			
7055, 7056	13488172	27	2.00E-12	Mesorhizobium loti MAFF303099	hypothetical protein ml9374 [Mesorhizobium loti MAFF303099] db BAB54981.1 ml9374 [Mesorhizobium loti MAFF303099]			
7057, 7058	57505523	35	1.00E-18	Campylobacter upsallensis RM3195	conserved hypothetical protein [Campylobacter upsallensis RM3195] gb EAL52857.1 conserved hypothetical protein [Campylobacter upsallensis RM3195]			
7059, 7060	34557616	35	2.00E-40	Wolinella succinogenes DSM 1740	HELICASE [Wolinella succinogenes DSM 1740] emb CAE10331.1 HELICASE [Wolinella succinogenes]			
7061, 7062	23126372	37	2.00E-13	Nostoc punctiforme PCC 73102	COG1943: Transposase and inactivated derivatives [Nostoc punctiforme PCC 73102]			
7063, 7064	32262499	49	3.00E-13	Helicobacter hepaticus ATCC 51449	hypothetical protein HH0949 [Helicobacter hepaticus ATCC 51449] ref NP_860480.1 hypothetical protein HH0949 [Helicobacter hepaticus ATCC 51449]			
7069, 7070	57505360	73	1.00E-122	Campylobacter upsallensis RM3195	ribonucleoside-diphosphate reductase, alpha subunit [Campylobacter upsallensis RM3195] gb EAL53281.1 ribonucleoside-diphosphate reductase, alpha subunit [Campylobacter upsallensis RM3195]			1.17.4.1
707, 708	34397903	51	2.00E-47	Porphyromonas gingivalis W83	excinuclease ABC, C subunit [Porphyromonas gingivalis W83] ref NP_906065.1 excinuclease ABC, C subunit [Porphyromonas gingivalis W83]			2.7.7.7
7071, 7072	57241418	33	9.00E-17	Campylobacter lari RM2100	Protein of unknown function (DUF452) superfamily [Campylobacter lari RM2100] gb EAL54530.1 Protein of unknown function (DUF452) superfamily [Campylobacter lari RM2100]			
7073, 7074	21672890	36	5.00E-18	Chlorobium tepidum TLS	biotin synthesis protein, putative [Chlorobium tepidum TLS] gb AAM71297.1 biotin synthesis protein, putative [Chlorobium tepidum TLS]			
7075, 7076	21672890	29	4.00E-24	Chlorobium tepidum TLS	biotin synthesis protein, putative [Chlorobium tepidum TLS] gb AAM71297.1 biotin synthesis protein, putative [Chlorobium tepidum TLS]			

7077,	52144430	26	1.00E-23	Bacillus cereus ZK	hypothetical protein BCZK0794 [Bacillus cereus ZK] gb AAU19449.1]			
7078				Bacillus cereus ZK	conserved hypothetical protein [Bacillus cereus ZK]			
7079,				Campylobacter coli	chemotaxis regulatory protein Cj1118c [Campylobacter coli RM2228]			
7080	57168004	38	7.00E-14	RM2228	gb EAL57047.1] chemotaxis regulatory protein Cj1118c [Campylobacter coli RM2228]			2.7.3.-
7081,				Wolfinella	PUTATIVE TRANSPOSASE [Wolfinella succinogenes DSM 1740]			
7082	34557717	74	3.00E-50	succinogenes DSM 1740	emb CAE10432.1] PUTATIVE TRANSPOSASE [Wolfinella succinogenes]			
7083,				Cytophaga	COG1512: Beta-propeller domains of methanol dehydrogenase type			
7084	48854336	37	6.00E-20	hutchinsonii	[Cytophaga hutchinsonii]			
7085,				Geobacter				
7086	39998549	26	3.00E-13	sulfurreducens PCA	glycosyl transferase, group 2 family protein [Geobacter sulfurreducens PCA]			
7087,				Wolfinella	DNA POLYMERASE III EPSILON SUBUNIT DNAQ [Wolfinella succinogenes DSM 1740] emb CAE09379.1] DNA POLYMERASE III EPSILON SUBUNIT DNAQ [Wolfinella succinogenes]			2.7.7.7
7088	34556664	46	1.00E-42	succinogenes DSM 1740	probable conjugal transfer protein TrbE [Desulfotalea psychrophila LSV54]			
7089,				Desulfotalea	emb CAG37878.1] probable conjugal transfer protein TrbE [Desulfotalea psychrophila LSV54]			
7090	51246985	44	7.00E-53	psychrophila LSV54	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			2.7.3.-
7093,	48831001	26	2.00E-26	Magnetococcus sp. MC-1	hypothetical protein [Klebsiella pneumoniae]			
7095,	7328117	26	5.00E-12	Klebsiella pneumoniae				
7096				Wolfinella	DNA PRIMASE PROTEIN [Wolfinella succinogenes DSM 1740]			2.7.7.-
7099,	34558196	33	2.00E-28	succinogenes DSM 1740	emb CAE10911.1] DNA PRIMASE PROTEIN [Wolfinella succinogenes]			
7100				Bacteroides	putative ABC transporter permease [Bacteroides thetaiotaomicron VPI-5482]			
71, 72	29346875	28	2.00E-16	thetaitaomicron VPI-5482	gb AAO76572.1] putative ABC transporter permease [Bacteroides thetaiotaomicron VPI-5482]			
7101,				Campylobacter	tRNA pseudouridine synthase B [Campylobacter jejuni RM1221]			4.2.1.70
7102	57237984	53	2.00E-47	jejun RM1221	gb AAW35567.1] tRNA pseudouridine synthase B [Campylobacter jejuni RM1221]			
7103,				Wolfinella	ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolfinella succinogenes DSM 1740] emb CAE09984.1] ATP-DEPENDENT DNA HELICASE EC 3.6.1.			3.6.1.-
7104	34557269	60	4.00E-93	succinogenes DSM 1740	[Wolfinella succinogenes]			
7105,				Helicobacter	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449]			2.6.1.17
7106	32261920	57	5.00E-49	hepaticus ATCC 51449	ref NP_859903.1] hypothetical protein HH0372 [Helicobacter hepaticus ATCC 51449]			
7107,	48853786	50	5.00E-78	Cytophaga hutchinsonii	COG0859: ADP-heptose-LPS heptosyltransferase [Cytophaga hutchinsonii]			

7109, 7110	32469872	29	2.00E-14	Campylobacter jejuni	hypothetical protein [Campylobacter jejuni] gb AAN46942.1 unknown [Campylobacter jejuni]			
7111, 7112	54029077	62	6.00E-41	Polaromonas sp. JS666	COG1089: GDP-D-mannose dehydratase [Polaromonas sp. JS666] Archaea bacterial proteins of unknown function family [Campylobacter lari RM2100] gb EAL54764.1 Archaea bacterial proteins of unknown function family [Campylobacter lari RM2100]		4.2.1.47	
7113, 7114	57241068	39	3.00E-15	Campylobacter lari RM2100	Desci-H. pylori ORF 06gp71906_25504187_f3_112 cytoplasmic protein.			
7115, 7116	AAW5565 5	60	1.00E-60		Org.Helicobacter pylori		1.8.-.-	
7117, 7118	21674237	43	2.00E-19	Chlorobium tepidum TLS	glycosyl transferase [Chlorobium tepidum TLS] gb AAM72644.1 glycosyl transferase [Chlorobium tepidum TLS]			
7119, 7120	52853852	37	2.00E-36	Psychrobacter sp. 273-4	COG0442: Prolyl-tRNA synthetase [Psychrobacter sp. 273-4]			
7121, 7122	32477471	28	5.00E-17	Rhodopirellula baltica SH 1	peroxiredoxin [Rhodopirellula baltica SH 1] emb CAD77542.1 peroxiredoxin [Pirellula sp.]			
7123, 7124	34397620	63	3.00E-76	Porphyromonas gingivalis W83	ABC transporter, ATP-binding protein [Porphyromonas gingivalis W83] ref NP_905783.1 ABC transporter, ATP-binding protein [Porphyromonas gingivalis W83]		1.8.-.-	
7127, 7128	34556661	42	2.00E-27	Wolinella succinogenes DSM 1740	PUTATIVE FRUCTOSE-1,6-BISPHOSPHATASE [Wolinella succinogenes DSM 1740] emb CAE09376.1 PUTATIVE FRUCTOSE-1,6- BISPHOSPHATASE [Wolinella succinogenes]		3.1.3.11	
7129, 7130	48856007	35	8.00E-11	Cytophaga hutchinsonii	COG0308: Aminopeptidase N [Cytophaga hutchinsonii]			
7131, 7132	39995395	31	4.00E-07	Geobacter sulfurreducens PCA	PBS lyase HEAT-like repeat protein [Geobacter sulfurreducens PCA] gb AAR33619.1 PBS lyase HEAT-like repeat protein [Geobacter sulfurreducens PCA]			
7133, 7134	51894433	46	5.00E-73	Symbiobacterium thermophilum IAM 14863	sigma-54-dependent transcriptional regulator [Symbiobacterium thermophilum IAM 14863] dbj BAD42280.1 sigma-54-dependent transcriptional regulator [Symbiobacterium thermophilum IAM 14863]			
7137, 7138	15678496	34	6.00E-22	Methanothermobac ter thermautotrophicus str. Delta H	sensory transduction histidine kinase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB84974.1 sensory transduction histidine kinase [Methanothermobacter thermotrophicus str. Delta H] pir C69161 sensory transduction histidine kinase - Methanobacterium thermautotrophicum (strain Delta H)		2.7.3.-	
7139, 7140	54302013	43	3.00E-29	Photobacterium profundum SS9	hypothetical protein PBPRB0333 [Photobacterium profundum SS9] emb CAG22206.1 hypothetical protein [Photobacterium profundum]			
7141, 7142	56707454	41	6.00E-26	Francisella tularensis subsp. tularensis Schu 4	hypothetical protein FTT0301 [Francisella tularensis subsp. tularensis Schu 4] gb AAV29706.1 NT02FT0891 [synthetic construct] emb CAG44934.1 hypothetical protein [Francisella tularensis subsp. tularensis]			

7143, 7144	56707453	36	1.00E-07	Francisella tularensis subsp. tularensis Schu 4	hypothetical protein FTT0300 [Francisella tularensis subsp. tularensis Schu 4] gb AAV29688.1 NT02FT0892 [synthetic construct] emb CAG44933.1 hypothetical protein [Francisella tularensis subsp. tularensis]				
7145, 7146	48855541	72	3.00E-50	Cytophaga hutchinsonii	COG1875: Predicted ATPase related to phosphate starvation-inducible protein PhoH [Cytophaga hutchinsonii]	Parachlamydia- related symbiont UWE25, complete genome	85	7.00E-08	
7147, 7148	29346304	56	1.00E-107	Bacteroides thetaiotaomicron VPI-5482	DNA ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76001.1 DNA ligase [Bacteroides thetaiotaomicron VPI-5482]			6.5.1.2	
7149, 7150	29346304	61	1.00E-77	Bacteroides thetaiotaomicron VPI-5482	DNA ligase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76001.1 DNA ligase [Bacteroides thetaiotaomicron VPI-5482]			6.5.1.2	
7151, 7152	52421238	53	2.00E-25	Bacteroides fragilis YCH46	hypothetical protein BFP0024 [Bacteroides fragilis YCH46] db BAD51351.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
7153, 7154	20091731	71	1.00E-96	Methanosarcina acetivorans C2A	2-oxoisovalerate ferredoxin oxidoreductase, beta subunit [Methanosarcina acetivorans C2A] gb AAM06286.1 2-oxoisovalerate ferredoxin oxidoreductase, beta subunit [Methanosarcina acetivorans str. C2A]			1.2.7.-	
7155, 7156	24372513	28	6.00E-16	Shewanella oneidensis MR-1	acetyltransferase, GNAT family [Shewanella oneidensis MR-1] gb AAN54000.1 acetyltransferase, GNAT family [Shewanella oneidensis MR- 1]				
7157, 7158	15791002	37	1.00E-11	Halobacterium salinarum NRC-1	hypothetical protein VNG2170H [Halobacterium salinarum NRC-1] gb AAG20306.1 Vng2170h [Halobacterium sp. NRC-1] pir F84367 hypothetical protein Vng2170h [imported] - Halobacterium sp. NRC-1				
7161, 7162	34557666	30	1.00E-39	Wolinella succinogenes DSM 1740	hypothetical protein WS1305 [Wolinella succinogenes DSM 1740] emb CAE10381.1 hypothetical protein [Wolinella succinogenes]				
7163, 7164	21241124	40	1.00E-26	Xanthomonas axonopodis pv. citri str. 306	hypothetical protein XAC0350 [Xanthomonas axonopodis pv. citri str. 306] gb AAM35242.1 conserved hypothetical protein [Xanthomonas axonopodis pv. citri str. 306]				
7165, 7166	29346750	54	2.00E-67	Bacteroides thetaiotaomicron VPI-5482	putative lipopolysaccharide biosynthesis glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76447.1 putative lipopolysaccharide biosynthesis glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.4.1.-	
7169, 7170	34558443	25	3.00E-07	Wolinella succinogenes DSM 1740	hypothetical protein WS2166 [Wolinella succinogenes DSM 1740] emb CAE11158.1 hypothetical protein [Wolinella succinogenes]				

7171,	34558443	36	2.00E-13	Wolinella succinogenes DSM 1740	hypothetical protein WS2166 [Wolinella succinogenes DSM 1740] emb[CAE11158.1] hypothetical protein [Wolinella succinogenes]				
7172									2.4.1.18
7173,	48855019	56	2.00E-66	Cytophaga hutchinsonii	COG0763: Lipid A disaccharide synthetase [Cytophaga hutchinsonii]				2
7174									
7175,									
7176	24373599	34	4.00E-09	Shewanella oneidensis MR-1	hypothetical protein SO2039 [Shewanella oneidensis MR-1] gb AAN55086.1 conserved domain protein [Shewanella oneidensis MR-1]				
7177,									
7178	54307149	52	6.00E-89	Bacteroides uniformis	hypothetical protein NBU1_09 [Bacteroides uniformis] gb AAF74441.1 unknown [Bacteroides uniformis]				
7179,									
7180	57241290	60	3.00E-31	Campylobacter lari RM2100	Uncharacterized BCR, YceG family COG1559 [Campylobacter lari RM2100] gb EAL54986.1 Uncharacterized BCR, YceG family COG1559 [Campylobacter lari RM2100]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6	97	2.00E-11	4.1.1.17
7185,	23474222	58	8.00E-53	Desulfovibrio desulfuricans G20	COG2998: ABC-type tungstate transport system, permease component [Desulfovibrio desulfuricans G20]				
7186									
7187,									
7188	34558490	65	1.00E-103	Wolinella succinogenes DSM 1740	GLUTAMYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb[CAE11205.1] GLUTAMYL-TRNA SYNTHETASE [Wolinella succinogenes] sp Q7M7L9 SYE_WOLSU Glutamyl-tRNA synthetase (Glutamate-tRNA ligase) (GluRS)	Helicobacter pylori, strain J99 section 38 of 132 of the complete genome	83	7.00E-07	6.1.1.17
7189,									
7190	48855372	32	3.00E-13	Cytophaga hutchinsonii	COG2931: RTX toxins and related Ca2+-binding proteins [Cytophaga hutchinsonii]				
719,									
720	48862211	47	5.00E-33	Microbulbifer degradans 2-40	COG2989: Uncharacterized protein conserved in bacteria [Microbulbifer degradans 2-40]				
7191,									
7192	48859660	38	2.00E-47	Clostridium thermocellum ATCC 27405	COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Clostridium thermocellum ATCC 27405]				3.4.21.-
7193,									
7194	19704426	29	1.00E-23	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Sigma factor sigB regulation protein rsbU [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95287.1 Sigma factor sigB regulation protein rsbU [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]				3.1.3.16
7197,									
7198	48831001	40	2.00E-41	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]				2.7.3.-
7199,									
7200	34557246	64	1.00E-35	Wolinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]				2.7.3.-
7203,									
7204	34556562	58	6.00E-53	Wolinella succinogenes DSM 1740	PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes DSM 1740] emb CAE09277.1 PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes]				

7209, 7210	51246604	66	6.00E-66	Desulfotalea psychrophila LSV54	probable arginyl-tRNA synthetase [Desulfotalea psychrophila LSV54] emb CAG37481.1 probable arginyl-tRNA synthetase [Desulfotalea psychrophila LSV54]			6.1.1.19
721, 722	53758638	37	2.00E-32	Methylococcus capsulatus str. Bath	conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_113480.1 hypothetical protein MCA1003 [Methylococcus capsulatus str. Bath]			
7211, 7212	57237610	57	2.00E-27	Campylobacter jejuni RM1221	histidyl-tRNA synthetase [Campylobacter jejuni RM1221] gb AAW35193.1 histidyl-tRNA synthetase [Campylobacter jejuni RM1221] emb CAB73030.1			
7213, 7214	53714483	40	3.00E-18	Bacteroides fragilis YCH46	histidyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281926.1 histidyl-tRNA synthetase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81347 histidine-tRNA ligase (EC 6.1.1.21) C 0765c [Imported] - Campylobacter jejuni (strain NCTC 11168) sp Q9PPF4 SYH_CAM JE Histidyl-tRNA synthetase (Histidine-tRNA ligase) (HISRS)			6.1.1.21
7215, 7216	29345593	36	3.00E-41	Bacteroides thetaiotaomicron VPI-5482	transglycosylase [Bacteroides fragilis YCH46] db BAD49941.1 transglycosylase [Bacteroides fragilis YCH46]			
7217, 7218	48891870	50	1.00E-56	Trichodesmium erythraeum IMS101	transglycosylase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75290.1 transglycosylase [Bacteroides thetaiotaomicron VPI-5482]			2.1.1.-
7219, 7220	49477542	29	7.00E-25	Bacillus thuringiensis serovar konkukian str. 97-27	COG0566: rRNA methylases [Trichodesmium erythraeum IMS101] UDP-N-acetylmuramoyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacillus thuringiensis serovar konkukian str. 97-27] gb AAAT59744.1 UDP-N-acetylmuramoyl-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D-alanyl ligase [Bacillus thuringiensis serovar konkukian str. 97-27]			6.3.2.15
7221, 7222	34558309	50	5.00E-36	Wolinella succinogenes DSM 1740	ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE11024.1 ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes]			1.8.-
7223, 7224	57240653	27	2.00E-17	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55046.1 conserved hypothetical protein [Campylobacter lari RM2100]			
7229, 7230	2313711	28	1.00E-07	Helicobacter pylori 26695	H. pylori predicted coding region HP0586 [Helicobacter pylori 26695] pir B64593 hypothetical protein HP0586 - Helicobacter pylori (strain 26695) ref NP_207381.1 hypothetical protein HP0586 [Helicobacter pylori 26695]			
723, 724	48855418	65	2.00E-84	Cytophaga hutchinsonii	COG0535: Predicted Fe-S oxidoreductases [Cytophaga hutchinsonii]			

7231, 7232	20094914	60	8.00E-14	Methanopyrus kandleri AV19	DNA-directed RNA polymerase, subunit N [Methanopyrus kandleri AV19] gb AAAM02691.1 DNA-directed RNA polymerase, subunit N [Methanopyrus kandleri AV19] sp Q8TVB4 RPON_METKA DNA-directed RNA polymerase subunit N	2.7.7.6
7233, 7234	34763018	32	5.00E-11	Fusobacterium nucleatum subsp. vincentii ATCC 49256	DNA TOPOLOGY MODULATION PROTEIN FLAR-RELATED PROTEIN [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24413.1 DNA TOPOLOGY MODULATION PROTEIN FLAR-RELATED PROTEIN [Fusobacterium nucleatum subsp. vincentii ATCC 49256]	
7235, 7236	9655841	46	2.00E-37	Vibrio cholerae O1 biovar eltor str. N16961	sensory box sensor histidine kinase/response regulator [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_230993.1 sensory box sensor histidine kinase/response regulator [Vibrio cholerae O1 biovar eltor str. N16961] pir H82211 sensory box sensor histidine kinase/response regulator VC1349 [imported] - Vibrio cholerae (strain N16961 serogroup O1)	2.7.3.-
7237, 7238	48833325	27	9.00E-26	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1] ispD/ispF bifunctional enzyme [Campylobacter jejuni RM1221]	2.7.3.-
7239, 7240	57238620	48	2.00E-26	Campylobacter jejuni RM1221	gb AAW36203.1 ispD/ispF bifunctional enzyme [Campylobacter jejuni RM1221]	2.7.7.60
7241, 7242	48856860	49	2.00E-29	Cytophaga hutchinsonii	COG0781: Transcription termination factor [Cytophaga hutchinsonii] probable methionyl-tRNA synthetase [Desulfotalea psychrophila LSV54] emb CAG35515.1 probable methionyl-tRNA synthetase [Desulfotalea psychrophila LSV54]	6.1.1.10
7243, 7244	51244638	61	9.00E-70	Desulfotalea psychrophila LSV54	hypothetical protein BF3086 [Bacteroides fragilis YCH46] db BAD49831.1 hypothetical protein [Bacteroides fragilis YCH46]	
7245, 7246	53714373	29	2.00E-21	Bacteroides fragilis YCH46	Small-conductance mechanosensitive channel [Idiomarina loihiensis L2TR] gb AAV82847.1 Small-conductance mechanosensitive channel [Idiomarina loihiensis L2TR]	
7249, 7250	56461115	48	2.00E-71	Idiomarina loihiensis L2TR	hypothetical protein BT0882 [Bacteroides thetaiotaomicron VPI-5482] gb AAO75989.1 conserved hypothetical protein [Bacteroides thetaitaomicron VPI-5482]	
7251, 7252	30721677	26	7.00E-07	Plasmodium falciparum	phosphoprotein 300 [Plasmodium falciparum]	
7253, 7254	47227859	29	1.00E-06	Tetraodon nigroviridis	unnamed protein product [Tetraodon nigroviridis]	
7255, 7256	34556947	41	4.00E-19	Wolinella succinogenes DSM 1740	hypothetical protein WS0526 [Wolinella succinogenes DSM 1740] emb CAE09662.1 hypothetical protein [Wolinella succinogenes]	

7257, 7258	34557269	58	1.00E-74	Wollinella succinogenes DSM 1740	ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes DSM 1740] emb CAE0984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes]			3.6.1.-
7259, 7260	34557268	62	2.00E-57	Wollinella succinogenes DSM 1740	TRANSCRIPTIONAL REGULATOR (LYSR FAMILY) [Wollinella succinogenes DSM 1740] emb CAE0983.1 TRANSCRIPTIONAL REGULATOR (LYSR FAMILY) [Wollinella succinogenes]			
7261, 7262	34556595	38	1.00E-35	Wollinella succinogenes DSM 1740	hypothetical protein WS0147 [Wollinella succinogenes DSM 1740] emb CAE09310.1 conserved hypothetical protein [Wollinella succinogenes]			
7263, 7264	34558202	40	6.00E-21	Wollinella succinogenes DSM 1740	LIPID A BIOSYNTHESIS ACYLTRANSFERASE [Wollinella succinogenes DSM 1740] emb CAE10917.1 LIPID A BIOSYNTHESIS ACYLTRANSFERASE [Wollinella succinogenes]			2.3.1.-
7267, 7268	52006955	25	4.00E-07	Thiobacillus denitrificans ATCC 25259	COG3660: Predicted nucleoside-diphosphate-sugar epimerase [Thiobacillus denitrificans ATCC 25259]			
7271, 7272	27365538	23	4.00E-14	Vibrio vulnificus CMCP6	hypothetical protein VV12211 [Vibrio vulnificus CMCP6] gb AAO10593.1 Conserved hypothetical protein [Vibrio vulnificus CMCP6]			
7273, 7274	34558170	46	1.00E-50	Wollinella succinogenes DSM 1740	RIBONUCLEASE [Wollinella succinogenes DSM 1740] emb CAE10885.1 RIBONUCLEASE [Wollinella succinogenes]			3.1.-.-
7275, 7276	57167878	32	5.00E-17	Campylobacter coli RM2228	conserved hypothetical protein [Campylobacter coli RM2228] gb EAL57664.1 conserved hypothetical protein [Campylobacter coli RM2228]			
7277, 7278	21242142	47	2.00E-27	Xanthomonas axonopodis pv. citri str. 306	ABC transporter ATP-binding protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM36260.1 ABC transporter ATP-binding protein [Xanthomonas axonopodis pv. citri str. 306]			
7283, 7284	20808914	22	2.00E-12	Thermoanaerobact er tengcongensis MB4	Transcription-repair coupling factor - superfamily II helicase [Thermoanaerobacter tengcongensis MB4] gb AAM25689.1 Transcription- repair coupling factor - superfamily II helicase [Thermoanaerobacter tengcongensis MB4]			
7285, 7286	34557966	56	1.00E-63	Wollinella succinogenes DSM 1740	ATP-DEPENDENT HELICASE [Wollinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wollinella succinogenes]			3.6.1.-
7287, 7288	48853613	33	3.00E-40	Cytophaga hutchinsonii	COG0037: Predicted ATPase of the PP-loop superfamily implicated in cell cycle control [Cytophaga hutchinsonii]			
7289, 7290	48833229	30	3.00E-30	Magnetococcus sp. MC-1	COG1226: Kef-type K+ transport systems, predicted NAD-binding component [Magnetococcus sp. MC-1]			
729, 730	48854473	29	4.00E-10	Cytophaga hutchinsonii	COG1648: Siroheme synthase (precorrin-2 oxidase/ferrochelatase domain) [Cytophaga hutchinsonii]			

7293, 7294	53713067	28	6.00E-19	Bacteroides fragilis YCH46	hypothetical protein BF1778 [Bacteroides fragilis YCH46] dbj BAD48525.1 hypothetical protein [Bacteroides fragilis YCH46]				
7295, 7296	14591697	46	6.00E-64	Pyrococcus horikoshii OT3	oligopeptide transport ATP-binding protein appF [Pyrococcus horikoshii OT3] dbj BAA31085.1 335aa long hypothetical oligopeptide transport ATP-binding protein appF [Pyrococcus horikoshii OT3] pir F71211 probable oligopeptide transport ATP-binding protein appF - Pyrococcus horikoshii				1.8.-.-
7297, 7298	34557268	49	3.00E-57	Wolinella succinogenes DSM 1740	TRANSCRIPTIONAL REGULATOR (LYSR FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09983.1 TRANSCRIPTIONAL REGULATOR (LYSR FAMILY) [Wolinella succinogenes]				
7299, 7300	34558285	55	3.00E-56	Wolinella succinogenes DSM 1740	PUTATIVE HEMOLYSIN [Wolinella succinogenes DSM 1740] emb CAE10980.1 PUTATIVE HEMOLYSIN [Wolinella succinogenes]	Wolinella succinogenes, complete genome; segment 6/7	87	1.00E-10	
73, 74	15644379	38	1.00E-09	Thermotoga maritima MSB8	hypothetical protein TM1631 [Thermotoga maritima MSB8] gb AAD36698.1 conserved hypothetical protein [Thermotoga maritima MSB8] pir G72229 conserved hypothetical protein - Thermotoga maritima (strain MSB8)				
7303, 7304	47568045	47	9.00E-21	Bacillus cereus G9241	glycogen synthase [Bacillus cereus G9241] gb EAL13693.1 glycogen synthase [Bacillus cereus G9241]				2.4.1.21
7307, 7308	57238299	50	1.00E-31	Campylobacter jejuni RM1221	hypothetical protein CJE0604 [Campylobacter jejuni RM1221] gb AAW35882.1 conserved hypothetical protein [Campylobacter jejuni RM1221] emb CAB75134.1 hypothetical protein Cj0496 [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281683.1 hypothetical protein Cj0496 [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81395 hypothetical protein Cj0496 [imported] - Campylobacter jejuni (strain NCTC 11168)				
7309, 7310	34558209	42	3.00E-48	Wolinella succinogenes DSM 1740	conserved hypothetical protein-SAM dependent methyltransferases [Wolinella succinogenes DSM 1740] emb CAE10924.1 conserved hypothetical protein-SAM dependent methyltransferases [Wolinella succinogenes]				2.1.1.52
731, 732	15613113	35	2.00E-37	Bacillus halodurans C-125	ABC transporter (ATP-binding protein) [Bacillus halodurans C-125] dbj BAB04269.1 ABC transporter (ATP-binding protein) [Bacillus halodurans C-125] pir F83718 ABC transporter (ATP-binding protein) BH0550 [imported] - Bacillus halodurans (strain C-125)				1.8.-.-
7311, 7312	57240846	58	2.00E-45	Campylobacter lari RM2100	UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate ligase [Campylobacter lari RM2100] gb EAL55039.1 UDP-N-acetylmuramoylalanyl- D-glutamyl-2, 6-diaminopimelate ligase [Campylobacter lari RM2100]				6.3.2.13

7313, 7314	34557905	50	Wolinella succinogenes DSM 1740	2.00E-69	50	PROLYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb[CAG10620.1] PROLYL-TRNA SYNTHETASE [Wolinella succinogenes]			6.1.1.15
7317, 7318	48858096	33	Clostridium thermocellum ATCC 27405	3.00E-37	33	COG0572: Uridine kinase [Clostridium thermocellum ATCC 27405]			2.7.1.48
7319, 7320	54308510	39	Photobacterium profundum SS9	3.00E-50	39	hypothetical protein PBPR1317 [Photobacterium profundum SS9] emb[CAG19728.1] hypothetical protein [Photobacterium profundum]			
7321, 7322	54308510	53	Photobacterium profundum SS9	5.00E-09	53	hypothetical protein PBPR1317 [Photobacterium profundum SS9] emb[CAG19728.1] hypothetical protein [Photobacterium profundum] DNA topoisomerase I [Thermosynechococcus elongatus BP-1] dbj[BAC09433.1] DNA topoisomerase I [Thermosynechococcus elongatus BP-1]			5.99.1.2
7323, 7324	22299424	34	Thermosynechococcus elongatus BP-1	4.00E-17	34	RESPONSE REGULATOR PROTEIN-CheY-like nd an HD-GYP domain [Wolinella succinogenes DSM 1740] emb[CAG10661.1] RESPONSE REGULATOR PROTEIN-CheY-like nd an HD-GYP domain [Wolinella succinogenes]			3.1.4.17
7327, 7328	34557946	41	Wolinella succinogenes DSM 1740	1.00E-42	41	hypothetical protein CT0328 [Chlorobium tepidum TLS] gb AAM71574.1 conserved hypothetical protein [Chlorobium tepidum TLS] polysaccharide biosynthesis protein [Shewanella oneidensis MR-1] gb AAN55507.1 polysaccharide biosynthesis protein [Shewanella oneidensis MR-1]			6.1.1.5
7329, 7330	21673167	40	Chlorobium tepidum TLS	4.00E-33	40	Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601]			3.1.3.16
733, 734	24374020	43	Shewanella oneidensis MR-1	1.00E-43	43	COG0507: ATP-dependent exoDNase (exonuclease V), alpha subunit - helicase superfamily I member [Desulfovibrio desulfuricans G20]			3.1.11.5
7331, 7332	24214122	35	Leptospira Interrogans serovar Lai str. 56601	5.00E-37	35	hypothetical protein [Deinococcus radiodurans] pir G75368 hypothetical protein - Deinococcus radiodurans (strain R1) ref NP_295399.1 hypothetical protein DR1676 [Deinococcus radiodurans R1]			
7333, 7334	53691714	53	Desulfovibrio desulfuricans G20	2.00E-51	53	S-adenosylmethionine:tRNA ribosyltransferase-isomerase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79078.1 S-adenosylmethionine:tRNA ribosyltransferase-isomerase [Bacteroides thetaiotaomicron VPI-5482]			5.---
7335, 7336	6459446	33	Deinococcus radiodurans	1.00E-18	33	COG0778: Nitroreductase [Nostoc punctiforme PCC 73102]			
7339, 7340	29349381	53	Bacteroides thetaiotaomicron VPI-5482	7.00E-75	53				
7343, 7344	23130537	36	Nostoc punctiforme PCC 73102	7.00E-24	36				

7349, 7350, 735, 736	34558196 40062985	57 50	4.00E-71 3.00E-39	Wolinella succinogenes DSM 1740 uncultured bacterium 443	DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes]	Wolinella succinogenes, complete genome; segment 6/7	91 5.00E-07	2.7.7.- 1.3.3.4
7353, 7354, 7355, 7356	40062985 54302734 41722784	50 31 55	3.00E-39 4.00E-30 1.00E-31	Photobacterium profundum SS9 Dechloromonas aromatica RCB Alvinella pompejana epibiont 7G3	phytoene dehydrogenase [uncultured bacterium 443] hypothetical dinitrification protein NorD [Photobacterium profundum SS9] emb CAG22927.1 hypothetical dinitrification protein NorD [Photobacterium profundum] COG4548: Nitric oxide reductase activation protein [Dechloromonas aromatica RCB]			1.7.99.7 1.7.99.7
7357, 7358	3455828	25	7.00E-08	Wolinella succinogenes DSM 1740	KIAA1005 protein [Alvinella pompejana epibiont 7G3] conserved hypothetical protein-Predicted amidohydrolase [Wolinella succinogenes DSM 1740] emb CAE10901.1 conserved hypothetical protein-Predicted amidohydrolase [Wolinella succinogenes]			
7359, 7360	34558186	52	3.00E-31	Wolinella succinogenes DSM 1740	HOMOSERINE O-ACETYLTRANSFERASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10903.1 HOMOSERINE O-ACETYLTRANSFERASE PROTEIN [Wolinella succinogenes]			2.3.1.31
7365, 7366	53714371	30	2.00E-32	Bacteroides fragilis YCH46 uncultured archaeon	putative ATPase involved in DNA repair [Bacteroides fragilis YCH46] dbj BAD49829.1 putative ATPase involved in DNA repair [Bacteroides fragilis YCH46]			
7369, 7370	52548475	36	1.00E-07	Wolinella succinogenes DSM 1740	prophage LambdaSa1 transcriptase/maturase family protein [uncultured archaeon GZfos14B8] PEROXIDE STRESS REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09880.1 PEROXIDE STRESS REGULATOR [Wolinella succinogenes]			
7371, 7372, 7373, 7374	34556965 48832225	45 63	1.00E-29 4.00E-61	Magnetococcus sp. MC-1	COG0840: Methyl-accepting chemotaxis protein [Magnetococcus sp. MC-1]			
7375, 7376	48854031	54	2.00E-77	Cytophaga hutchinsonii	COG0445: NAD/FAD-utilizing enzyme apparently involved in cell division [Cytophaga hutchinsonii]	Desc:Mycoplasma genitalium genome. Org:Mycoplasma genitalium	83 3.00E-12	
7377, 7378	45657719	26	9.00E-08	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	hypothetical protein LIC11856 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AAST0442.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			

7381, 7382	48858283	53	6.00E-63	Clostridium thermocellum ATCC 27405	COG2304: Uncharacterized protein containing a von Willebrand factor type A (vWA) domain [Clostridium thermocellum ATCC 27405]				
7383, 7384	23099115	37	1.00E-46	Oceanobacillus ihayensis HTE831	sulfur deprivation response regulator [Oceanobacillus ihayensis HTE831] dbj BAC13616.1 sulfur deprivation response regulator [Oceanobacillus ihayensis HTE831]				
7385, 7386	53715139	33	3.00E-43	Bacteroides fragilis YCH46	putative acetyltransferase [Bacteroides fragilis YCH46] dbj BAD50597.1				2.3.1.-
7387, 7388	48786589	50	2.00E-58	Burkholderia fungorum LB400	putative acetyltransferase [Bacteroides fragilis YCH46]				
739, 740	48855418	62	1.00E-101	Cytophaga hutchinsonii	COG2202: FOG: PAS/PAC domain [Burkholderia fungorum LB400]				
7391, 7392	57237984	42	1.00E-38	Campylobacter jejuni RM1221	COG0535: Predicted Fe-S oxidoreductases [Cytophaga hutchinsonii] tRNA pseudouridine synthase B [Campylobacter jejuni RM1221] gb AAW35567.1 tRNA pseudouridine synthase B [Campylobacter jejuni RM1221]				4.2.1.70
7393, 7394	34557273	37	2.00E-11	Wolinella succinogenes DSM 1740	hypothetical protein WS0881 [Wolinella succinogenes DSM 1740] emb CAE09988.1 hypothetical protein [Wolinella succinogenes]				2.7.1.14 8
7395, 7396	48845647	43	1.00E-46	Geobacter metallireducens GS 15	hypothetical protein Gmet02001892 [Geobacter metallireducens GS-15]				
7399, 7400	39995205	60	2.00E-46	Geobacter sulfurreducens PCA	DNA polymerase III, gamma and tau subunits [Geobacter sulfurreducens PCA] gb AAR33429.1 DNA polymerase III, gamma and tau subunits [Geobacter sulfurreducens PCA]				2.7.7.7
7401, 7402	34556460	51	2.00E-62	Wolinella succinogenes DSM 1740	DNA POLYMERASE III, BETA CHAIN [Wolinella succinogenes DSM 1740] emb CAE09175.1 DNA POLYMERASE III, BETA CHAIN [Wolinella succinogenes]				2.7.7.7
7403, 7404	23003425	53	1.00E-31	Lactobacillus gasseri	COG1207: N-acetylglucosamine-1-phosphate uridylyltransferase (contains nucleotidyltransferase and l-patch acetyltransferase domains) [Lactobacillus gasseri]				2.7.7.23
7407, 7408	45508536	39	3.00E-20	Anabaena variabilis ATCC 29413	COG0535: Predicted Fe-S oxidoreductases [Anabaena variabilis ATCC 29413] gb AAA93025.1 NifX2				
7409, 7410	23023289	34	1.00E-33	Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293	COG4928: Predicted P-loop ATPase [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]				

741, 742	53713222	34	4.00E-16	Bacteroides fragilis YCH46	polysialic acid transport protein [Bacteroides fragilis YCH46] dbj BAD48680.1 polysialic acid transport protein [Bacteroides fragilis YCH46]				
7413, 7414	17231532	28	3.00E-14	Nostoc sp. PCC 7120	hypothetical protein all4040 [Nostoc sp. PCC 7120] pir A12310 hypothetical protein all4040 [imported] - Nostoc sp. (strain PCC 7120) dbj BAB75739.1 all4040 [Nostoc sp. PCC 7120]				
7415, 7416	48856157	39	1.00E-46	Cytophaga hutchinsonii	COG0046: Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Cytophaga hutchinsonii]				
7417, 7418	56475703	44	2.00E-26	Azoarcus sp. Ebn1	putative transposase [Azoarcus sp. Ebn1] emb CA106391.1 putative transposase [Azoarcus sp. Ebn1]				
7419, 7420	56477204	62	8.00E-90	Azoarcus sp. Ebn1	2-oxoglutarate ferredoxin oxidoreductase beta subunit [Azoarcus sp. Ebn1] emb CA107892.1 2-oxoglutarate ferredoxin oxidoreductase beta subunit [Azoarcus sp. Ebn1]				1.2.7.3
7423, 7424	34556768	68	5.00E-95	Wolinella succinogenes DSM 1740	DIAMINOPIMELATE DECARBOXYLASE DAP DECARBOXYLASE [Wolinella succinogenes DSM 1740] emb CAE09483.1 DIAMINOPIMELATE DECARBOXYLASE DAP DECARBOXYLASE [Wolinella succinogenes]			83	1.00E-08 4.1.1.20
7425, 7426	34556736	27	6.00E-13	Wolinella succinogenes DSM 1740	hypothetical protein WS0300 [Wolinella succinogenes DSM 1740] emb CAE09451.1 hypothetical protein [Wolinella succinogenes]				
7427, 7428	34557003	48	3.00E-59	Wolinella succinogenes DSM 1740	PUTATIVE RIBOFLAVIN KINASE /FMN ADENYLYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09718.1 PUTATIVE RIBOFLAVIN KINASE /FMN ADENYLYLTRANSFERASE [Wolinella succinogenes]				2.7.1.26
7429, 7430	56420170	64	8.00E-57	Geobacillus kaustophilus HTA426	hypothetical protein GK1635 [Geobacillus kaustophilus HTA426] dbj BAD75920.1 hypothetical conserved protein [Geobacillus kaustophilus HTA426]				
743, 744	48854498	59	3.00E-68	Cytophaga hutchinsonii	hypothetical protein Chut02002697 [Cytophaga hutchinsonii]				
7431, 7432	34556550	22	9.00E-09	Wolinella succinogenes DSM 1740	hypothetical protein WS0098 [Wolinella succinogenes DSM 1740] emb CAE09265.1 hypothetical protein [Wolinella succinogenes]				
7433, 7434	57234107	32	8.00E-11	Dehalococcoides ethenogenes 195	hypothetical protein DET1110 [Dehalococcoides ethenogenes 195] gb AAW39612.1 conserved hypothetical protein [Dehalococcoides ethenogenes 195]				
7435, 7436	34557509	64	4.00E-44	Wolinella succinogenes DSM 1740	hypothetical protein WS1135 [Wolinella succinogenes DSM 1740] emb CAE10224.1 hypothetical protein [Wolinella succinogenes]	Wolinella succinogenes, complete genome; segment 4/7	##	6.00E-09	

7437, 7438	48853602	50	1.00E-63	Cytophaga hutchinsonii	COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii]	Oceanobacillus theysensis HTE831 genomic DNA, section 1/13	91	6.00E-07	
7439, 7440	48853602	57	9.00E-76	Cytophaga hutchinsonii	COG0593: ATPase involved in DNA replication initiation [Cytophaga hutchinsonii]				
7441, 7442	34558244	32	1.00E-21	Wolinella succinogenes DSM 1740	SIGNAL TRANSDUCTION REGULATORY PROTEIN-CheY like receiver domain [Wolinella succinogenes DSM 1740] emb[CAB10959.1] SIGNAL TRANSDUCTION REGULATORY PROTEIN-CheY like receiver domain [Wolinella succinogenes]			2.7.3.-	
7443, 7444	53712102	50	3.00E-61	Bacteroides fragilis YCH46	putative dNDP-4-keto-6-deoxy-glucose-2,3- dehydratase [Bacteroides fragilis YCH46] dbj[BAD47560.1] putative dNDP-4-keto-6-deoxy-glucose-2,3- dehydratase [Bacteroides fragilis YCH46]				
7445, 7446	17547595	28	1.00E-07	Ralstonia solanacearum GMI1000	PUTATIVE MEMBRANE-BOUND LYTIC MUREIN TRANSGLYCOSYLASE A TRANSMEMBRANE PROTEIN [Ralstonia solanacearum GMI1000] emb[CAD16583.1] PUTATIVE MEMBRANE-BOUND LYTIC MUREIN TRANSGLYCOSYLASE A TRANSMEMBRANE PROTEIN [Ralstonia solanacearum]			3.2.1.-	
7447, 7448	37525725	41	1.00E-57	Photorhabdus luminescens subsp. laumondii TTO1	hypothetical protein plu1791 [Photorhabdus luminescens subsp. laumondii TTO1] emb[CAB14084.1] unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1]				
7449, 7450	20807293	42	7.00E-36	Thermoanaerobact er tengcongensis MB4	Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Thermoanaerobacter tengcongensis MB4] gb AAM24068.1] Phosphoribosylformylglycinamide (FGAM) synthase, synthetase domain [Thermoanaerobacter tengcongensis MB4] sp Q8RBK5 PURL_THETN Phosphoribosylformylglycinamide synthase II (FGAM synthase II) ABC transporter [Synecocystis sp. PCC 6803] dbj BAA16900.1 ABC transporter [Synecocystis sp. PCC 6803] pir S74749 ABC-type transport protein sir082 - Synecocystis sp. (strain PCC 6803)			6.3.5.3	
745, 746	16329492	74	4.00E-90	Synechocystis sp. PCC 6803	carbamyl phosphate synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75664.1] carbamyl phosphate synthetase [Bacteroides thetaiotaomicron VPI-5482]			1.8.-	
7451, 7452	29345967	58	4.00E-58	Bacteroides thetaiotaomicron VPI-5482	ISSod5, transposase [Shewanella oneidensis MR-1] gb AAN55452.1 ISSod5, transposase [Shewanella oneidensis MR-1]			6.3.5.5	
7453, 7454	24373965	54	1.00E-34	Shewanella oneidensis MR-1					

7455, 7456	34556892	66	3.00E-94	Wolnella succinogenes DSM 1740	DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wolnella succinogenes DSM 1740] emb CAE09607.1 DNA-DIRECTED RNA POLYMERASE, BETA SUBUNIT RPOB [Wolnella succinogenes] sp Q7MA56 RPBC_WOLSU Bifunctional DNA-directed RNA polymerase, beta and beta' chain [Includes: DNA-directed RNA polymerase beta chain (Transcriptase beta chain) (RNA polymerase beta subunit); DNA-directed RNA polymerase beta' chain (Transcriptase beta' chain) (RNA polymerase beta' subunit)]	Helicobacter hepaticus ATCC 51449 section 2 of 6 of the complete genome	82	9.00E-15	2.7.7.6
7461, 7462	57238474	44	7.00E-45	Campylobacter jejuni RM1221	deoxyuridine triphosphatase domain protein [Campylobacter jejuni RM1221] gb AAW36057.1 deoxyuridine triphosphatase domain protein				
7465, 7466	57168280	62	1.00E-103	Campylobacter coli RM2228	[Campylobacter jejuni RM1221] conserved hypothetical protein TIGR00423 [Campylobacter coli RM2228] gb EAL57323.1 conserved hypothetical protein TIGR00423 [Campylobacter coli RM2228]				
7469, 7470	17227449	33	2.00E-41	Nostoc sp. PCC 7120	hypothetical protein all8075 [Nostoc sp. PCC 7120] pir AD2560 hypothetical protein all8075 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120gamma dbj BAB77405.1 ORF_ID:all8075~probable helicase [Nostoc sp. PCC 7120]				3.1.21.3
747, 748	49484307	44	3.00E-18	Staphylococcus aureus subsp. aureus MRSA252	putative UDP-N-acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate-- D- alanine-D-alanine ligase [Staphylococcus aureus subsp. aureus MRSA252] emb CAG41150.1 putative UDP-N-acetylmuramoylalanine-D-glutamate-2, 6- diaminopimelate-- D-alanine-D-alanine ligase [Staphylococcus aureus subsp. aureus MRSA252]				6.3.2.15
7471, 7472	42520897	34	1.00E-08	Wolbachia endosymbiont of Drosophila melanogaster	methyltransferase, putative [Wolbachia endosymbiont of Drosophila melanogaster] gb AAS14746.1 methyltransferase, putative [Wolbachia endosymbiont of Drosophila melanogaster] sp Q73G71 TRMB_WOLPM tRNA (guanine-N(7))-methyltransferase (tRNA(m7G46)-methyltransferase)				2.1.1.-
7475, 7476	28852723	58	3.00E-59	Pseudomonas syringae pv. tomato str. DC3000	hydrolase, haloacid dehalogenase-like family [Pseudomonas syringae pv. tomato str. DC3000] ref NP_792100.1 hydrolase, haloacid dehalogenase- like family [Pseudomonas syringae pv. tomato str. DC3000]				3.1.3.3
7477, 7478	50083834	28	4.00E-15	Acinetobacter sp. ADP1	hypothetical protein ACIAD0599 [Acinetobacter sp. ADP1] emb CAG67522.1 conserved hypothetical protein [Acinetobacter sp. ADP1]				
7479, 7480	50955568	30	3.00E-21	Leifsonia xyl subsp. xyl str. CTCB07	glycosyltransferase [Leifsonia xyl subsp. xyl str. CTCB07] gb AAT89751.1 glycosyltransferase [Leifsonia xyl subsp. xyl str. CTCB07]				

7481, 7482	20807825	32	4.00E-24	Thermoanaerobacter tengcongensis MB4	DNA segregation ATPase FtsK/SpoIIIE and related proteins [Thermoanaerobacter tengcongensis MB4] gb AAM24600.1 DNA segregation ATPase FtsK/SpoIIIE and related proteins [Thermoanaerobacter tengcongensis MB4] sp Q8R5S4 FTSK THETN DNA translocase ftsK			
7483, 7484	45658174	35	5.00E-14	Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130	hypothetical protein LIC12328 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] gb AAS70897.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]			
7487, 7488	57241004	23	3.00E-10	Campylobacter lari RM2100	probable transmembrane protein Cj0390 [Campylobacter lari RM2100] gb EAL54700.1 probable transmembrane protein Cj0390 [Campylobacter lari RM2100]			
7489, 7490	16328450	42	1.00E-47	Synechocystis sp. PCC 6803	regulatory components of sensory transduction system [Synechocystis sp. PCC 6803] dbj BAA16858.1 regulatory components of sensory transduction system [Synechocystis sp. PCC 6803] pir S74707 nltrogen fixation positive activator protein - Synechocystis sp. (strain PCC 6803)			2.7.3.-
749, 750	28377119	43	2.00E-28	Lactobacillus plantarum WCFS1	alpha-amylase [Lactobacillus plantarum WCFS1] emb CAD62849.1 alpha-amylase [Lactobacillus plantarum WCFS1]			3.2.1.1
7493, 7494	30019367	55	1.00E-57	Bacillus cereus ATCC 14579	dTDP-glucose 4,6-dehydratase [Bacillus cereus ATCC 14579] gb AAP08199.1 dTDP-glucose 4,6-dehydratase [Bacillus cereus ATCC 14579]			4.2.1.46
7495, 7496	48855000	61	4.00E-94	Cytophaga hutchinsonii	COG2509: Uncharacterized FAD-dependent dehydrogenases [Cytophaga hutchinsonii]			
7497, 7498	23129971	33	1.00E-07	Nostoc punctiforme PCC 73102	hypothetical protein Npun02001199 [Nostoc punctiforme PCC 73102]			
7499, 7500	19881279	35	7.00E-14	Campylobacter jejuni	RioB [Campylobacter jejuni] gb AAM00862.1 RioB [Campylobacter jejuni] gb AAM00829.1 RioB [Campylobacter jejuni]			
75, 76	48853747	56	6.00E-27	Cytophaga hutchinsonii	COG0441: Threonyl-tRNA synthetase [Cytophaga hutchinsonii]			6.1.1.3
7507, 7508	42524004	32	1.00E-15	Bdellovibrio bacteriovorus HD100	cell wall surface anchor family protein [Bdellovibrio bacteriovorus HD100] emb CAE80377.1 cell wall surface anchor family protein [Bdellovibrio bacteriovorus HD100]			
7509, 7510	53735875	38	3.00E-36	Crocospaera watsonii WH 8501	COG5421: Transposase [Crocospaera watsonii WH 8501]			
7511, 7512	53715023	55	8.00E-42	Bacteroides fragilis YCH46	hypothetical protein BF3739 [Bacteroides fragilis YCH46] db BAD50481.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			

7513,	48855619	53	6.00E-29	Cytophaga hutchinsonii	COG1587: Uroporphyrinogen-III synthase [Cytophaga hutchinsonii]				
7514					ATP-dependent DNA helicase RecQ [Coxiella burnetii RSA 493]				
7515,	29653815	36	8.00E-48	Coxiella burnetii RSA 493	gb AAO90021.1 ATP-dependent DNA helicase RecQ [Coxiella burnetii RSA 493]				3.6.1.-
7517,	23509126	40	3.00E-10	Plasmodium falciparum 3D7	hypothetical protein PFL2170c [Plasmodium falciparum 3D7]				
7518					gb AAN36518.1 hypothetical protein PFL2170c [Plasmodium falciparum 3D7]				
7519,	18000405	41	5.00E-09	Halovirus HF2	putative methyltransferase-endonuclease [Halovirus HF2] ref NP_861654.1				
7520					putative methyltransferase-endonuclease [Halovirus HF1] gb AAO61365.1				
7521,					putative methyltransferase-endonuclease [Halovirus HF1] ref NP_542568.1				2.1.1.72
7522,	2984552	50	5.00E-32	Aquifex aeolicus VF5	putative methyltransferase-endonuclease [Halovirus HF2]				
7523,	48839272	30	8.00E-15	Methanosarcina barkeri str. fusaro	putative protein [Aquifex aeolicus VF5] ref NP_046399.1 hypothetical protein aq_aa03 [Aquifex aeolicus VF5] sp O66399 YZ03_AQUAE Hypothetical protein AA03				
7524					COG1401: GTPase subunit of restriction endonuclease [Methanosarcina barkeri str. fusaro]				3.1.21.-
7525,	34558485	44	6.00E-73	Wolinella succinogenes DSM 1740	hypothetical protein WS2211 [Wolinella succinogenes DSM 1740]				
7526					emb CAE11200.1 hypothetical protein [Wolinella succinogenes]				2.7.3.-
7527,					hypothetical protein aq_1630 [Aquifex aeolicus VF5] gb AAC07520.1				
7528	15606737	36	2.00E-13	Aquifex aeolicus VF5	hypothetical protein [Aquifex aeolicus VF5] pir F70440 conserved hypothetical protein aq_1630 - Aquifex aeolicus				
7529,					hypothetical protein WS1882 [Wolinella succinogenes DSM 1740]				2.7.1.37
7530	34558177	22	3.00E-12	Wolinella succinogenes DSM 1740	emb CAE10892.1 hypothetical protein [Wolinella succinogenes]				
7531,					hypothetical protein WS1305 [Wolinella succinogenes DSM 1740]				
7532	34557666	24	1.00E-10	Wolinella succinogenes DSM 1740	emb CAE10381.1 hypothetical protein [Wolinella succinogenes]				
7533,					hypothetical protein WS1243 [Wolinella succinogenes DSM 1740]				
7534	34557608	25	2.00E-14	Wolinella succinogenes DSM 1740	emb CAE10323.1 conserved hypothetical protein [Wolinella succinogenes]				
7535,					folypolyglutamate synthase (folC) [Campylobacter coli RM2228]				
7536	57167971	51	2.00E-25	Campylobacter coli RM2228	gb EAL57014.1 folypolyglutamate synthase (folC) [Campylobacter coli RM2228]				6.3.2.17
7537,					RNA POLYMERASE SIGMA FACTOR [Wolinella succinogenes DSM 1740]				
7538	34558185	76	1.00E-110	Wolinella succinogenes DSM 1740	emb CAE10900.1 RNA POLYMERASE SIGMA FACTOR [Wolinella succinogenes]				
					Streptococcus thermophilus LMG 18311, complete genome			88	3.00E-24

7539, 7540	57167942	46	5.00E-46	Campylobacter coli RM2228	Isoleucyl-tRNA synthetase [Campylobacter coli RM2228] gb EAL56985.1 Isoleucyl-tRNA synthetase [Campylobacter coli RM2228]			6.1.1.5
7543, 7544	34557246	42	1.00E-18	Wolinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]			
7545, 7546	48858827	53	1.00E-25	Cytophaga hutchinsonii	COG2315: Uncharacterized protein conserved in bacteria [Cytophaga hutchinsonii]			
7547, 7548	57237512	63	3.00E-64	Campylobacter jejuni RM1221	tRNA-(6)A37 thiotransferase enzyme MiaB [Campylobacter jejuni RM1221] gb AAW35095.1 tRNA-(6)A37 thiotransferase enzyme MiaB [Campylobacter jejuni RM1221]			1.8.--
7549, 7550	34558082	51	1.00E-41	Wolinella succinogenes DSM 1740	LIPOPROTEIN [Wolinella succinogenes DSM 1740] emb CAE10797.1 LIPOPROTEIN [Wolinella succinogenes]			
755, 756	20093112	77	6.00E-74	Methanosarcina acetivorans C2A	hypothetical protein MA4324 [Methanosarcina acetivorans C2A] gb AAM07667.1 conserved hypothetical protein [Methanosarcina acetivorans str. C2A]	Methanosarcina acetivorans str. C2A, section 213 of 534 of the complete genome	84	1.00E-77 3.4.24.-
7551, 7552	34556740	34	1.00E-42	Wolinella succinogenes DSM 1740	hypothetical protein WS0304 [Wolinella succinogenes DSM 1740] emb CAE09455.1 conserved hypothetical protein [Wolinella succinogenes] conserved hypothetical protein [Pseudomonas aeruginosa PAO1] pir E83031 conserved hypothetical protein PA4927 [Imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_253614.1 hypothetical protein PA4927 [Pseudomonas aeruginosa PAO1]			
7553, 7554	9951205	36	1.00E-23	Pseudomonas aeruginosa PAO1	Hemin receptor [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA24234.1 Hemin receptor [Fusobacterium nucleatum subsp. vincentii ATCC 49256]			
7555, 7556	34763190	27	3.00E-19	Fusobacterium nucleatum subsp. vincentii ATCC 49256		Desc:Borrelia burgdorferi polynucleotide sequence #1. Org:Borrelia burgdorferi	93	2.00E-13
7557, 7558	52673266	57	1.00E-99	Bacillus amyloliquefaciens	UvrABC system protein B [Bacillus amyloliquefaciens] DNA topoisomerase I [Bacteroides fragilis YCH46] db BAD51157.1 DNA topoisomerase I [Bacteroides fragilis YCH46]			5.99.1.2
7559, 7560	53715699	53	9.00E-64	Bacteroides fragilis YCH46				

7561, 7562	37528384	43	1.00E-47	Photorhabdus luminescens subsp. laumondii TTO1	hypothetical protein plu4565 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE16937.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1]			2.-.-.-	
7565, 7566	57285642	61	5.00E-69	Staphylococcus aureus subsp. aureus COL	uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus COL] ref NP_645353.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus MW2] ref NP_373792.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus N315] dbj BAB56743.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus Mu50] dbj BAB94401.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus MW2] dbj BAB41770.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus N315] ref NP_371105.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus Mu50] pir G89826 uracil-DNA glycosylase ung [imported] - Staphylococcus aureus (strain N315) sp P67075 UNG_STAAM Uracil-DNA glycosylase (UDG) sp P67077 UNG_STAAM Uracil-DNA glycosylase (UDG) sp P67076 UNG_STAAM Uracil-DNA glycosylase (UDG) ref YP_185512.1 uracil-DNA glycosylase [Staphylococcus aureus subsp. aureus COL]	Blochmannia floridanus complete genome; segment 3/3	81	1.00E-07	3.2.2.-
757, 758	23501128	58	1.00E-39	Brucella suis 1330	transcriptional regulator, MerR family [Brucella suis 1330] gb AAN29170.1 transcriptional regulator, MerR family [Brucella suis 1330]			5.4.1.2	
7571, 7572	48855446	36	7.00E-10	Cytophaga hutchinsonii	COG1173: ABC-type dipeptide/oligopeptide/nickel transport systems, permease components [Cytophaga hutchinsonii]				
7573, 7574	53712874	48	3.00E-63	Bacteroides fragilis YCH46	ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] dbj BAD48332.1 ABC transporter ATP-binding protein [Bacteroides fragilis YCH46]			1.8.-.-	
7583, 7584	34556902	40	1.00E-29	NADP+	FORMATE DEHYDROGENASE, BETA SUBUNIT (FORMATE DEHYDROGENASE [NADP+]) [Wolinnella succinogenes DSM 1740] emb CAE09617.1 FORMATE DEHYDROGENASE, BETA SUBUNIT (FORMATE DEHYDROGENASE [NADP+]) [Wolinnella succinogenes] response regulator [Thermotoga maritima MSB8] gb AAD35484.1 response regulator [Thermotoga maritima MSB8] pir H72382 response regulator - Thermotoga maritima (strain MSB8)			1.6.5.3	
7585, 7586	15643165	36	9.00E-39	Thermotoga maritima MSB8	COG0479: Succinate dehydrogenase/fumarate reductase, Fe-S protein subunit [Magnetococcus sp. MC-1]			2.7.3.-	
7587, 7588	48834056	35	5.00E-32	Magnetococcus sp. MC-1	methyl-accepting chemotaxis protein, putative [Campylobacter upsaliensis RM3195] gb EAL53448.1 methyl-accepting chemotaxis protein, putative [Campylobacter upsaliensis RM3195]			1.3.99.1	
7589, 7590	57242735	40	2.00E-21	Campylobacter upsaliensis RM3195					

759, 760	29349012	41	2.00E-14	Bacteroides thetaiotaomicron VPI-5482	putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482] gb AAO78709.1 putative outer membrane protein, probably involved in nutrient binding [Bacteroides thetaiotaomicron VPI-5482]			
7591, 7592	48855125	48	1.00E-59	Cytophaga hutchinsonii	COG2081: Predicted flavoproteins [Cytophaga hutchinsonii]			
7593, 7594	22094882	31	3.00E-09	Flavobacterium johnsoniae	GldH [Flavobacterium johnsoniae]			
7595, 7596	21668035	31	5.00E-11	Bacteroides fragilis	hypothetical transposase [Bacteroides fragilis]			
7597, 7598	57159487	35	1.00E-42	Thermococcus kodakaraensis	probable molybdenum cofactor biosynthesis protein A [Thermococcus kodakaraensis] ref YP_18384.1 probable molybdenum cofactor biosynthesis protein A [Thermococcus kodakaraensis]			
7599, 7600	57240895	40	3.00E-51	Campylobacter lari RM2100	proline dehydrogenase [Campylobacter lari RM2100] gb EAL55288.1 proline dehydrogenase [Campylobacter lari RM2100]			1.5.99.8
7601, 7602	34558306	44	7.00E-53	Wolinella succinogenes DSM 1740	PUTATIVE RIBOFLAVIN-SPECIFIC DEAMINASE EC 3.5.4. [Wolinella succinogenes DSM 1740] emb CAE11021.1 PUTATIVE RIBOFLAVIN- SPECIFIC DEAMINASE EC 3.5.4. [Wolinella succinogenes]			3.5.4.26
7603, 7604	11498376	31	2.00E-21	Archaeoglobus fulgidus DSM 4304	signal-transducing histidine kinase [Archaeoglobus fulgidus DSM 4304] gb AAE90464.1 signal-transducing histidine kinase [Archaeoglobus fulgidus DSM 4304] pir B69346 signal-transducing histidine kinase homolog - Archaeoglobus fulgidus			2.7.3.-
7609, 7610	28379430	30	5.00E-10	Lactobacillus plantarum WCFS1	ABC transporter, ATP-binding and permease protein [Lactobacillus plantarum WCFS1] emb CAD65182.1 ABC transporter, ATP-binding and permease protein [Lactobacillus plantarum WCFS1]			
761, 762	48729246	28	2.00E-15	Pseudomonas fluorescens PFO-1	COG0457: FOG: TPR repeat [Pseudomonas fluorescens Pfo-1]			
7611, 7612	57168857	57	4.00E-58	Campylobacter coli RM2228	anaerobic glycerol-3-phosphate dehydrogenase, subunit C [glpC] [Campylobacter coli RM2228] gb EAL56379.1 anaerobic glycerol-3- phosphate dehydrogenase, subunit C [glpC] [Campylobacter coli RM2228]			
7613, 7614	52840519	52	8.00E-48	Legionella pneumophila subsp. pneumophila str. Philadelphia 1	hypothetical protein [pg0264 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1] gb AAU2637.1 hypothetical protein [pg0264 [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]			
7615, 7616	16415962	38	2.00E-41	Acinetobacter lwoffi	Alol restriction modification enzyme [Acinetobacter lwoffi]			2.1.1.72
7617, 7618	53715164	30	1.00E-16	Bacteroides fragilis YCH46	hypothetical protein BF3880 [Bacteroides fragilis YCH46] dbj BAD50622.1 conserved hypothetical protein [Bacteroides fragilis YCH46]			

7619, 7620	34557635	43	3.00E-54	Wollinella succinogenes DSM 1740	RND PUMP PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10350.1 RND PUMP PROTEIN [Wollinella succinogenes]				
7623, 7624	34558169	33	1.00E-23	Wollinella succinogenes DSM 1740	conserved hypothetical protein-DNA polymerase III delta subunit [Wollinella succinogenes DSM 1740] emb CAE10884.1 conserved hypothetical protein-DNA polymerase III delta subunit [Wollinella succinogenes]				
7625, 7626	34557200	30	1.00E-37	Wollinella succinogenes DSM 1740	hypothetical protein WS0802 [Wollinella succinogenes DSM 1740] emb CAE09915.1 conserved hypothetical protein [Wollinella succinogenes]				
7627, 7628	34557237	29	8.00E-08	Wollinella succinogenes DSM 1740	COMPONENTS OF SENSORY TRANSDUCTION SYSTEM [Wollinella succinogenes DSM 1740] emb CAE09952.1 COMPONENTS OF SENSORY TRANSDUCTION SYSTEM [Wollinella succinogenes]				
7629, 7630	34557202	63	2.00E-57	Wollinella succinogenes DSM 1740	ATP PHOSPHORIBOSYLTRANSFERASE [Wollinella succinogenes DSM 1740] emb CAE09917.1 ATP PHOSPHORIBOSYLTRANSFERASE [Wollinella succinogenes] sp Q7M9N0 HIS1_WOLSU ATP phosphoribosyltransferase (ATP-PRTase) (ATP-PRT)				2.4.2.17
763, 764	29349976	27	2.00E-24	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT4568 [Bacteroides thetaiotaomicron VPI-5482] gb AAO79673.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]				
7631, 7632	53711927	29	4.00E-16	Bacteroides fragilis YCH46	hypothetical protein BF0636 [Bacteroides fragilis YCH46] dbj BAD47385.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
7633, 7634	22036085	35	2.00E-15	Vibrio parahaemolyticus	hypothetical ATP-binding protein [Vibrio parahaemolyticus]				
7635, 7636	53731251	41	7.00E-23	Methanococcoides burtonii DSM 6242	COG0642: Signal transduction histidine kinase [Methanococcoides burtonii DSM 6242]				2.7.3.-
7637, 7638	57241137	48	5.00E-75	Campylobacter lari RM2100	oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter lari RM2100] gb EAL54833.1 oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter lari RM2100]				1.-.-.-
7643, 7644	57168975	59	1.00E-31	Campylobacter coli RM2228	3'(2''),5'-bisphosphate nucleotidase [Campylobacter coli RM2228] gb EAL56330.1 3'(2''),5'-bisphosphate nucleotidase [Campylobacter coli RM2228]				

7645, 7646	54639980	69	1.00E-75	Campylobacter jejuni	putative adenylylsulfate kinase [Campylobacter jejuni]	Campylobacter jejuni OH4384 peptide chain release factor 2 (prfB) gene, partial cds; alpha-2,3- sialyltransferase (cst-I), sulfate adenylyltransferase subunit CysD (cysD), sulfate adenylyltransferase subunit CysN (cysN), putative sodium/sulfate symporter (sodium sulfate symporter), putative adenylylsulfate kinase (cysC), hypothetical protein, putative glycosyltransferase, and hypothetical protein genes, complete cds; and cj1457c gene, partial cds	84	4.00E-07	2.7.1.25	
7647, 7648	24373737	50	8.00E-72	Shewanella oneidensis MR-1	peptidase, M23/M37 family [Shewanella oneidensis MR-1] gb AAN55224.1 peptidase, M23/M37 family [Shewanella oneidensis MR-1]				3.5.1.-	
7649, 7650	53711855	40	5.00E-21	Bacteroides fragilis YCH46 Bradyrhizobium japonicum USDA 110	putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides fragilis YCH46] dbj BAD47313.1 putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides fragilis YCH46]				3.1.4.16	
765, 766	27382256	49	4.00E-31	Trichodesmium erythraeum IMS101	hypothetical protein bli7145 [Bradyrhizobium japonicum USDA 110] dbj BAC52410.1 bli7145 [Bradyrhizobium japonicum USDA 110]					
7651, 7652	48892249	33	3.00E-30	Trichodesmium erythraeum IMS101	COG4886: Leucine-rich repeat (LRR) protein [Trichodesmium erythraeum IMS101]					

7653, 7654	23112865	45	2.00E-44	Desulfotobacterium hafniense DCB-2	COG4636: Uncharacterized protein conserved in cyanobacteria [Desulfotobacterium hafniense DCB-2]			
7655, 7656	32262541	70	1.00E-100	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860522.1 hypothetical protein HH0591 [Helicobacter hepaticus ATCC 51449]	80	2.00E-16	
7657, 7658	AAB5256 4	45	1.00E-53		Desc:Helicobacter pylori bait polypeptide #82. Org:Helicobacter pylori			3.4.-.-
7661, 7662	52008034	28	5.00E-14	Thiobacillus denitrificans ATCC 25259	COG2202: FOG: PAS/PAC domain [Thiobacillus denitrificans ATCC 25259] hypothetical protein BCZK0794 [Bacillus cereus ZK] gb AAU19449.1			2.7.3.-
7663, 7664	52144430	27	6.00E-30	Bacillus cereus ZK	conserved hypothetical protein [Bacillus cereus ZK]			
7665, 7666	52007674	33	3.00E-16	Thiobacillus denitrificans ATCC 25259	COG1959: Predicted transcriptional regulator [Thiobacillus denitrificans ATCC 25259]			
7667, 7668	57159034	51	2.00E-57	Thermococcus kodakaraensis	deblocking aminopeptidase [Thermococcus kodakaraensis] ref YP_183188.1 deblocking aminopeptidase [Thermococcus kodakaraensis]			3.4.11.-
7675, 7676	31747866	58	1.00E-68	Fritschea bemisiae	unknown [Fritschea bemisiae] related to iron (III) ABC transporter, ATP-binding protein [Desulfotalea psychrophila LSv54] emb CAG37707.1 related to iron (III) ABC transporter, ATP-binding protein [Desulfotalea psychrophila LSv54]			
7677, 7678	51246830	28	1.00E-10	Desulfotalea psychrophila LSv54	transcriptional regulatory protein KdpE, putative [Campylobacter coli RM2228] gb EAL56224.1 transcriptional regulatory protein KdpE, putative [Campylobacter coli RM2228]			2.7.3.-
7679, 7680	57169075	29	5.00E-19	Campylobacter coli RM2228	hypothetical protein HH0539 [Helicobacter hepaticus ATCC 51449] ref NP_860070.1 hypothetical protein HH0539 [Helicobacter hepaticus ATCC 51449]			
7681, 7682	32262087	38	2.00E-10	Helicobacter hepaticus ATCC 51449	L-SERYL-TRNA(SEC) SELENIUM TRANSFERASE [Wolfinella succinogenes DSM 1740] emb CAE0951.1 L-SERYL-TRNA(SEC) SELENIUM TRANSFERASE [Wolfinella succinogenes] sp Q7M9L1 SELA_WOLSU L- seryl-tRNA(SEC) selenium transferase (CysteinyI-tRNA(SEC) selenium transferase) (Selenocysteine synthase) (Selenocysteinyl-tRNA(SEC) synthase)			2.9.1.1
7683, 7684	34557236 34557385	60 40	6.00E-94 3.00E-39	Wolfinella succinogenes DSM 1740 Wolfinella succinogenes DSM 1740	SELENOPHOSPHATE SYNTHETASE [Wolfinella succinogenes DSM 1740] emb CAE10100.1 SELENOPHOSPHATE SYNTHETASE [Wolfinella succinogenes]			2.7.9.3

7689, 7690	34558184	29	1.00E-07	Wolinella succinogenes DSM 1740	hypothetical protein WS1889 [Wolinella succinogenes DSM 1740] emb CAE10899.1 hypothetical protein [Wolinella succinogenes] flagellar basal-body P-ring formation protein FigA, putative [Shewanella oneidensis MR-1] gb AAAN56251.1 flagellar basal-body P-ring formation protein FigA, putative [Shewanella oneidensis MR-1] COG0451: Nucleoside-diphosphate-sugar epimerases [Cytophaga hutchinsonii]				
7691, 7692	24374764	27	3.00E-23	Shewanella oneidensis MR-1					
7693, 7694	48853513	74	2.00E-52	Cytophaga hutchinsonii					4.2.1.46
7695, 7696	34556844	27	1.00E-17	Wolinella succinogenes DSM 1740	SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes DSM 1740] emb CAE09559.1 SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes]				
7697, 7698	34557698	31	5.00E-11	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10413.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]				2.7.3.-
7699, 7700	13123737	67	5.00E-51	Campylobacter jejuni	putative acetyltransferase [Campylobacter jejuni]	Campylobacter jejuni strain TGH 9011 contig147 Tgh114, Tgh020, Tgh021, Tgh022, Tgh160, Tgh011, Tgh42, Tgh043, Tgh004, Tgh001, Tgh002, and Tgh003s genes, complete cds	79	4.00E-10	2.3.1.-
77, 78	20090869	47	3.00E-39	Methanosarcina acetivorans C2A	hypothetical protein MA2021 [Methanosarcina acetivorans C2A] gb AAM05424.1 hypothetical protein [Methanosarcina acetivorans str. C2A] DNA topoisomerase I [Thermosynechococcus elongatus BP-1] db BAC09433.1 DNA topoisomerase I [Thermosynechococcus elongatus BP-1]				1.14.17. 3
7703, 7704	22289424	41	2.00E-50	Thermosynechococ cus elongatus BP-1	excinuclease ABC, B subunit [Geobacter sulfurreducens PCA] gb AAR36653.1 excinuclease ABC, B subunit [Geobacter sulfurreducens PCA]				5.99.1.2
7709, 7710	39998352	67	2.00E-55	Geobacter sulfurreducens PCA					
771, 772	48855742	51	4.00E-77	Cytophaga hutchinsonii	COG0514: Superfamily II DNA helicase [Cytophaga hutchinsonii]				3.6.1.-
7711, 7712	34557410	55	1.00E-16	Wolinella succinogenes DSM 1740	hypothetical protein WS1024 [Wolinella succinogenes DSM 1740] emb CAE10125.1 conserved hypothetical protein [Wolinella succinogenes]				

7719, 7720	28378865	25	1.00E-09	Lactobacillus plantarum WCFS1	DNA mismatch repair protein MutS2 [Lactobacillus plantarum WCFS1] emb CAD64608.1 DNA mismatch repair protein MutS2 [Lactobacillus plantarum WCFS1]				
7721, 7722	57241750	26	3.00E-10	Campylobacter lari RM2100	conserved domain protein [Campylobacter lari RM2100] gb EAL54420.1 conserved domain protein [Campylobacter lari RM2100]				
7723, 7724	20089933	27	5.00E-23	Methanosarcina acetivorans C2A	capsular polysaccharide biosynthesis protein [Methanosarcina acetivorans C2A] gb AAM04488.1 capsular polysaccharide biosynthesis protein [Methanosarcina acetivorans str. C2A]				
7725, 7726	16077744	43	7.00E-40	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU06760 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12496.1 yeeA [Bacillus subtilis subsp. subtilis str. 168] pir E69792 conserved hypothetical protein yeeA - Bacillus subtilis				
773, 774	29346376	35	7.00E-19	Bacteroides thetaiotaomicron VPI-5482	RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI- 5482] gb AAO76073.1 RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482]				
7731, 7732	56459864	43	5.00E-33	Idiomarina loliensis L2TR	Signaling protein with a MHYT sensor domain, PAS, GGDEF and EAL domains [Idiomarina loliensis L2TR] gb AAV81596.1 Signaling protein with a MHYT sensor domain, PAS, GGDEF and EAL domains [Idiomarina loliensis L2TR]				
7735, 7736	57240666	39	2.00E-35	Campylobacter lari RM2100	radical SAM domain protein [Campylobacter lari RM2100] gb EAL55059.1 radical SAM domain protein [Campylobacter lari RM2100]				
7737, 7738	57240666	40	5.00E-30	Campylobacter lari RM2100	radical SAM domain protein [Campylobacter lari RM2100] gb EAL55059.1 radical SAM domain protein [Campylobacter lari RM2100]				
7743, 7744	46142119	63	5.00E-73	Methanococcus burtonii DSM 6242	COG0439: Biotin carboxylase [Methanococcus burtonii DSM 6242]				
7745, 7746	48855088	38	3.00E-21	Cytophaga hutchinsonii	COG0243: Anaerobic dehydrogenases, typically selenocysteine-containing [Cytophaga hutchinsonii]				1.2.1.2
7747, 7748	37523321	30	9.00E-12	Gloeobacter violaceus PCC 7421	probable oxidoreductase [Gloeobacter violaceus PCC 7421] dbj BAC91693.1 glj3752 [Gloeobacter violaceus PCC 7421]				
7749, 7750	21244626	50	8.00E-19	Xanthomonas axonopodis pv. citri str. 306	mitomycin resistance protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM38744.1 mitomycin resistance protein [Xanthomonas axonopodis pv. citri str. 306]				
775, 776	34396946	29	4.00E-20	Porphyrionas gingivalis W83	type IIS restriction endonuclease, putative [Porphyrionas gingivalis W83] ref NP_905111.1 type IIS restriction endonuclease, putative [Porphyrionas gingivalis W83]				2.1.1.72

[illegible]

7777,	21226672	39	3.00E-17	Methanosarcina mazel Go1	ABC transporter, ATP-binding protein [Methanosarcina mazel Go1]				
7778,				Wolinella succinogenes DSM 1740	hypothetical protein WS0265 [Wolinella succinogenes DSM 1740]				3.6.1.13
7779,	34556704	48	4.00E-34	Photobacterium profundum SS9	emb CAE09419.1 conserved hypothetical protein [Wolinella succinogenes]				
7780,				Photobacterium profundum SS9	emb CAG22359.1 conserved hypothetical protein [Photobacterium profundum]				
7781,	54302166	30	4.00E-21	Ralstonia eutropha JMP134	COG1073: Hydrolases of the alpha/beta superfamily [Ralstonia eutropha JMP134]				
7782,	53762765	34	7.00E-40	Clostridium perfringens str. 13	two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13]				
7783,				Cytophaga hutchinsonii	hypothetical protein Chut02000101 [Cytophaga hutchinsonii]				
7784,	18310494	35	2.00E-20	Cytophaga hutchinsonii	COG0044: Dihydroorotase and related cyclic amidohydrolases [Cytophaga hutchinsonii]				3.5.2.3
7785,	48856384	23	3.00E-13	Campylobacter coli RM2228	conserved hypothetical protein [Campylobacter coli RM2228]				
7786,	48856383	40	6.00E-35	Campylobacter coli RM2228	gb EAL56259.1 conserved hypothetical protein [Campylobacter coli RM2228]				
7787,	57169024	31	4.00E-11	Campylobacter coli RM2228	conserved hypothetical protein [Campylobacter coli RM2228]				
7788,				Streptococcus pyogenes MGAS8232	putative ABC transporter (ATP-binding protein) [Streptococcus pyogenes MGAS8232]				1.8.-.-
7789,	57169025	39	8.00E-49	Dechloromonas aromatica RCB	COG1988: Predicted membrane-bound metal-dependent hydrolases [Dechloromonas aromatica RCB]				
7790,	19745834	40	8.00E-30	Nostoc punctiforme PCC 73102	COG0642: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102]				2.7.3.-
7791,	41724574	45	2.00E-27	Bacteroides fragilis YCH46	O-methyltransferase [Bacteroides fragilis YCH46]				2.1.1.-
7792,	23129412	30	6.00E-23	Geobacter metallireducens GS-15	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]				
7793,	53715760	50	4.00E-56	Cytophaga hutchinsonii	COG2319: FOG: WD40 repeat [Cytophaga hutchinsonii]				
7794,				Campylobacter coli RM2228	proline dehydrogenase [Campylobacter coli RM2228]				
7795,	48845444	54	1.00E-59		proline dehydrogenase [Campylobacter coli RM2228]				1.5.99.8
7796,	48845444	54	1.00E-59						
7797,	48845444	54	1.00E-59						
7798,	48845444	54	1.00E-59						
7799,	48845444	54	1.00E-59						
7800,	48845444	54	1.00E-59						
7801,	48845444	54	1.00E-59						
7802,	48845444	54	1.00E-59						
7803,	48845444	54	1.00E-59						
7804,	48845444	54	1.00E-59						
7805,	48845444	54	1.00E-59						
7806,	48845444	54	1.00E-59						
7807,	48845444	54	1.00E-59						
7808,	48845444	54	1.00E-59						
7809,	48845444	54	1.00E-59						
7810,	48845444	54	1.00E-59						
7811,	48845444	54	1.00E-59						
7812,	48845444	54	1.00E-59						
7813,	48845444	54	1.00E-59						
7814,	48845444	54	1.00E-59						
7815,	48845444	54	1.00E-59						
7816,	48845444	54	1.00E-59						

7817, 7818	53715668	47	3.00E-33	Bacteroides fragilis YCH46	putative amidophosphoribosyl-transferase [Bacteroides fragilis YCH46] dbj BAD51126.1 putative amidophosphoribosyl-transferase [Bacteroides fragilis YCH46]			
7819, 7820	50122191	34	4.00E-47	Erwinia carotovora subsp. atroseptica SCRI1043	HlyD family secretion protein [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG76167.1 HlyD family secretion protein [Erwinia carotovora subsp. atroseptica SCRI1043]			3.1.11.-
7821, 7822	20095135	98	6.00E-59	Providencia rettgeri	TraC [Providencia rettgeri]	Providencia rettgeri conjunctive genomic island R391, complete sequence	97 #####	
7823, 7824	29349895	49	3.00E-71	Bacteroides thetaiotaomicon VPI-5482	putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicon VPI-5482] gb AAO79592.1 putative membrane-bound lytic murein transglycosylase [Bacteroides thetaiotaomicon VPI-5482]			3.2.1.-
7825, 7826	48853332	39	5.00E-21	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]			
7827, 7828	20090484	33	2.00E-08	Methanosarcina acetivorans C2A	transposase [Methanosarcina acetivorans C2A] gb AAM05039.1 transposase [Methanosarcina acetivorans str. C2A]			
7829, 7830	53684697	26	1.00E-08	Desulfotobacterium hafnense DCB-2	COG2984: ABC-type uncharacterized transport system, periplasmic component [Desulfotobacterium hafnense DCB-2]			
7831, 7832	48856849	51	2.00E-77	Cytophaga hutchinsonii	COG0525: Valyl-tRNA synthetase [Cytophaga hutchinsonii]	Bacteroides fragilis YCH46 DNA, complete genome	88 4.00E-08	6.1.1.9
7835, 7836	34557654	42	5.00E-33	Wolinella succinogenes DSM 1740	hypothetical protein WS1291 [Wolinella succinogenes DSM 1740] emb CAE10369.1 conserved hypothetical protein [Wolinella succinogenes] PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09897.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes]			
7837, 7838	34557182	48	3.00E-38	Wolinella succinogenes DSM 1740	TPR domain protein [Porphyromonas gingivalis W83] ref NP_906029.1 TPR domain protein [Porphyromonas gingivalis W83]			
7839, 7840	34397867	24	1.00E-21	Porphyromonas gingivalis W83	UDP-N-acetylmuramoylalanine-D-glutamate-2, 6-diaminopimelate ligase [Bacteroides fragilis YCH46] dbj BAD47059.1 UDP-N-acetylmuramoylalanine- D-glutamate-2, 6-diaminopimelate ligase [Bacteroides fragilis YCH46]			6.3.2.13
7843, 7844	53711601	51	5.00E-78	Bacteroides fragilis YCH46	COG2202: FOG: PAS/PAC domain [Geobacter metallireducens GS-15]			2.7.3.-
7849, 7850	48846045	36	1.00E-22	Geobacter metallireducens GS				

785, 786	48853824	50	4.00E-62	Cytophaga hutchinsonii	COG0859: ADP-heptose:LPS heptosyltransferase [Cytophaga hutchinsonii]			
7851, 7852	14521387	33	2.00E-34	Pyrococcus abyssi GE5	hypothetical protein PAB0790 [Pyrococcus abyssi GE5] emb CAB50093.1 Hypothetical protein [Pyrococcus abyssi] pir H75098 hypothetical protein PAB0790 - Pyrococcus abyssi (strain Orsay)		3.6.1.-	
7853, 7854	15643214	26	2.00E-13	Thermotoga maritima MSB8	hypothetical protein TM0448 [Thermotoga maritima MSB8] gb AAD35531.1 hypothetical protein TM0448 [Thermotoga maritima MSB8] pir A72375 hypothetical protein - Thermotoga maritima (strain MSB8)			
7855, 7856	34558194	65	8.00E-53	Wolinella succinogenes DSM 1740	RIBONUCLEASE HI [Wolinella succinogenes DSM 1740] emb CAE10909.1 RIBONUCLEASE HI [Wolinella succinogenes]		3.1.26.4	
7857, 7858	54302166	27	5.00E-09	Photobacterium profundum SS9	hypothetical protein PBPRB0486 [Photobacterium profundum SS9] emb CAG22359.1 hypothetical protein [Photobacterium profundum]			
7859, 7860	14718642	30	3.00E-21	Sus scrofa	estrogen sulfotransferase [Sus scrofa] ref NP_999157.1 estrogen sulfotransferase [Sus scrofa]		2.8.2.4	
7861, 7862	32262892	24	1.00E-17	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860872.1 hypothetical protein HH1341 [Helicobacter hepaticus ATCC 51449]			
7867, 7868	34556675	30	2.00E-34	Wolinella succinogenes DSM 1740	hypothetical protein WS0233 [Wolinella succinogenes DSM 1740] emb CAE09390.1 conserved hypothetical protein [Wolinella succinogenes]		5.2.1.8	
7869, 7870	53713306	45	2.00E-49	Bacteroides fragilis YCH46	ATP-independent RNA helicase [Bacteroides fragilis YCH46] dbj BAD48764.1 ATP-independent RNA helicase [Bacteroides fragilis YCH46]		2.7.7.-	
787, 788	48853824	44	7.00E-64	Cytophaga hutchinsonii	COG0859: ADP-heptose:LPS heptosyltransferase [Cytophaga hutchinsonii] cytochrome c551 peroxidase [Campylobacter jejuni RM1221] gb AAW34515.1 cytochrome c551 peroxidase [Campylobacter jejuni RM1221]			
7871, 7872	57236932	45	6.00E-22	Campylobacter jejuni RM1221	ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes DSM 1740] emb CAE10562.1 ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes]		1.11.1.5	
7875, 7876	34557847	29	4.00E-07	Wolinella succinogenes DSM 1740	putative glycosyltransferase [Serratia marcescens]		2.4.1.-	
7877, 7878	4753136	38	1.00E-32	Serratia marcescens	putative glycosyltransferase [Serratia marcescens]		2.4.1.-	
7879, 7880	4753136	35	3.00E-37	Serratia marcescens	putative glycosyltransferase [Serratia marcescens]		2.4.1.-	

7883, 7884, 7885, 7886	34558247	58	1.00E-69	Wolinella succinogenes DSM 1740	PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907863.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907529.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907441.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907411.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907300.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907278.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907223.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907162.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_907120.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_906960.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes DSM 1740] ref NP_906534.1 TRANSPOSASE [Wolinella succinogenes DSM 1740] emb CAE10763.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes] emb CAE10429.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes] emb CAE10341.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes] emb CAE10311.1 PUTATIVE TRANSPOSASE [Wolinella succinogenes] em COG0688: Phosphatidylserine decarboxylase [Pseudomonas fluorescens PfO-1]				4.1.1.65
7887, 7888	34557306	68	1.00E-47	Wolinella succinogenes DSM 1740	NOSZ PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10021.1 NOSZ PROTEIN [Wolinella succinogenes] PUTATIVE D-ALANINE-D-ALANINE LIGASE [Wolinella succinogenes DSM 1740] emb CAE09580.1 PUTATIVE D-ALANINE-D-ALANINE LIGASE [Wolinella succinogenes] sp Q7MA71 DDL_WOLSU D-alanine-D-alanine ligase (D-alanylalanine synthetase) (D-Ala-D-Ala ligase)				6.3.2.4
7889, 790	34556865	54	5.00E-40	Wolinella succinogenes DSM 1740	inorganic pyrophosphatase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] ref NP_714220.1 Soluble inorganic pyrophosphatase [Leptospira interrogans serovar Lai str. 56601] gb AAN51238.1 Soluble inorganic pyrophosphatase [Leptospira interrogans serovar lai str. 56601] sp Q8EZ21 PYR_LEPIN Inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase) (PPase) gb AAS71768.1 inorganic pyrophosphatase [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]				3.6.1.1

7893, 7894	6968117	50	6.00E-47	Campylobacter jejuni subsp. jejuni NCTC 11168	putative ATP /GTP binding protein [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281833.1 putative ATP /GTP binding protein [Campylobacter jejuni subsp. jejuni NCTC 11168] pir A81414 probable ATP /GTP binding protein C0650 [imported] - Campylobacter jejuni (strain NCTC 11168) sp Q9PHL7 ENGB_CAMJE Probable GTP-binding protein engB				
7897, 7898	53714509	26	3.00E-17	Bacteroides fragilis YCH46	hypothetical protein BF3222 [Bacteroides fragilis YCH46] db BAD49867.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
7899, 7900	56489415	25	2.00E-07	Plasmodium berghiei	Pb-reticulocyte binding protein [Plasmodium berghiei]				
79, 80	34398333	45	2.00E-50	Porphyromonas gingivalis W83	conserved domain protein [Porphyromonas gingivalis W83] ref NP_904501.1 hypothetical protein PG0160 [Porphyromonas gingivalis W83]				
7901, 7902	55819425	26	1.00E-13	Mimivirus	putative DNA repair protein [Mimivirus] gb AAV50819.1 putative DNA repair protein [Mimivirus]				
7903, 7904	34557690	54	2.00E-21	Wolinella succinogenes DSM 1740	hypothetical protein WS1330 [Wolinella succinogenes DSM 1740] emb CAE10405.1 hypothetical protein [Wolinella succinogenes]				
7905, 7906	28899263	43	2.00E-33	Vibrio parahaemolyticus RIMD 2210633	iron(III) ABC transporter, ATP-binding protein [Vibrio parahaemolyticus RIMD 2210633] db JBAC60752.1 iron(III) ABC transporter, ATP-binding protein [Vibrio parahaemolyticus]				1.8.-.-
7907, 7908	34557200	34	5.00E-17	Wolinella succinogenes DSM 1740	hypothetical protein WS0802 [Wolinella succinogenes DSM 1740] emb CAE09915.1 conserved hypothetical protein [Wolinella succinogenes]				
7909, 7910	23025125	46	5.00E-21	Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293	COG4974: Site-specific recombinase XerD [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]				
7911, 7912	15896153	50	4.00E-26	Clostridium acetobutylicum ATCC 824	Spore photoproduct lyase, SPL related protein [Clostridium acetobutylicum ATCC 824] gb AAK80842.1 Spore photoproduct lyase, SPL related protein [Clostridium acetobutylicum ATCC 824] pir G97256 spore photoproduct lyase, SPL related protein [imported] - Clostridium acetobutylicum				4.1.99.-
7913, 7914	34557291	45	2.00E-58	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10006.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]				2.7.3.-
7915, 7916	48831167	39	1.00E-36	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]				2.7.3.-

7917, 7918	34558004	56	4.00E-92	Wolinella succinogenes DSM 1740	RNA POLYMERASE ALPHA SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10719.1 RNA POLYMERASE ALPHA SUBUNIT [Wolinella succinogenes] sp Q7M8F7 RPOA_WOLSU DNA-directed RNA polymerase alpha chain (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit)			2.7.7.6
7923, 7924	45658174	32	2.00E-13	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	hypothetical protein LIC12326 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] gb AA570897.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]			
793, 794	48856683	32	4.00E-15	Cytophaga hutchinsonii	COG4258: Predicted exporter [Cytophaga hutchinsonii]			
7933, 7934	57234354	42	1.00E-34	Dehalococcoides ethenogenes 195	hydrogenase, group 4, EchE subunit, putative [Dehalococcoides ethenogenes 195] gb AAW39859.1 hydrogenase, group 4, EchE subunit, putative [Dehalococcoides ethenogenes 195]			1.-.-
7937, 7938	34557782	41	4.00E-37	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]			2.7.3.-
7939, 7940	29654150	47	1.00E-58	Coxiella burnetii RSA 493	hypothetical protein CBU0822 [Coxiella burnetii RSA 493] gb AAO90356.1 conserved hypothetical protein [Coxiella burnetii RSA 493]			
7943, 7944	53798300	61	2.00E-32	Chloroflexus aurantiacus	COG3945: ABC-type uncharacterized transport systems, ATPase components [Chloroflexus aurantiacus]			1.8.-.-
7945, 7946	48854975	56	2.00E-79	Cytophaga hutchinsonii	COG0247: Fe-S oxidoreductase [Cytophaga hutchinsonii]			1.3.99.1
7949, 7950	34558149	37	7.00E-44	Wolinella succinogenes DSM 1740	SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes DSM 1740] emb CAE10864.1 SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes]			2.7.3.-
7951, 7952	51573026	26	4.00E-15	Borrelia garinii PBI	conserved hypothetical protein [Borrelia garinii PBI] ref YP_072643.1 hypothetical protein BG0193 [Borrelia garinii PBI]			
7953, 7954	17227393	60	6.00E-61	Nostoc sp. PCC 7120	hypothetical protein air8019 [Nostoc sp. PCC 7120] pir AD2553 hypothetical protein air8019 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120gamma dbj BAB77349.1 ORF_ID:air8019-transposase-unknown protein [Nostoc sp. PCC 7120]			
7955, 7956	48854025	37	1.00E-16	Cytophaga hutchinsonii	hypothetical protein Chut02003116 [Cytophaga hutchinsonii]			
7957, 7958	29348766	45	1.00E-38	Bacteroides thetaiotaomicron VPI-5482	ribonuclease III [Bacteroides thetaiotaomicron VPI-5482] gb AAO78463.1 ribonuclease III [Bacteroides thetaiotaomicron VPI-5482]			3.1.26.3

7959, 7960	41205694	30	1.00E-26	Geobacillus stearothermophilus	putative rhamnosyltransferase [Geobacillus stearothermophilus] heme biosynthesis protein (nirJ-2) [Archaeoglobus fulgidus DSM 4304] gb AAB89245.1 heme biosynthesis protein (nirJ-2) [Archaeoglobus fulgidus DSM 4304] pir H69500 heme biosynthesis protein (nirJ-2) homolog - Archaeoglobus fulgidus				2.4.1.-	
7963, 7964	11499591	28	9.00E-10	Archaeoglobus fulgidus DSM 4304	putative response regulator receiver protein [Azoarcus sp. EbN1] emb CAI07934.1 putative response regulator receiver protein [Azoarcus sp. EbN1]					
7965, 7966	56477246	43	1.00E-26	Azoarcus sp. EbN1						
7967, 7968	34558196	32	7.00E-11	Wolinella succinogenes DSM 1740	DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes]					
7969, 7970	15927758	28	1.00E-08	Staphylococcus aureus subsp. aureus N315	hypothetical protein SA1980 [Staphylococcus aureus subsp. aureus N315] dbj BAB58340.1 conserved hypothetical protein [Staphylococcus aureus subsp. aureus Mu50] pir E90013 conserved hypothetical protein SA1980 [Imported] - Staphylococcus aureus (strain N315) dbj BAB43270.1 conserved hypothetical protein [Staphylococcus aureus subsp. aureus N315] ref NP_372702.1 hypothetical protein SAV2178 [Staphylococcus aureus subsp. aureus Mu50]					
7971, 7972	53730639	32	2.00E-16	Dechloromonas aromatica RCB	hypothetical protein Daro03001950 [Dechloromonas aromatica RCB]					
7973, 7974	56708496	61	4.00E-50	Francisella tularensis subsp. tularensis Schu 4	sugar transamine/perosamine synthetase [Francisella tularensis subsp. tularensis Schu 4] emb CAG46088.1 sugar transamine/perosamine synthetase [Francisella tularensis subsp. tularensis] gb AAS60273.1 perosamine synthetase [Francisella tularensis subsp. tularensis]					
7977, 7978	24374604	30	5.00E-26	Shewanella oneidensis MR-1	sensory box protein [Shewanella oneidensis MR-1] gb AAN56091.1 sensory box protein [Shewanella oneidensis MR-1]					
7979, 7980	24374604	81	1.00E-49	Shewanella oneidensis MR-1	sensory box protein [Shewanella oneidensis MR-1] gb AAN56091.1 sensory box protein [Shewanella oneidensis MR-1]			88	1.00E-21	
7981, 7982	15669217	50	9.00E-71	Methanocaldococ- us jannaschii DSM 2661	DNA topoisomerase VI, subunit B (top6B) [Methanocaldococcus jannaschii DSM 2661] gb AAB99032.1 DNA topoisomerase VI, subunit B (top6B) [Methanocaldococcus jannaschii DSM 2661] pir C64428 hypothetical protein MJ1028 - Methanocaldococcus jannaschii					5.99.1.3

7985, 7986	15612340	45	1.00E-48	Helicobacter pylori J99	PHOSPHATIDYL SERINE DECARBOXYLASE [Helicobacter pylori J99] sp Q9ZJN0 PSD_HELPJ Phosphatidylserine decarboxylase proenzyme [Contains: Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine decarboxylase beta chain] gb AAD06847.1				4.1.1.65
7987, 7988	30248124	31	1.00E-18	Nitrosomonas europaea ATCC 19718	PHOSPHATIDYL SERINE DECARBOXYLASE [Helicobacter pylori J99] pir J71628 phosphatidylserine decarboxylase (EC 4.1.1.65) precursor - Helicobacter pylori (strain J99)				
7993, 7994	31195897	43	7.00E-29	Anopheles gambiae	recQ; ATP-dependent DNA helicase [Nitrosomonas europaea ATCC 19718] emb CAD84004.1 recQ; ATP-dependent DNA helicase [Nitrosomonas europaea ATCC 19718]				3.6.1.-
7995, 7996	48857810	48	9.00E-66	Clostridium thermocellum	ENSANGP00000003278 [Anopheles gambiae]				3.4.13.9
7997, 7998	34557234	66	8.00E-77	Wolinella succinogenes DSM 1740	COG0249: Mismatch repair ATPase (MutS family) [Clostridium thermocellum ATCC 27405]				
7999, 8000	51246841	56	2.00E-32	Desulfotalea psychrophila LSV54	FDHD PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09949.1				
8003, 8004	57241759	41	3.00E-31	Campylobacter lari	FDHD PROTEIN [Wolinella succinogenes] related to molybdenum transport protein (ModE) [Desulfotalea psychrophila LSV54] emb CAG37718.1 related to molybdenum transport protein (ModE) [Desulfotalea psychrophila LSV54]				
8005, 8006	50085326	49	5.00E-25	Acinetobacter sp. ADP1	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54429.1 conserved hypothetical protein [Campylobacter lari RM2100]				
8007, 8008	15893643	34	7.00E-12	Clostridium acetobutylicum ATCC 824	hypothetical protein ACIAD2218 [Acinetobacter sp. ADP1] emb CAG69014.1 conserved hypothetical protein [Acinetobacter sp. ADP1]				
801, 802	15894734	29	7.00E-22	Clostridium acetobutylicum ATCC 824	Uncharacterized conserved membrane protein, SANA family [Clostridium acetobutylicum ATCC 824] gb AAK78332.1 Uncharacterized conserved membrane protein, SANA family [Clostridium acetobutylicum ATCC 824] pir J96943 uncharacterized conserved membrane protein, SANA family CAC0352 [Imported] - Clostridium acetobutylicum				
					Two-component system regulator (CheY domain and HTH-like DNA-binding domain) [Clostridium acetobutylicum ATCC 824] gb AAK79423.1 Two-component system regulator (CheY domain and HTH-like DNA-binding domain) [Clostridium acetobutylicum ATCC 824] pir J97079 two-component system regulator (CheY domain and HTH-like DNA-binding domain) [Imported] - Clostridium acetobutylicum				

8011, 8012	29345904	43	8.00E-42	Bacteroides thetaiotaomicron VPI-5482	protoporphyrin IX magnesium chelatase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75601.1 protoporphyrin IX magnesium chelatase [Bacteroides thetaiotaomicron VPI-5482]				
8013, 8014	34557313	50	3.00E-50	Wolinella succinogenes DSM 1740	ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10028.1 ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes]				1.8.-
8015, 8016	50914506	63	1.00E-64	Streptococcus pyogenes MGAS10394	Type II restriction-modification system methylation subunit [Streptococcus pyogenes MGAS10394] gb AAT87295.1 Type II restriction-modification system methylation subunit [Streptococcus pyogenes MGAS10394] gb AAT72355.1 methylase [Streptococcus pyogenes] gb AAR83196.1 type II modification methylase [Streptococcus pyogenes]	Bacteroides sp. 139 plasmid p139EF putative resolvase, putative C-5 cytosine-specific DNA methylase, putative HylD secretion protein, and putative ABC transporter protein genes, complete cds; and unknown gene	83	7.00E-12	2.1.1.73
8017, 8018	57238060	56	8.00E-69	Campylobacter jejuni RM1221	glucose inhibited division protein A [Campylobacter jejuni RM1221] gb AAW35643.1 glucose inhibited division protein A [Campylobacter jejuni RM1221]	Desc:Haemophilus influenzae DNA for cellular proliferation protein #11. Org:Haemophilus influenzae	89	6.00E-10	
8023, 8024	57234157	42	3.00E-51	Dehalococcoides ethenogenes 195	portal protein, HK97 family, putative [Dehalococcoides ethenogenes 195] gb AAW39662.1 portal protein, HK97 family, putative [Dehalococcoides ethenogenes 195]				
8025, 8026	15893941	46	7.00E-46	Clostridium acetobutylicum ATCC 824	Response regulator (CheY-like receiver domain and HTH DNA binding domain) [Clostridium acetobutylicum ATCC 824] gb AAK78630.1 Response regulator (CheY-like receiver domain and HTH DNA binding domain) [Clostridium acetobutylicum ATCC 824] pir C96980 response regulator (CheY-like receiver domain and HTH DNA binding domain) [imported] - Clostridium acetobutylicum				2.7.3.-
8029, 8030	34557593	44	4.00E-43	Wolinella succinogenes DSM 1740	hypothetical protein WS1227 [Wolinella succinogenes DSM 1740] emb CAE10308.1 hypothetical protein [Wolinella succinogenes] sp P59893 TRUD_WOLSU tRNA pseudouridine synthase D (Pseudouridylyl synthase) [Uracil hydrolyase]				

803, 804	48853695	59	6.00E-81	Cytophaga hutchinsonii	hypothetical protein Chut02003551 [Cytophaga hutchinsonii]				
8033, 8034	4838141	34	1.00E-23	Bacteroides fragilis	BatD [Bacteroides fragilis]				
8035, 8036	1488662	35	1.00E-10	Bacillus subtilis	phosphatase-associated protein [Bacillus subtilis] sp P54421 LYTE_BACSU Probable endopeptidase lytE precursor (Gamma-D-glutamate-meso- diaminopimelate mureopeptidase lytE) (Phosphatase-associated protein papQ) (Cell wall-associated polypeptide CWBP33)				
8037, 8038	57506273	59	6.00E-42	Campylobacter upsaliensis RM3195	Fic family protein [Campylobacter upsaliensis RM3195] gb EAL52255.1 Fic family protein [Campylobacter upsaliensis RM3195]				
8039, 8040	34557297	53	3.00E-28	Wolfinella succinogenes DSM 1740	PUTATIVE TRANSPORTER [Wolfinella succinogenes DSM 1740] emb CAE10012.1 PUTATIVE TRANSPORTER [Wolfinella succinogenes]				1.8.-
8043, 8044	34556770	36	4.00E-18	Wolfinella succinogenes DSM 1740	Putative Dethiobiotin synthetase [Wolfinella succinogenes DSM 1740] emb CAE09485.1 Putative Dethiobiotin synthetase [Wolfinella succinogenes]				6.3.3.3
8049, 8050	48856170	34	2.00E-09	Cytophaga hutchinsonii	COG1452: Organic solvent tolerance protein OstA [Cytophaga hutchinsonii]				
805, 806	21226435	60	6.00E-55	Methanosarcina mazel Go1	Methyl-accepting chemotaxis protein [Methanosarcina mazel Go1] gb AAM30029.1 Methyl-accepting chemotaxis protein [Methanosarcina mazel Go1]				
8051, 8052	48855476	52	7.00E-76	Cytophaga hutchinsonii	COG0437: Fe-S-cluster-containing hydrogenase components 1 [Cytophaga hutchinsonii]				1.2.7.-
8053, 8054	16080273	37	7.00E-10	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU32200 [Bacillus subtilis subsp. subtilis str. 168] emb CAB15210.1 yutJ [Bacillus subtilis subsp. subtilis str. 168] pir D70024 NADH dehydrogenase homolog yutJ - Bacillus subtilis				1.6.99.3
8059, 8060	53713209	45	1.00E-15	Bacteroides fragilis YCH46	hypothetical protein BF1919 [Bacteroides fragilis YCH46] dbj BAD48667.1 hypothetical protein [Bacteroides fragilis YCH46]				
8061, 8062	46143358	48	2.00E-30	Actinobacillus pleuropneumoniae serovar 1 str. 4074	COG0242: N-formylmethionyl-tRNA deformylase [Actinobacillus pleuropneumoniae serovar 1 str. 4074]				3.5.1.88
8065, 8066	34556591	46	4.00E-26	Wolfinella succinogenes DSM 1740	PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolfinella succinogenes DSM 1740] emb CAE09306.1 PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolfinella succinogenes]				4.2.1.70

8067, 8068	19699220	35	6.00E-34	Arabidopsis thaliana	At1g49820/F10F5_1 [Arabidopsis thaliana] gb AAL09753.1 At1g49820/F10F5_1 [Arabidopsis thaliana] gb AAG51775.1 unknown protein; 11341-13243 [Arabidopsis thaliana] pir A96535 unknown protein, 11341-13243 [imported] - Arabidopsis thaliana ref NP_564555.1 5- methylthioribose kinase family [Arabidopsis thaliana]				2.7.1.10 0
8069, 8070	48855291	41	1.00E-06	Cytophaga hutchinsonii	COG2919: Septum formation Initiator [Cytophaga hutchinsonii]				
8071, 8072	48864065	43	2.00E-22	Microbulbifer degradans 2-40	COG0328: Ribonuclease HI [Microbulbifer degradans 2-40]				
8073, 8074	48864040	38	1.00E-35	Microbulbifer degradans 2-40	hypothetical protein Mdeg02000406 [Microbulbifer degradans 2-40]				
8075, 8076	28854869	24	2.00E-17	Pseudomonas syringae pv. tomato str. DC3000	conserved hypothetical protein [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794236.1 hypothetical protein PSPTO4482 [Pseudomonas syringae pv. tomato str. DC3000]				
8079, 8080	13661984	30	5.00E-13	Rhizobium etli	LpeA [Rhizobium etli]				
8081, 8082	48855832	43	6.00E-48	Cytophaga hutchinsonii	hypothetical protein Chut02001044 [Cytophaga hutchinsonii]				
8085, 8086	34557849	41	6.00E-61	Wollinella succinogenes DSM 1740	INTEGRAL MEMBRANE PROTEIN-Small-conductance mechanosensitive channel [Wollinella succinogenes DSM 1740] emb CAE10564.1 INTEGRAL MEMBRANE PROTEIN-Small-conductance mechanosensitive channel [Wollinella succinogenes]				
8087, 8088	5091686	39	1.00E-40	Pediococcus pentosaceus	unknown [Pediococcus pentosaceus] ref NP_037556.1 unknown [Pediococcus pentosaceus]				
8091, 8092	16801535	37	4.00E-49	Listeria innocua Clp11262	hypothetical protein lin2473 [Listeria innocua Clp11262] emb CAC97700.1 lin2473 [Listeria innocua] pir AD1741 aspartate kinase homolog lin2473 [imported] - Listeria innocua (strain Clp11262)				2.7.2.4
8093, 8094	56707343	41	5.00E-19	Francisella tularensis subsp. tularensis Schu 4	Acetyltransferase [Francisella tularensis subsp. tularensis Schu 4] emb CAG44810.1 Acetyltransferase [Francisella tularensis subsp. tularensis]				2.3.1.12 8
8097, 8098	16330629	40	4.00E-11	Synechocystis sp. PCC 6803	hypothetical protein sil1411 [Synechocystis sp. PCC 6803] dbj BAA18037.1 sil1411 [Synechocystis sp. PCC 6803] pir S75476 hypothetical protein sil1411 - Synechocystis sp. (strain PCC 6803)				
8099, 8100	57241805	47	6.00E-12	Campylobacter lari RM2100	glutamyl-tRNA(Gln) amidotransferase, C subunit [Campylobacter lari RM2100] gb EAL54223.1 glutamyl-tRNA(Gln) amidotransferase, C subunit [Campylobacter lari RM2100]				2.7.7.- 6.3.5.-

81, 82	29346485	36	1.00E-29	Bacteroides thetaiotaomicron VPI-5482	putative two-component system sensor protein, but no histidine kinase domain [Bacteroides thetaiotaomicron VPI-5482] gblAAO76182.1 putative two-component system sensor protein, but no histidine kinase domain [Bacteroides thetaiotaomicron VPI-5482]				2.7.3.-
8101,	48854159	36	7.00E-28	Cytophaga hutchinsonii	COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii]				3.1.1.24
8103,	AAB1996								
8104	1	36	3.00E-09		Desc:Staphylococcus aureus 509RR protein. Org:Staphylococcus aureus				
8105,				Wolinella succinogenes DSM	hypothetical protein WS0414 [Wolinella succinogenes DSM 1740]				
8106	34556843	40	3.00E-41	1740	emb CAE09558.1 conserved hypothetical protein [Wolinella succinogenes]				2.7.3.-
8107,				Wolinella succinogenes DSM	PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR				
8108	34557235	49	1.00E-72	1740	[Wolinella succinogenes DSM 1740] emb CAE09950.1 PUTATIVE SELENOCYSTEINE-SPECIFIC ELONGATION FACTOR [Wolinella succinogenes]				3.6.1.48
8109,				Campylobacter jejuni RM1221	selenocysteine-specific elongation factor [Campylobacter jejuni RM1221]				
8110	57238422	44	7.00E-42		gb AAW36005.1 selenocysteine-specific elongation factor [Campylobacter jejuni RM1221]				
811,	ABU0070	33	7.00E-33		Desc:S. pneumoniae type 4 strain protein from coding region #273.				5.1.3.14
8112	57241386	45	5.00E-48	Campylobacter lari RM2100	Org:Streptococcus pneumoniae type 4 strain RNA methyltransferase, TrmH family, group 3 [Campylobacter lari RM2100]				
8113,				Bacteroides fragilis YCH46	gb AL54498.1 RNA methyltransferase, TrmH family, group 3 [Campylobacter lari RM2100]				2.1.1.-
8114	53714371	24	4.00E-15		putative ATPase involved in DNA repair [Bacteroides fragilis YCH46]				
8117,				Campylobacter upsaliensis RM3195	conserved hypothetical protein [Campylobacter upsaliensis RM3195]				
8118	57242699	51	1.00E-38		gb EAL53412.1 conserved hypothetical protein [Campylobacter upsaliensis RM3195]		80	9.00E-11	
8121,				Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449]				
8122	32261677	52	2.00E-41		ref NP_859661.1 hypothetical protein HH0130 [Helicobacter hepaticus ATCC 51449]		92	1.00E-10	
8123,				Campylobacter upsaliensis RM3195	response regulator, putative [Campylobacter upsaliensis RM3195]				
8124	57242734	37	3.00E-34		gb EAL53447.1 response regulator, putative [Campylobacter upsaliensis RM3195]				2.7.3.-
8125,				Geobacter metallireducens GS	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]				
8126	48846591	28	1.00E-16	15					2.7.3.-

8127, 8128	32262467	41	3.00E-17	51449	Helicobacter hepaticus ATCC	hypothetical protein HH0918 [Helicobacter hepaticus ref NP_860449.1 hypothetical protein HH0918 [Helicobacter hepaticus ATCC 51449]			
813, 814	21227977	53	4.00E-28	1740	Methanosarcina mazei Go1	hypothetical protein MM1875 [Methanosarcina mazei Go1] gb AAM31571.1 conserved protein [Methanosarcina mazei Goe1]			
8131, 8132	34557564	34	1.00E-20	1740	Wolinella succinogenes DSM	PUTATIVE MOLYBDOPTEIN BIOSYNTHESIS PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10279.1 PUTATIVE MOLYBDOPTEIN BIOSYNTHESIS PROTEIN [Wolinella succinogenes]			
8133, 8134	57504783	47	2.00E-13	RM2228	Campylobacter coli RM2228	probable molybdopterin biosynthesis protein Cj1519 [Campylobacter coli RM2228] gb EAL56045.1 probable molybdopterin biosynthesis protein Cj1519 [Campylobacter coli RM2228]			
8135, 8136	56750401	30	2.00E-16	6301	Synechococcus elongatus PCC	hypothetical protein syc0392_d [Synechococcus elongatus PCC 6301] db BAD78582.1 hypothetical protein [Synechococcus elongatus PCC 6301]			2.7.3.-
8137, 8138	45524550	35	6.00E-14	8501	Crocospaera watsonii WH 8501	hypothetical protein Cwat03005121 [Crocospaera watsonii WH 8501]			
8139, 8140	57168616	61	5.00E-77	RM2228	Campylobacter coli RM2228	MloA [Campylobacter coli RM2228] gb EAL56577.1 MloA [Campylobacter coli RM2228]	Campylobacter jejuni strain RM2240 HsdR (hsdR) gene, hsdR- 1 allele, complete cds; RloD (rloD) gene, complete cds; HsdS (hsdS) gene, hsdS-3 allele, complete cds; MloA (mloA) gene, complete cds; and HsdM (hsdM) gene, hsdM-1 allele, complete cds	85	2.00E-16

8143, 8144	57168973	72	1.00E-100	Campylobacter coli RM2228	sulfate adenylyltransferase, subunit 1/adenylylsulfate kinase [Campylobacter coli RM2228] gb EAL56328.1 sulfate adenylyltransferase, subunit 1/adenylylsulfate kinase [Campylobacter coli RM2228]	Campylobacter jejuni OH4384 peptide chain release factor 2 (prfB) gene, partial cds; alpha-2,3-sialyltransferase (cst-I), sulfate adenylyltransferase subunit CysD (cysD), sulfate adenylyltransferase subunit CysN (cysN), putative sodium/sulfate symporter (sodium sulfate symporter), putative adenylylsulfate kinase (cysC), hypothetical protein, putative glycosyltransferase, and hypothetical protein genes, complete cds; and cj1457c gene, partial cds	82	5.00E-32	2.7.7.4	
8149, 8150	56421524	29	9.00E-19	Geobacillus kaustophilus HTA426	transposase [Geobacillus kaustophilus HTA426] dbj BAD77274.1 transposase [Geobacillus kaustophilus HTA426]					
815, 816	18312740	28	1.00E-28	Pyrobaculum aerophilum str. IM2	aminopeptidase [Pyrobaculum aerophilum str. IM2] gb AAL63589.1 aminopeptidase [Pyrobaculum aerophilum str. IM2]					3.4.11.-
8151, 8152	ABP7901 3	54	1.00E-80		Desc.N. gonorrhoeae amino acid sequence SEQ ID 4556. Org:Neisseria gonorrhoeae					3.1.21.3
8153, 8154	16078046	47	3.00E-49	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU09810 [Bacillus subtilis subsp. subtilis str. 168] emb CAA74443.1 hypothetical protein [Bacillus subtilis] emb CAB12820.1 yhaZ [Bacillus subtilis subsp. subtilis str. 168] pir D69820 hypothetical protein yhaZ - Bacillus subtilis					

8159, 8160	34556772	58	1.00E-77	Wolinnella succinogenes DSM 1740	ENDOPEPTIDASE CLP ATP-BINDING CHAIN A [Wolinnella succinogenes DSM 1740] embjCAE09487.1] ENDOPEPTIDASE CLP ATP-BINDING CHAIN A [Wolinnella succinogenes]				
8161, 8162	11282475	39	1.00E-43	imported	hypothetical protein wblA [imported] - Vibrio cholerae dbj[BAA33632.1] probable beta-D-galactoside 2-alpha-L-fucosyl transferase [Vibrio cholerae] proline iminopeptidase, putative [Bacillus cereus ATCC 10987] gbjAAS40103.1] proline iminopeptidase, putative [Bacillus cereus ATCC 10987]				2.4.1.69
8163, 8164	42780248	32	2.00E-27	Bacillus cereus ATCC 10987	COG2065: Pyrimidine operon attenuation protein/uracil phosphoribosyltransferase [Cytophaga hutchinsonii] beta-galactosidase [Bacteroides thetaiotaomicron VPI-5482] gbjAAO76733.1] beta-galactosidase [Bacteroides thetaiotaomicron VPI-5482]				3.4.11.5
8165, 8166	48855920	36	1.00E-28	Cytophaga hutchinsonii	COG2172: Anti-sigma regulatory factor (Ser/Thr protein kinase) [Cytophaga hutchinsonii]				2.4.2.8
8167, 8168	29347036	35	3.00E-31	Bacteroides thetaitaomicron VPI-5482	16S rRNA processing protein RimM, putative [Campylobacter coli RM2228] gbjEAL57510.1] 16S rRNA processing protein RimM, putative [Campylobacter coli RM2228]				3.2.1.23
8169, 8170	48854029	31	5.00E-08	Cytophaga hutchinsonii	hypothetical protein WS1210 [Wolinnella succinogenes DSM 1740] embjCAE10292.1] conserved hypothetical protein [Wolinnella succinogenes]				
8171, 8172	57167724	43	4.00E-31	Campylobacter coli RM2228	Methyltransferase [Bacillus cereus ATCC 14579] gbjAAP11449.1] Methyltransferase [Bacillus cereus ATCC 14579]				
8177, 8178	34557577	36	5.00E-33	Wolinnella succinogenes DSM 1740	arginine repressor, transcriptional regulator of arginine metabolism [Bacteroides thetaiotaomicron VPI-5482] gbjAAO78867.1] arginine repressor, transcriptional regulator of arginine metabolism [Bacteroides thetaiotaomicron VPI-5482]				
8179, 8180	30022617	62	8.00E-30	Bacillus cereus ATCC 14579	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinnella succinogenes DSM 1740] embjCAE09961.1] SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinnella succinogenes]				2.7.3.-
8181, 8182	29349170	45	3.00E-17	Bacteroides thetaitaomicron VPI-5482	PUTATIVE TWO-COMPONENT SENSOR [Wolinnella succinogenes DSM 1740] embjCAE10497.1] PUTATIVE TWO-COMPONENT SENSOR [Wolinnella succinogenes]				2.7.3.-
8183, 8184	34557246	37	6.00E-53	Wolinnella succinogenes DSM 1740	COG1741: Pirin-related protein [Burkholderia fungorum LB400] Desc:Helicobacter pylori cellular proliferation protein #241. Org:Helicobacter pylori				
8185, 8186	34557782	45	3.00E-34	Wolinnella succinogenes DSM 1740	COG1544: Ribosome-associated protein Y (PSrp-1) [Moorella thermoacetica ATCC 39073]				4.6.1.4
8189, 820	48783002	49	9.00E-41	Burkholderia fungorum LB400					
8191, 8192	AAU3592 8	62	6.00E-46						
8193, 8194	49236237	51	1.00E-27	Moorella thermoacetica ATCC 39073					

8195, 8196	48846331	35	5.00E-37	15	Geobacter metallireducens GS	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]			2.7.3.-
8197, 8198	54308791	45	4.00E-41		Photobacterium profundum SS9	hypothetical ATP-dependent helicase [Photobacterium profundum SS9] emb CAG20009.1 hypothetical ATP-dependent helicase [Photobacterium profundum]			3.6.1.-
8199, 8200	32261920	55	2.00E-47	51449	Helicobacter hepaticus ATCC	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_859903.1 hypothetical protein HH0372 [Helicobacter hepaticus ATCC 51449]			2.6.1.17
8201, 8202	34556481	33	2.00E-44	1740	Wolinella succinogenes DSM	hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes]			
8203, 8204	17233315	39	4.00E-08	7120	Nostoc sp. PCC	hypothetical protein air7299 [Nostoc sp. PCC 7120] dbj BAB78383.1 air7299 [Nostoc sp. PCC 7120] pir JAC2515 hypothetical protein air7299 [Imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha			
8205, 8206	34556510	38	3.00E-40	1740	Wolinella succinogenes DSM	PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09225.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes]			
8207, 8208	48855393	32	8.00E-27		Cytophaga hutchinsonii	COG0665: Glycine/D-amino acid oxidases (deaminating) [Cytophaga hutchinsonii]			
821, 822	24371725	44	1.00E-22	oneidensis MR-1	Shewanella	hypothetical protein SO0125 [Shewanella oneidensis MR-1] gb AAN53212.1 conserved hypothetical protein [Shewanella oneidensis MR-1]			
8211, 8212	23129348	51	6.00E-69	PCC 73102	Nostoc punctiforme	COG4804: Uncharacterized conserved protein [Nostoc punctiforme PCC 73102]			
8213, 8214	34557912	41	8.00E-36	1740	Wolinella succinogenes DSM	hypothetical protein WS1588 [Wolinella succinogenes DSM 1740] emb CAE10627.1 conserved hypothetical protein [Wolinella succinogenes]			
8215, 8216	57241469	34	3.00E-14	RM2100	Campylobacter lari	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54581.1 conserved hypothetical protein [Campylobacter lari RM2100]			
8219, 8220	15605716	59	3.00E-33	VF5	Aquifex aeolicus	cytochrome c peroxidase [Aquifex aeolicus VF5] gb AAC06485.1 cytochrome c peroxidase [Aquifex aeolicus VF5] pir B70313 cytochrome-c peroxidase (EC 1.11.1.5) - Aquifex aeolicus			1.11.1.5

8221, 8222	21672563	46	2.00E-23	Buchnera aphidicola str. Sg (Schizaphis graminum)	hypothetical ABC transporter ATP-binding protein [Buchnera aphidicola str. Sg (Schizaphis graminum)] gb AAM67841.1 hypothetical ABC transporter ATP-binding protein [Buchnera aphidicola str. Sg (Schizaphis graminum)] sp Q44613 LOLD_BUCAP Lipoprotein releasing system ATP-binding protein [Buchnera aphidicola] pir I40068 probable ABC-type transport protein - Buchnera aphidicola prf 2107191B ORF C	1,8,-,-
8223, 8224	53728282	33	5.00E-11	Haemophilus somnus 2336	COG1396: Predicted transcriptional regulators [Haemophilus somnus 2336] ref ZP_00123339.1 COG1396: Predicted transcriptional regulators [Haemophilus somnus 129PT]	
8225, 8226	19705186	33	8.00E-11	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	Esterase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL93980.1 Esterase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]	3,-,-,-
8227, 8228	57236803	50	7.00E-19	Flavobacterium johnsoniae	SecDF [Flavobacterium johnsoniae] peptidase (M20/M25/M40 family) [Xylella fastidiosa Temecula1] gb AAO29682.1 peptidase (M20/M25/M40 family) [Xylella fastidiosa Temecula1]	
823, 824	28199719	33	2.00E-25	Xylella fastidiosa Temecula1	DNA mismatch repair ATPase MutS [Mimivirus] gb AAV50628.1 DNA mismatch repair ATPase MutS [Mimivirus]	3,4,17,2 1
8235, 8236	55819234	22	2.00E-09	Mimivirus	COG0726: Predicted xylanase/chitin deacetylase [Geobacter metallireducens GS-15]	3,5,1,- 3,4,17,2 1
8237, 8238	48847340	47	4.00E-37	Geobacter metallireducens GS-15	COG2234: Predicted aminopeptidases [Cytophaga hutchinsonii]	
8241, 8242	48854772	41	1.00E-52	Cytophaga hutchinsonii	COG1775: Benzoyl-CoA reductase/2-hydroxyglutaryl-CoA dehydratase subunit, BcrC/BadH/HgdB [Magnetospirillum magnetotacticum MS-1]	
8243, 8244	46202765	44	3.00E-19	Magnetospirillum magnetotacticum MS-1	short-chain alcohol dehydrogenase family [Synechocystis sp. PCC 6803] dbj BAA17390.1 short-chain alcohol dehydrogenase family [Synechocystis sp. PCC 6803] pir IS77543 short-chain alcohol dehydrogenase-related protein, 72K - Synechocystis sp. (strain PCC 6803)	1,-,-,-
8249, 8250	16329982	43	2.00E-34	Synechocystis sp. PCC 6803	hydrogenase expression/information protein HypA [Shewanella oneidensis MR-1] gb AAN55136.1 hydrogenase expression/information protein HypA [Shewanella oneidensis MR-1]	
8251, 8252	24373649	57	4.00E-31	Shewanella oneidensis MR-1	thymidylate kinase [Picrophilus torridus DSM 9790] gb AAT44007.1 thymidylate kinase [Picrophilus torridus DSM 9790]	
8255, 8256	48478494	30	3.00E-13	Picrophilus torridus DSM 9790		

8257, 8258	53712165	40	1.00E-47	Bacteroides fragilis YCH46	Trk system K+ uptake protein TrkA [Bacteroides fragilis YCH46] dbj BAD47623.1 Trk system K+ uptake protein TrkA [Bacteroides fragilis YCH46]				
8259, 8260	53711484	30	6.00E-12	Bacteroides fragilis YCH46	hypothetical protein BF0193 [Bacteroides fragilis YCH46] dbj BAD46942.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
8261, 8262	52007843	48	6.00E-32	Thiobacillus denitrificans ATCC 25259	COG0607: Rhodanese-related sulfurtransferase [Thiobacillus denitrificans ATCC 25259]				
8263, 8264	42523774	35	2.00E-38	Bdellovibrio bacteriovorus HD100	HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] emb CAE80147.1 HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100]				
8265, 8266	48861439	33	1.00E-22	Microbulbifer degradans 2-40	hypothetical protein Mdeg02003392 [Microbulbifer degradans 2-40] hypothetical protein DP0517 [Desulfotalea psychrophila LSV54] emb CAG35246.1 conserved hypothetical protein [Desulfotalea psychrophila LSV54]				
8269, 8270	51244369	21	6.00E-17	Desulfotalea psychrophila LSV54	Desc:Acetobacter turbidans alpha-amino ester hydrolase protein #5. Org:Acetobacter turbidans				
827, 828	AAE3396	5	2.00E-10						
8271, 8272	48856045	21	8.00E-09	Cytophaga hutchinsonii	hypothetical protein Chut02001277 [Cytophaga hutchinsonii] hypothetical carboxypeptidase G2 [Photobacterium profundum SS9] emb CAG22583.1 hypothetical carboxypeptidase G2 [Photobacterium profundum]				3.4.17.1 1
8273, 8274	54302390	52	3.00E-53	Photobacterium profundum SS9	NADH-ubiquinone dehydrogenase chain E 1 [Mesorhizobium loti MAFF303099] dbj BAB48755.1 NADH-ubiquinone dehydrogenase chain E 1 [Mesorhizobium loti MAFF303099]				1.6.5.3
8277, 8278	13471403	40	2.00E-12	Mesorhizobium loti MAFF303099	HD_GYP hydrolase domain fused to HD hydrolase domain [Clostridium acetobutylicum ATCC 824] gb AAK80486.1 HD_GYP hydrolase domain fused to HD hydrolase domain [Clostridium acetobutylicum ATCC 824] pir C97212 HD_GYP hydrolase domain fused to HD hydrolase domain [imported] - Clostridium acetobutylicum				
8279, 8280	15895797	44	8.00E-39	Clostridium acetobutylicum ATCC 824	conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_230490.1 hypothetical protein VC0842 [Vibrio cholerae O1 biovar eltor str. N16961] gb AAK20799.1 unknown [Vibrio cholerae] gb AAK20769.1 unknown [Vibrio cholerae] pir G82273 conserved hypothetical protein VC0842 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				
8281, 8282	9655294	32	1.00E-12	Vibrio cholerae O1 biovar eltor str. N16961	conjugative transposon protein TraG, putative [Campylobacter upsaliensis RM3195] gb EAL52545.1 conjugative transposon protein TraG, putative [Campylobacter upsaliensis RM3195]				
8283, 8284	57505955	52	2.00E-38	Campylobacter upsaliensis RM3195					

8285, 8286	57505955	36	8.00E-32	Campylobacter upsaliensis RM3195	conjugative transposon protein TraG, putative [Campylobacter upsaliensis RM3195] gb EAL52545.1 conjugative transposon protein TraG, putative [Campylobacter upsaliensis RM3195]			
8287, 8288	34557851	31	2.00E-34	Wolinella succinogenes DSM 1740	hypothetical protein WS1518 [Wolinella succinogenes DSM 1740] emb CAE10566.1 conserved hypothetical protein [Wolinella succinogenes]			
8289, 8290	50120714	64	5.00E-42	Erwinia carotovora subsp. atroseptica SCRI1043	rhodanese-like protein [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG74886.1 rhodanese-like protein [Erwinia carotovora subsp. atroseptica SCRI1043]			
829, 830	48895464	31	1.00E-26	Trichodesmium erythraeum IMS101	COG0463: Glycosyltransferases involved in cell wall biogenesis [Trichodesmium erythraeum IMS101]			2.4.1.83
8291, 8292	57236963	47	4.00E-29	Campylobacter jejuni RM1221	GTP-binding protein [Campylobacter jejuni RM1221] gb AAW34546.1 GTP- binding protein [Campylobacter jejuni RM1221]			
8293, 8294	54309817	70	1.00E-32	Photobacterium profundum SS9	putative UDP-glucose dehydrogenase [Photobacterium profundum SS9] emb CAG21035.1 putative UDP-glucose dehydrogenase [Photobacterium profundum]	Escherichia coli kpsS, kfoG, kfoF, kfoE, kfoD, kfoS, kfoC, kfoB, kfoA, kpsT genes for KpsS hypothetical protein, predicted glycosyltransferase, UDP-glucose dehydrogenase, KfoE hypothetical protein, KfoD hypothetical protein, IS hypothetical protein, chondroitin polymerase, KfoB hypothetical protein, UDP-glucose 4- epimerase, ABC transporter, partial and complete cds	84	2.00E-07/1.1.1.22

8295, 8296	34556483	67	7.00E-49	Wolinella succinogenes DSM 1740	PUTATIVE UDP-GLUCURONIC ACID EPIMERASE [Wolinella succinogenes DSM 1740] emb CAE09198.1 PUTATIVE UDP- GLUCURONIC ACID EPIMERASE [Wolinella succinogenes]			5.1.3.-
8297, 8298	53715387	58	1.00E-92	Bacteroides fragilis YCH46	ABC transporter ATP-binding protein [Bacteroides fragilis dbj BAD50845.1 ABC transporter ATP-binding protein [Bacteroides fragilis YCH46]			1.8.-.-
8299, 8300	53715387	43	4.00E-19	Bacteroides fragilis YCH46	ABC transporter ATP-binding protein [Bacteroides fragilis YCH46] dbj BAD50845.1 ABC transporter ATP-binding protein [Bacteroides fragilis YCH46]			
83. 84	32474477	27	5.00E-08	Rhodopirellula baltica SH 1	hypothetical protein-transmembrane prediction [Rhodopirellula baltica SH 1] emb CAD75017.1 hypothetical protein-transmembrane prediction [Pirellula sp.]			
8305, 8306	26988521	60	3.00E-71	Pseudomonas putida KT2440	acyneuraminase cytidyltransferase, putative [Pseudomonas putida KT2440] gb AAN67410.1 acylneuraminase cytidyltransferase, putative [Pseudomonas putida KT2440]			2.7.7.43
8307, 8308	18310494	29	4.00E-25	Clostridium perfringens str. 13	two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13] dbj BAB81218.1 two-component sensor histidine kinase/response regulator [Clostridium perfringens str. 13]			
8309, 8310	48854548	35	8.00E-46	Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]			
831, 832	55380037	28	1.00E-06	Haloarcula marismortui ATCC 43049	probable translation initiation factor 2 alpha subunit [Haloarcula marismortui ATCC 43049] gb AAV48181.1 probable translation initiation factor 2 alpha subunit [Haloarcula marismortui ATCC 43049]			
8311, 8312	45528473	37	3.00E-37	Crocospaera watsonii WH 8501	COG0457: FOG: TPR repeat [Crocospaera watsonii WH 8501]			5.2.1.8
8313, 8314	29349210	41	6.00E-32	Bacteroides thetaiotaomicron VPI-5482	peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Bacteroides thetaiotaomicron VPI-5482] gb AAO78907.1 peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Bacteroides thetaiotaomicron VPI-5482]			5.2.1.8
8315, 8316	34557362	37	3.00E-15	Wolinella succinogenes DSM 1740	TWO-COMPONENT HYBRID PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10077.1 TWO-COMPONENT HYBRID PROTEIN [Wolinella succinogenes]			2.7.3.-
8317, 8318	34556704	49	3.00E-36	Wolinella succinogenes DSM 1740	hypothetical protein WS0265 [Wolinella succinogenes DSM 1740] emb CAE09419.1 conserved hypothetical protein [Wolinella succinogenes]			3.6.1.13
8319, 8320	48832341	31	6.00E-17	Magnetococcus sp. MC-1	COG0842: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			
8321, 8322	34557444	49	6.00E-44	Wolinella succinogenes DSM 1740	hypothetical protein WS1061 [Wolinella succinogenes DSM 1740] emb CAE10159.1 conserved hypothetical protein [Wolinella succinogenes]			

8323, 8324	57241252	45	1.00E-34	Campylobacter lari RM2100	signal-transducing protein, histidine kinase [Campylobacter lari RM2100] gb EAL54948.1 signal-transducing protein, histidine kinase [Campylobacter lari RM2100]			2.7.3.-
8327, 8328	34557494	41	1.00E-53	Wolinella succinogenes DSM 1740	PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes DSM 1740] emb CAE10209.1 PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes]			6.3.4.6
8329, 8330, 8331, 8332	21673303	43	3.00E-55	Chlorobium tepidum TLS	hypothetical protein CT0467 [Chlorobium tepidum TLS] gb AAM71710.1 conserved hypothetical protein [Chlorobium tepidum TLS]			
8333, 8334	48856395	58	5.00E-51	Cytophaga hutchinsonii	COG0327: Uncharacterized conserved protein [Cytophaga hutchinsonii]			
8331, 8332	57505714	42	2.00E-29	Campylobacter upsallensis RM3195	AVG-specific adenine glycosylase [Campylobacter upsallensis RM3195] gb EAL52775.1 AVG-specific adenine glycosylase [Campylobacter upsallensis RM3195]			3.2.2.-
8335, 8336	34557297	55	2.00E-30	Wolinella succinogenes DSM 1740	PUTATIVE TRANSPORTER [Wolinella succinogenes DSM 1740] emb CAE10012.1 PUTATIVE TRANSPORTER [Wolinella succinogenes]			1.8.-
8337, 8338	57240764	44	3.00E-32	Campylobacter lari RM2100	proline dipeptidase TC0863 [Campylobacter lari RM2100] gb EAL55157.1 proline dipeptidase TC0863 [Campylobacter lari RM2100]			3.4.11.9
8339, 8340	34556556	31	2.00E-21	Wolinella succinogenes DSM 1740	POSSIBLE PHOSPHATASE [Wolinella succinogenes DSM 1740] emb CAE0927.1 POSSIBLE PHOSPHATASE [Wolinella succinogenes]			3.6.1.11
8341, 8342	53691630	50	3.00E-74	Desulfovibrio desulfuricans G20	COG1109: Phosphomannomutase [Desulfovibrio desulfuricans G20]			5.4.2.8
8343, 8344	53736033	47	4.00E-72	Crocospaera watsonii WH 8501	COG0488: ATPase components of ABC transporters with duplicated ATPase domains [Crocospaera watsonii WH 8501]			1.8.-
8347, 8348	57237455	43	5.00E-30	Campylobacter jejuni RM1221	ferric uptake regulation protein [Campylobacter jejuni RM1221] gb AAW35038.1 ferric uptake regulation protein [Campylobacter jejuni RM1221]			
8349, 8350	48863156	35	7.00E-15	Microbulbifer degradans 2-40	COG4067: Uncharacterized protein conserved in archaea [Microbulbifer degradans 2-40]			
8355, 8356	29349761	65	1.00E-106	Bacteroides thetaiotaomicron VPI-5482	valyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79458.1 valyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI- 5482]			6.1.1.9
8357, 8358	48844990	62	1.00E-104	Geobacter metallireducens GS-15	COG0365: Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases [Geobacter metallireducens GS-15]			6.2.1.1
8359, 8360	23007833	34	1.00E-06	Magnetospirillum magnetotacticum MS-1	COG1409: Predicted phosphohydrolases [Magnetospirillum magnetotacticum MS-1]			

8363, 8364	48855923	32	1.00E-24	Cytophaga hutchinsonii	COG2812: DNA polymerase III, gamma/tau subunits [Cytophaga hutchinsonii]			2.7.7.7
8367, 8368	39933606	26	6.00E-15	Rhodopseudomonas palustris CGA009	putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) [Rhodopseudomonas palustris CGA009] emb[CAE25973.1] putative diguanylate cyclase (GGDEF)/phosphodiesterase (EAL) [Rhodopseudomonas palustris CGA009]			
8369, 8370	34556462	72	2.00E-46	Wolinella succinogenes DSM 1740	hypothetical protein WS0003 [Wolinella succinogenes DSM 1740] emb[CAE09177.1] conserved hypothetical protein [Wolinella succinogenes]			
837, 838	48856607	46	2.00E-48	Cytophaga hutchinsonii	COG1321: Mn-dependent transcriptional regulator [Cytophaga hutchinsonii] oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter lari RM2100] gb[EA54833.1] oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter lari RM2100]			1.---
8373, 8374	57241137	45	5.00E-48	Campylobacter lari RM2100	hypothetical protein WS1876 [Wolinella succinogenes DSM 1740] emb[CAE10886.1] conserved hypothetical protein [Wolinella succinogenes]			
8375, 8376	34558171	32	7.00E-21	Wolinella succinogenes DSM 1740	hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb[CAE09196.1] conserved hypothetical protein [Wolinella succinogenes]			
8377, 8378	34556481	30	5.00E-36	Wolinella succinogenes DSM 1740	orf, hypothetical protein [Escherichia coli O157:H7] ref NP_286822.1 hypothetical protein Z1297 [Escherichia coli O157:H7 EDL933] ref NP_309058.1 hypothetical protein ECs1031 [Escherichia coli O157:H7] pir [E85621] hypothetical protein Z1297 [imported] - Escherichia coli (strain O157:H7, substrain EDL933) dbj BA34454.1 hypothetical protein [Escherichia coli O157:H7] pir [G90757] hypothetical protein ECs1031 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952) ABC transporter, ATP-binding protein/permease protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AA595497.1 ABC transporter, ATP-binding protein/permease protein [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			3.4.21.-
8381, 8382	12514126	40	2.00E-51	Escherichia coli O157:H7	oligopeptidase [Gloeobacter violaceus PCC 7421] dbj BAC88070.1 oligopeptidase [Gloeobacter violaceus PCC 7421]			3.4.21.8 3
8385, 8386	46579430	43	2.00E-39	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	hypothetical protein BL02075 [Bacillus licheniformis ATCC 14580] gb AAU40965.1] conserved hypothetical protein [Bacillus licheniformis DSM 133]			
8387, 8388	37519698	58	1.00E-84	Gloeobacter violaceus PCC 7421	general glycosylation pathway protein [Campylobacter jejuni RM1221] gb AAW35584.1] general glycosylation pathway protein [Campylobacter jejuni RM1221]			
8389, 8390	52785829	39	1.00E-44	Bacillus licheniformis ATCC 14580				
8389, 8390	57238001	36	2.00E-25	Campylobacter jejuni RM1221				

839, 840	15679035	30	6.00E-23	Methanothermobacter thermautotrophicus str. Delta H	hypothetical protein MTH1017 [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85513.1] conserved protein [Methanothermobacter thermautotrophicus str. Delta H] pir JF69002 conserved hypothetical protein MTH1017 - Methanothermobacterium thermoautotrophicum (strain Delta H) sp O27096[GCH3_METTH GTP cyclohydrolase III]				
8391, 8392	53712294	53	3.00E-66	Bacteroides fragilis YCH46	putative glycogen synthase [Bacteroides fragilis YCH46] dbj BAD47752.1] putative glycogen synthase [Bacteroides fragilis YCH46]				2.4.1.21
8395, 8396	28555201	44	1.00E-21	Pseudomonas syringae pv. tomato str. DC3000	sensory box histidine kinase [Pseudomonas syringae pv. tomato str. DC3000] ref NP_794567.1] sensory box histidine kinase [Pseudomonas syringae pv. tomato str. DC3000]				2.7.3.-
8399, 8400	16330855	49	6.00E-10	Synechocystis sp. PCC 6803	cytochrome b6/f complex iron-sulfur subunit [Synechocystis sp. PCC 6803] dbj BAA18263.1] cytochrome b6/f complex iron-sulfur subunit [Synechocystis sp. PCC 6803] pir J575804 plastocyanin reductase (EC 1.10.99.1) Rieske iron-sulfur protein patC - Synechocystis sp. (strain PCC 6803)				1.10.99. 1
8405, 8406	57241290	56	2.00E-23	Campylobacter lari RM2100	Uncharacterized BCR, YoeG family COG1559 [Campylobacter lari RM2100] gb EAL54986.1] Uncharacterized BCR, YoeG family COG1559 [Campylobacter lari RM2100]				4.-.-
8407, 8408	32034341	33	1.00E-15	Actinobacillus pleuropneumoniae serovar 1 str. 4074	COG0357: Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division [Actinobacillus pleuropneumoniae serovar 1 str. 4074]				
8409, 8410	28275200	55	2.00E-37	Shewanella oneidensis MR-1	hypothetical cheY-homologous receiver domain protein [Shewanella oneidensis MR-1]				2.7.3.-
8411, 8412	57240902	42	1.00E-32	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55295.1] conserved hypothetical protein [Campylobacter lari RM2100]				
8413, 8414	34557024	56	6.00E-84	Wolinella succinogenes DSM 1740	PROTEASE [Wolinella succinogenes DSM 1740] emb CAE09739.1] PROTEASE [Wolinella succinogenes]				3.4.21.-
8415, 8416	16077746	47	8.00E-55	Bacillus subtilis subsp. subtilis str. 168	hypothetical protein BSU06780 [Bacillus subtilis subsp. subtilis str. 168] emb CAB12498.1] yeeC [Bacillus subtilis subsp. subtilis str. 168] gb AAB66476.1] YeeC [Bacillus subtilis] pir G69792 hypothetical protein yeeC - Bacillus subtilis				
8417, 8418	41689105	60	8.00E-35	Psychrobacter sp. 273-4	COG0178: Excinuclease ATPase subunit [Psychrobacter sp. 273-4]				

8419, 8420	42528141	51	4.00E-62	Treponema denticola ATCC 35405	Fic family protein [Treponema denticola ATCC 35405] gb AAS13158.1 Fic family protein [Treponema denticola ATCC 35405]	Fusobacterium nucleatum subsp. nucleatum ATCC 25586, section 146 of 197 of the complete genome	90	1.00E-10	
8421, 8422	56416014	78	3.00E-72	Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150	putative pseudouridine synthase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150] gb AAV79777.1 putative pseudouridine synthase [Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150]			4.2.1.70	
8427, 8428	23472302	24	9.00E-18	Pseudomonas syringae pv. syringae B728a	COG0385: Predicted Na ⁺ -dependent transporter [Pseudomonas syringae pv. syringae B728a]				
8429, 8430	58422018	63	6.00E-71	Geobacillus kaustophilus HTA426	hypothetical protein GK3483 [Geobacillus kaustophilus HTA426] db BAD77768.1 hypothetical conserved protein [Geobacillus kaustophilus HTA426]	Fusobacterium nucleatum subsp. nucleatum ATCC 25586, section 183 of 197 of the complete genome	##	2.00E-09	
8431, 8432	29844552	50	5.00E-32	Aquifex aeolicus VF5	putative protein [Aquifex aeolicus VF5] ref NP_046399.1 hypothetical protein aq_aa03 [Aquifex aeolicus VF5] sp O66399 YZ03_AQUAE Hypothetical protein AA03				
8433, 8434	39998400	40	5.00E-48	Geobacter sulfurreducens PCA	hypothetical protein GSU3311 [Geobacter sulfurreducens PCA] gb AAR36701.1 hypothetical protein GSU3311 [Geobacter sulfurreducens PCA]				
8435, 8436	46119952	24	5.00E-16	Crocospaera watsonii WH 8501	COG2319: FOG: WD40 repeat [Crocospaera watsonii WH 8501] cytochrome c family protein, putative [Geobacter sulfurreducens PCA]			2.7.1.37	
8437, 8438	39998517	33	1.00E-13	Geobacter sulfurreducens PCA	gb AAR36818.1 cytochrome c family protein, putative [Geobacter sulfurreducens PCA]				
8439, 8440	29348769	51	2.00E-26	Bacteroides thetaiotaomicron VPI-5482	phosphoribosylglycinamide formyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76466.1 phosphoribosylglycinamide formyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.1.2.2	
8441, 8442	51245405	36	2.00E-27	Desulfotalea psychrophila LSV54	hypothetical protein DP1553 [Desulfotalea psychrophila LSV54] emb CAG36282.1 unknown protein [Desulfotalea psychrophila LSV54]				
8443, 8444	48113481	31	5.00E-27	Exiguobacterium sp. 255-15	COG1459: Type II secretory pathway, component PulF [Exiguobacterium sp. 255-15]				

8445, 8446	34557014	41	4.00E-57	Wollinella succinogenes DSM 1740	hypothetical protein WS0597 [Wollinella succinogenes DSM 1740] emb CAE09729.1 conserved hypothetical protein [Wollinella succinogenes]			
8447, 8448	28974235	37	2.00E-33	Campylobacter fetus	putative putative two-component sensor Cf0035 [Campylobacter fetus]			2.7.3.-
8449, 8450	38637719	23	2.00E-08	Cupriavidus necator	hypothetical protein PHG054 [Cupriavidus necator] gb AAP85807.1			
845, 846	15966356	31	5.00E-45	Sinorhizobium meliloti 1021	PUTATIVE OXIDOREDUCTASE PROTEIN [Sinorhizobium meliloti 1021] emb CAC47182.1 PUTATIVE OXIDOREDUCTASE PROTEIN [Sinorhizobium meliloti]			1.1.1.-
8451, 8452	29346992	42	6.00E-41	Bacteroides thetaiotaomicron VPI-5482	putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76689.1 putative methyltransferase [Bacteroides thetaiotaomicron VPI-5482]			
8453, 8454	34557573	35	5.00E-35	Wollinella succinogenes DSM 1740	SENSORY BOX/GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wollinella succinogenes]			2.7.3.-
8455, 8456	2314726	38	3.00E-44	Helicobacter pylori 26695	folypolyglutamate synthase (folC) [Helicobacter pylori 26695] ref NP_208336.1 folypolyglutamate synthase (folC) [Helicobacter pylori 26695] pir A64713 folypolyglutamate synthase - Helicobacter pylori (strain 26695)			6.3.2.17
8457, 8458	34556481	48	7.00E-48	Wollinella succinogenes DSM 1740	hypothetical protein WS0023 [Wollinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wollinella succinogenes]			2.7.3.-
8459, 8460	23897238	50	4.00E-67	Aeromonas salmonicida subsp. salmonicida	putative transposase [Aeromonas salmonicida subsp. salmonicida] ref NP_710165.1 putative transposase [Aeromonas salmonicida subsp. salmonicida]			
8461, 8462	29348968	42	2.00E-15	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT3559 [Bacteroides thetaiotaomicron VPI-5482] gb AAO78665.1 conserved hypothetical protein [Bacteroides thetaiotaomicron VPI-5482]			
8467, 8468	53758726	37	7.00E-33	Methylococcus capsulatus str. Bath	oxygen-independent coproporphyrinogen III oxidase family protein, putative [Methylococcus capsulatus str. Bath] ref YP_113360.1 oxygen-independent coproporphyrinogen III oxidase family protein, putative [Methylococcus capsulatus str. Bath]			
8469, 8470	26990982	27	3.00E-08	Pseudomonas putida KT2440	hypothetical protein PP4291 [Pseudomonas putida KT2440] gb AAN6987.1.1 conserved hypothetical protein [Pseudomonas putida KT2440]			
847, 848	48854395	52	4.00E-37	Cytophaga hutchinsonii	COG3832: Uncharacterized conserved protein [Cytophaga hutchinsonii]			
8473, 8474	48855757	44	7.00E-39	Cytophaga hutchinsonii	COG4772: Outer membrane receptor for Fe3+-dicitrate [Cytophaga hutchinsonii]			

8475, 8476	17938356	66	1.00E-104	C58	Agrobacterium tumefaciens str. C58	ABC transporter, nucleotide binding/ATPase protein [Agrobacterium tumefaciens str. C58] gb AAL45461.1 ABC transporter, nucleotide binding/ATPase protein [Agrobacterium tumefaciens str. C58] pir AG3130 hypothetical protein Atu4667 [imported] - Agrobacterium tumefaciens (strain C58; Dupont)	Pasteurella multocida subsp. multocida str. Pm70 section 201 of 204 of the complete genome	87	4.00E-08	1.8--
8477, 8478	29346178	41	9.00E-27	VPI-5482	Bacteroides thetaiotaomicron VPI-5482	putative para-aminobenzoate synthase component I [Bacteroides thetaiotaomicron VPI-5482] gb AAO75875.1 putative para-aminobenzoate synthase component I [Bacteroides thetaiotaomicron VPI-5482]				4.---
8479, 8480	18310884	28	8.00E-10	perfringens str. 13	Clostridium perfringens str. 13	hypothetical protein CPE1902 [Clostridium perfringens str. 13] dbj BAB81608.1 conserved hypothetical protein [Clostridium perfringens str. 13]				
8481, 8482	24374626	50	3.00E-45	MR-1	Shewanella oneidensis MR-1	hypothetical protein SO3107 [Shewanella oneidensis MR-1] gb AAN56113.1 conserved hypothetical protein [Shewanella oneidensis MR-1]				
8483, 8484	48864371	22	3.00E-08	degradans 2-40	Microbulbifer degradans 2-40	COG0541: Signal recognition particle GTPase [Microbulbifer degradans 2- 40]				
8487, 8488	53715793	50	3.00E-40	YCH46	Bacteroides fragilis YCH46	FKBP-type peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46] dbj BAD51251.1 FKBP-type peptidyl-prolyl cis-trans isomerase [Bacteroides fragilis YCH46]				5.2.1.8
8489, 8490	54030565	46	6.00E-30	JS666	Polaromonas sp. JS666	COG2030: Acyl dehydratase [Polaromonas sp. JS666]				
849, 850	54030565	46	6.00E-30	JS666		Desc: Human carbamyl phosphate synthase protein. Org: Homo sapiens				3.5.2.3
8493, 8494	5739402	48	3.00E-34	Johnstoniae	Flavobacterium Johnstoniae	TruB [Flavobacterium johnsoniae] sp Q9RB36 TRUB_CYTJO tRNA pseudouridine synthase B (tRNA pseudouridine 55 synthase) (Psi55 synthase) [Pseudouridylyl synthase] (Uracil hydrolyase)				4.2.1.70
85, 86	48854525	67	1.00E-102	hutchinsonii	Cytophaga hutchinsonii	COG0143: Methionyl-tRNA synthetase [Cytophaga hutchinsonii]				6.1.1.10
8501, 8502	34557661	50	1.00E-34	1740	Wolinella succinogenes DSM 1740	hypothetical protein WS1299 [Wolinella succinogenes DSM 1740] emb CAE10376.1 hypothetical protein [Wolinella succinogenes]				
8507, 8508	29348887	36	9.00E-19	VPI-5482	Bacteroides thetaiotaomicron VPI-5482	integrase [Bacteroides thetaiotaomicron VPI-5482] gb AAO78584.1 integrase [Bacteroides thetaiotaomicron VPI-5482]				
8509, 8510	29346738	36	6.00E-17	VPI-5482	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BT1328 [Bacteroides thetaiotaomicron VPI-5482] gb AAO76435.1 hypothetical protein [Bacteroides thetaiotaomicron VPI- 5482]				

851, 852	42523143	39	1.00E-19	Bdellovibrio bacteriovorus HD100	hypothetical protein Bd1641 [Bdellovibrio bacteriovorus HD100] emb CAE79516.1 conserved hypothetical protein [Bdellovibrio bacteriovorus HD100]			
8513, 8514	AAW9831 1	35	1.00E-28		Desc:H. pylori GHPO 881 protein. Org:Helicobacter pylori			
8515, 8516	29350071	39	1.00E-47	Bacteroides thetaiotaomicron VPI-5482	two-component system sensor histidine kinase/response [Bacteroides thetaiotaomicron VPI-5482] gb AAO79768.1 two-component system sensor histidine kinase/response [Bacteroides thetaiotaomicron VPI-5482]			2.7.3.-
8517, 8518	23129857	48	5.00E-23	Nostoc punctiforme PCC 73102	COG3920: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102]			2.7.3.-
8519, 8520	48862078	42	3.00E-30	Microbulbifer degradans 2-40	COG2162: Arylamine N-acetyltransferase [Microbulbifer degradans 2-40]			2.3.1.11 8
8521, 8522	34557352	27	3.00E-07	Wolinella succinogenes DSM 1740	hypothetical protein WS0964 [Wolinella succinogenes DSM 1740] emb CAE10067.1 conserved hypothetical protein [Wolinella succinogenes]			
8523, 8524	48854031	54	4.00E-86	Cytophaga hutchinsonii	COG0445: NAD/FAD-utilizing enzyme apparently involved in cell division [Cytophaga hutchinsonii]	Desc:Mycoplasma genitalium genome. Org:Mycoplasma genitalium	86	4.00E-11
8525, 8526	39935542	32	4.00E-32	Rhodopseudomonas palustris CGA009	putative diguanylate cyclase (GGDEF) [Rhodopseudomonas palustris CGA009] emb CAE27917.1 putative diguanylate cyclase (GGDEF) [Rhodopseudomonas palustris CGA009]			2.7.3.-
8527, 8528	28898100	33	5.00E-17	Vibrio parahaemolyticus RIMD 2210633	hypothetical protein VP1326 [Vibrio parahaemolyticus RIMD 2210633] db BAC59589.1 hypothetical protein [Vibrio parahaemolyticus]			
8529, 8530	21674737	40	2.00E-40	Chlorobium tepidum TLS	transposase [Chlorobium tepidum TLS] ref NP_661348.1 transposase [Chlorobium tepidum TLS] gb AAM73144.1 transposase [Chlorobium tepidum TLS] gb AAM71690.1 transposase [Chlorobium tepidum TLS]			
853, 854	51892061	38	4.00E-34	Symbiobacterium thermophilum IAM 14863	two-component response regulator [Symbiobacterium thermophilum IAM 14863] db BAD39908.1 two-component response regulator [Symbiobacterium thermophilum IAM 14863]			3.1.1.61
8531, 8532	34557782	38	4.00E-33	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]			2.7.3.-
8533, 8534	42524534	43	3.00E-29	Bdellovibrio bacteriovorus HD100	long-chain fatty-acid-CoA ligase [Bdellovibrio bacteriovorus HD100] emb CAE80907.1 long-chain fatty-acid-CoA ligase [Bdellovibrio bacteriovorus HD100]			6.2.1.3

8539, 8540	48834107	38	1.00E-40	Magnetococcus sp. MC-1	COG2301: Citrate lyase beta subunit [Magnetococcus sp. MC-1]			4.1.3.6
8541, 8542	48855753	51	5.00E-73	Cytophaga hutchinsonii	COG0058: Glucan phosphorylase [Cytophaga hutchinsonii]			2.4.1.1
8543, 8544	45358014	35	5.00E-11	Methanococcus maripaludis S2	hypothetical protein MPP0451 [Methanococcus maripaludis S2] emb CAF30007.1 conserved hypothetical protein [Methanococcus maripaludis S2]			
8549, 8550	32262172	28	9.00E-07	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860155.1 hypothetical protein HH0624 [Helicobacter hepaticus ATCC 51449]			
855, 856	15834252	31	6.00E-09	Escherichia coli O157:H7	putative DNA modification protein [Escherichia coli O157:H7] dbj BAB38421.1 putative DNA modification protein [Escherichia coli O157:H7] pir F91253 probable DNA modification protein [imported] - Escherichia coli (strain O157:H7, substrain RMD 0509952)			
8551, 8552	34557782	40	6.00E-11	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]			
8553, 8554	48833745	28	7.00E-34	Magnetococcus sp. MC-1	COG0840: Methyl-accepting chemotaxis protein [Magnetococcus sp. MC-1]			
8555, 8556	34558488	67	1.00E-107	Wolinella succinogenes DSM 1740	PUTATIVE ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE1203.1 PUTATIVE ABC TRANSPORTER, ATP-BINDING PROTEIN [Wolinella succinogenes]			1.8.-.-
8557, 8558	54310629	44	6.00E-26	Photobacterium profundum SS9	hypothetical protein PBPRA3591 [Photobacterium profundum SS9] emb CAG21847.1 Conserved hypothetical protein [Photobacterium profundum]			
8559, 8560	57240652	55	3.00E-53	Campylobacter lari RM2100	ABC transporter, ATP-binding protein (H11087) [Campylobacter lari RM2100] gb EAL55045.1 ABC transporter, ATP-binding protein (H11087) [Campylobacter lari RM2100]			1.8.-.-
8561, 8562	32262256	48	4.00E-51	Helicobacter hepaticus ATCC 51449	guanylate kinase [Helicobacter hepaticus ATCC 51449] ref NP_860238.1 guanylate kinase [Helicobacter hepaticus ATCC 51449] sp Q7VIA1 KGUA_HELHP Guanylate kinase (GMP kinase)			2.7.4.8
8563, 8564	21328619	40	1.00E-14	uncultured proteobacterium	photopigment and puc expression activator, putative [uncultured proteobacterium]			
8565, 8566	29346910	58	4.00E-84	Bacteroides thetaiotaomicron VPI-5482	Ribonuclease G [Bacteroides thetaiotaomicron VPI-5482] gb AAO76607.1 Ribonuclease G [Bacteroides thetaiotaomicron VPI-5482]			3.1.4.-
8567, 8568	53711964	38	3.00E-30	Bacteroides fragilis YCH46	aminopeptidase N [Bacteroides fragilis YCH46] aminopeptidase N [Bacteroides fragilis YCH46]			

8569, 8570	24214122	44	1.00E-26	Leptospira Interrogans serovar Lai str. 56601	Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601]				
857, 858	47565585	40	2.00E-42	Bacillus cereus G9241	beta-lactamase [Bacillus cereus G9241] gb EAL15902.1 beta-lactamase [Bacillus cereus G9241]				3.5.2.6
8575, 8576	57169066	28	2.00E-10	Campylobacter coli RM2228	conserved hypothetical protein [Campylobacter coli RM2228]				
8579, 8580	50120871	32	1.00E-41	Erwinia carotovora subsp. atroseptica SCRI1043	aconitate hydratase 1 [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG74844.1 aconitate hydratase 1 [Erwinia carotovora subsp. atroseptica SCRI1043]				4.2.1.3
8581, 8582	34556958	25	8.00E-10	Wolonia succinogenes DSM 1740	HYPOTHETICAL PROTEIN ; WS0538 [Wolonia succinogenes DSM 1740] emb CAE09673.1 HYPOTHETICAL PROTEIN ; WS0538 [Wolonia succinogenes]				
8583, 8584	53713067	30	1.00E-15	Bacteroides fragilis YCH46	hypothetical protein BF1778 [Bacteroides fragilis YCH46] db BAD48525.1 hypothetical protein [Bacteroides fragilis YCH46]				
8585, 8586	57240997	37	1.00E-17	Campylobacter lari RM2100	probable periplasmic protein Cj0943 [Campylobacter lari RM2100] gb EAL54693.1 probable periplasmic protein Cj0943 [Campylobacter lari RM2100]				
8587, 8588	29347851	36	5.00E-29	Bacteroides thetaiotaomicron VPI-5482	putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77548.1 putative 5'-nucleotidase/2',3'-cyclic phosphodiesterase [Bacteroides thetaiotaomicron VPI-5482]				3.1.4.16
8589, 8590	34558210	30	6.00E-33	Wolonia succinogenes DSM 1740	METHYL ACCEPTING CHEMOTAXIS PROTEIN [Wolonia succinogenes DSM 1740] emb CAE10925.1 METHYL ACCEPTING CHEMOTAXIS PROTEIN [Wolonia succinogenes]				2.7.3.-
8591, 8592	51587625	36	1.00E-26	Pseudomonas putida	3-phosphoshikimate 1-carboxyvinyltransferase [Pseudomonas putida]				2.5.1.19
8593, 8594	1944167	31	1.00E-06	Actinobacillus actinomycetemcom itans	unnamed protein product [Actinobacillus actinomycetemcomitans]				
8595, 8596	15607008	33	6.00E-18	Aquifex aeolicus VF5	hypothetical protein aq_2027 [Aquifex aeolicus VF5] gb AAC07788.1 hypothetical protein [Aquifex aeolicus VF5] pir A70474 conserved hypothetical protein aq_2027 - Aquifex aeolicus sp O67821 YK27_AQUAE Hypothetical protein AQ_2027				
8597, 8598	48845271	39	2.00E-49	Geobacter metallireducens GS 15	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]				2.7.3.-

8601, 8602	48763336	27	1.00E-37	Rhodospirillum rubrum	COG2905: Predicted signal-transduction protein containing cAMP-binding and CBS domains [Rhodospirillum rubrum]				
8603, 8604	34557014	44	3.00E-38	Wollinella succinogenes DSM 1740	hypothetical protein WS0597 [Wollinella succinogenes DSM 1740] emb CAE09729.1 conserved hypothetical protein [Wollinella succinogenes]				
8605, 8606	53756218	34	7.00E-10	Methylococcus capsulatus str. Bath	killer suppression protein HigA, putative [Methylococcus capsulatus str. Bath] ref YP_112810.1 killer suppression protein HigA, putative [Methylococcus capsulatus str. Bath]				
8607, 8608	14518367	36	4.00E-46	Microscilla sp. PRE1	hypothetical protein MS162 [Microscilla sp. PRE1] MS162, hypothetical protein [Microscilla sp. PRE1]				
8609, 8610	57169043	54	2.00E-66	Campylobacter coli RM2228	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Campylobacter coli RM2228] gb EAL56278.1 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Campylobacter coli RM2228]				2.1.1.61
861, 862	56707657	53	5.00E-29	Francisella tularensis subsp. tularensis Schu 4	hypothetical protein FTT0522 [Francisella tularensis subsp. tularensis Schu 4] emb CAG45155.1 conserved hypothetical protein [Francisella tularensis subsp. tularensis]				2.1.1.72
8611, 8612	34558300	58	4.00E-52	3-HYDROXYMYRISTOYL	UDP-3-O-[3-HYDROXYMYRISTOYL] N-ACETYLGLUCOSAMINE DEACETYLASE [Wollinella succinogenes DSM 1740] emb CAE11015.1 UDP-3-O-[3-HYDROXYMYRISTOYL] N-ACETYLGLUCOSAMINE DEACETYLASE [Wollinella succinogenes]				3.5.1.-
8613, 8614	57168696	49	3.00E-19	Campylobacter coli RM2228	conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56657.1 conserved hypothetical protein [Campylobacter coli RM2228]				
8615, 8616	34557246	66	3.00E-36	Wollinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wollinella succinogenes]				2.7.3.-
8617, 8618	48856320	27	2.00E-13	Cytophaga hutchinsonii	COG2885: Outer membrane protein and related peptidoglycan-associated (lipo)proteins [Cytophaga hutchinsonii]				
8619, 8620	34558835	63	3.00E-88	Alvinella pompejana epibiont 7G3	hydroxymethylbutenyl pyrophosphate reductase [Alvinella pompejana epibiont 7G3]				
8621, 8622	48856760	44	1.00E-25	Cytophaga hutchinsonii	COG2062: Phosphohistidine phosphatase SixA [Cytophaga hutchinsonii]				
8625, 8626	34557550	36	9.00E-21	Wollinella succinogenes DSM 1740	hypothetical protein WS1180 [Wollinella succinogenes DSM 1740] emb CAE10265.1 hypothetical protein [Wollinella succinogenes]				
8627, 8628	23475621	34	3.00E-15	Desulfovibrio desulfuricans G20	COG0071: Molecular chaperone (small heat shock protein) [Desulfovibrio desulfuricans G20]				

8629, 8630, 863, 864, 8631, 8632, 8635, 8636, 8637, 8638, 8639, 8640	15895537 57339644 38348674 34556481 57238619 34557261	77 49 37 40 56 47	1.00E-120 1.00E-49 8.00E-32 6.00E-58 1.00E-22 3.00E-42	Clostridium acetobutylicum ATCC 824 synthetic construct Microcystis aeruginosa Wolinella succinogenes DSM 1740 Campylobacter jejuni RM1221 Wolinella succinogenes DSM 1740	Aspartyl-tRNA synthetase [Clostridium acetobutylicum ATCC 824] gb AAK80226.1 Aspartyl-tRNA synthetase [Clostridium acetobutylicum ATCC 824] pir G97179 aspartyl-tRNA synthetase [imported] - Clostridium acetobutylicum sp Q97GU6 SYD_CLOAB Aspartyl-tRNA synthetase (Aspartate-tRNA ligase) (AspRS) hypothetical protein FTT0520 [synthetic construct] putative transposase [Microcystis aeruginosa] hypothetical protein WS0023 [Wolinella succinogenes DSM 1740] emb CAE09196.1 conserved hypothetical protein [Wolinella succinogenes] ATP/GTP-binding protein [Campylobacter jejuni RM1221] gb AAW36202.1 ATP/GTP-binding protein [Campylobacter jejuni RM1221] GLUCOSE INHIBITED DIVISION PROTEIN B [Wolinella succinogenes DSM 1740] emb CAE09976.1 GLUCOSE INHIBITED DIVISION PROTEIN B [Wolinella succinogenes] sp Q7M8J8 GIDB_WOLSU Methyltransferase gidB (Glucose inhibited division protein B)	Clostridium tetani E88, section 8 of 10 of the complete genome 81 3.00E-61 6.1.1.12	
8643, 8644, 8645, 8646, 8647, 8648	29348816 34557656 57241264	75 59 25	3.00E-91 1.00E-91 6.00E-12	Bacteroides thetaiotaomicron VPI-5482 Wolinella succinogenes DSM 1740 Campylobacter lari RM2100	ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI- 5482] gb AAO78513.1 ABC transporter ATP-binding protein [Bacteroides thetaiotaomicron VPI-5482] CLPY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10371.1 CLPY PROTEIN [Wolinella succinogenes] conserved hypothetical protein [Campylobacter lari RM2100] gb EAL54960.1 conserved hypothetical protein [Campylobacter lari RM2100]	Cerarium horridum extrachromosomal minicircle putative ABC transporter membrane protein Ycf24 (ycf24) gene, partial cds; and putative ATP- dependent transporter Ycf16 (ycf16) gene, complete cds 88 1.00E-07 1.8.-.- Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6 84 2.00E-13	

8649, 8650	34557188	46	4.00E-79	Wollinella succinogenes DSM 1740	TRANSCRIPTIONAL REGULATORY PROTEIN HYPF [Wollinella succinogenes DSM 1740] emb CAE09903.1 TRANSCRIPTIONAL REGULATORY PROTEIN HYPF [Wollinella succinogenes]			
8651, 8652	37527394	62	2.00E-50	Photorhabdus luminescens subsp. laumondii TTO1	hypothetical protein plu3521 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15894.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1]			
8653, 8654	37527394	50	8.00E-80	Photorhabdus luminescens subsp. laumondii TTO1	hypothetical protein plu3521 [Photorhabdus luminescens subsp. laumondii TTO1] emb CAE15894.1 unnamed protein product [Photorhabdus luminescens subsp. laumondii TTO1] COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00301665.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00301374.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00300257.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00300170.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00298468.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15] ref ZP_00298384.1 COG3385: FOG: Transposase and inactivated derivatives [Geobacter metallireducens GS-15]			
8655, 8656	48847450	39	3.00E-15	Geobacter metallireducens GS-15	ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ66097.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65681.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65455.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAQ65413.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_905778.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_905198.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904782.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904556.1 ISPg4, transposase [Porphyromonas gingivalis W83] ref NP_904514.1 ISPg4, transposase [Porphyromonas gingivalis W83] gb AAD38020.1 transposase [Porphyromonas gingivalis] hypothetical protein lin2473 [Listeria innocua Clip11262] emb CAC97700.1 lin2473 [Listeria innocua] pir AD1741 aspartate kinase homolog lin2473 [imported] - Listeria innocua (strain Clip11262)			
8657, 8658	34397615	30	8.00E-20	Porphyromonas gingivalis W83	TWO-COMPONENT REGULATOR [Wollinella succinogenes DSM 1740] emb CAE09457.1 TWO-COMPONENT REGULATOR [Wollinella succinogenes]			2.7.2.4
8659, 8660	16801535	35	3.00E-22	Listeria innocua Clip11262				
8661, 8662	34556742	36	6.00E-16	Wollinella succinogenes DSM 1740				

8663, 8664	AAB9666 2	41	3.00E-25			Desc: Putative high-affinity branched amino acid transport system ATPase #7. Org: <i>Pyrococcus abyssi</i>			1.8.-.-
8665, 8666	32262912 55		1.00E-44	Helicobacter hepaticus ATCC 51449		lipopolysaccharide core biosynthesis protein [Helicobacter hepaticus ATCC 51449] ref NP_860892.1 lipopolysaccharide core biosynthesis protein [Helicobacter hepaticus ATCC 51449]			2.7.7.3
8667, 8668	15643586 22		1.00E-09	Thermotoga maritima MSB8		transcriptional regulator, TetR family [Thermotoga maritima MSB8] gb AAD35905.1 transcriptional regulator, TetR family [Thermotoga maritima MSB8] pir B72330 transcription regulator, TetR family - Thermotoga maritima (strain MSB8)			
8669, 8670	34557966 56		1.00E-63	Wolinella succinogenes DSM 1740		ATP-DEPENDENT HELICASE [Wolinella succinogenes DSM 1740] emb CAE10681.1 ATP-DEPENDENT HELICASE [Wolinella succinogenes]			3.6.1.-
8673, 8674	29349715 57		5.00E-72	Bacteroides thetaiotaomicron VPI-5482		putative glycogen synthase [Bacteroides thetaiotaomicron VPI-5482] gb AAO79412.1 putative glycogen synthase [Bacteroides thetaiotaomicron VPI-5482]			2.4.1.21
8675, 8676	39959299 52		1.00E-86	Geobacter sulfurreducens PCA		ATP-dependent RNA helicase DbpA [Geobacter sulfurreducens PCA] gb AAR33523.1 ATP-dependent RNA helicase DbpA [Geobacter sulfurreducens PCA]			2.7.7.-
8677, 8678	50083983 24		6.00E-10	Acinetobacter sp. ADP1		hypothetical protein; putative membrane protein [Acinetobacter sp. ADP1] emb CAG67671.1 hypothetical protein; putative membrane protein [Acinetobacter sp. ADP1]			
8679, 8680	29348209 46		8.00E-60	Bacteroides thetaiotaomicron VPI-5482		putative amidophosphoribosyl-transferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77906.1 putative amidophosphoribosyl-transferase [Bacteroides thetaiotaomicron VPI-5482]			
8681, 8682	45656836 46		3.00E-62	Leptospira interrogans serovar Copenhagen str. Fio Cruz L1-130		ABC transporter, ATP-binding protein [Leptospira interrogans serovar Copenhagen str. Fio Cruz L1-130] gb AAS69559.1 ABC transporter, ATP-binding protein [Leptospira interrogans serovar Copenhagen str. Fio Cruz L1-130]			1.8.-.-
8685, 8686	34557269 60		1.00E-107	Wolinella succinogenes DSM 1740		ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolinella succinogenes DSM 1740] emb CAE09984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wolinella succinogenes]			3.6.1.-
8687, 8688	57241387 27		1.00E-12	Campylobacter lari RM2100		probable membrane protein Cj0152c [Campylobacter lari RM2100] gb EAL54499.1 probable membrane protein Cj0152c [Campylobacter lari RM2100]			
8689, 8690	53715862 56		1.00E-75	Bacteroides fragilis YCH46		DNA mismatch repair protein mutS [Bacteroides fragilis YCH46] db BAD51320.1 DNA mismatch repair protein mutS [Bacteroides fragilis YCH46]			

8691, 8692	34556651	27	5.00E-17	Wollinella succinogenes DSM 1740	hypothetical protein WS0208 [Wollinella succinogenes DSM 1740] emb CAE09386.1 hypothetical protein [Wollinella succinogenes]			
8693, 8694	6967725	24	6.00E-08	Campylobacter jejuni subsp. jejuni NCTC 11168	hypothetical protein Cj0248 [Campylobacter jejuni subsp. jejuni NCTC 11168] pir G81442 hypothetical protein Cj0248 [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_281442.1 hypothetical protein Cj0248 [Campylobacter jejuni subsp. jejuni NCTC 11168]			
8695, 8696	48855460	25	9.00E-22	Cytophaga hutchinsonii	hypothetical protein Chui02001797 [Cytophaga hutchinsonii]			
8699, 8700	54023411	27	5.00E-09	Nocardia farcinica IFM 10152	hypothetical protein nfa14440 [Nocardia farcinica IFM 10152] dbj BAD56289.1 hypothetical protein [Nocardia farcinica IFM 10152]			
87, 88	50907355	32	7.00E-16	Oryza sativa (japonica cultivar- group)	putative guanylate binding protein [Oryza sativa (japonica cultivar-group)] dbj BAD23587.1 putative guanylate binding protein [Oryza sativa (japonica cultivar-group)]			
8701, 8702	48845445	43	1.00E-28	Geobacter metallireducens GS 15	COG3437: Response regulator containing a CheY-like receiver domain and an HD-GYP domain [Geobacter metallireducens GS-15]			2.7.3.-
8703, 8704	42528087	28	6.00E-12	Treponema denticola ATCC 35405	endonuclease/exonuclease/phosphatase family protein [Treponema denticola ATCC 35405] gb AAS13104.1 endonuclease/exonuclease/phosphatase family protein [Treponema denticola ATCC 35405]			
8707, 8708	21231126	37	3.00E-31	Xanthomonas campestris pv. campestris str. ATCC 33913	glycosyl transferase [Xanthomonas campestris pv. campestris str. ATCC 33913] gb AAM40967.1 glycosyl transferase [Xanthomonas campestris pv. campestris str. ATCC 33913]			2.4.1.-
8709, 8710	21673717	39	7.00E-25	Chlorobium tepidum TLS	phosphoglycolate phosphatase [Chlorobium tepidum TLS] gb AAM72124.1 phosphoglycolate phosphatase [Chlorobium tepidum TLS]			3.1.3.18
871, 872	53712247	50	2.00E-68	Bacteroides fragilis YCH46	putative oxidoreductase [Bacteroides fragilis YCH46] dbj BAD47705.1 putative oxidoreductase [Bacteroides fragilis YCH46]			
8711, 8712	2314022	60	6.00E-85	Helicobacter pylori 26695	cysteinyI-tRNA synthetase (cysS) [Helicobacter pylori 26695] pir F64630 cysteine-tRNA ligase (EC 6.1.1.16) - Helicobacter pylori (strain 26695) ref NP_207679.1 cysteinyI-tRNA synthetase (cysS) [Helicobacter pylori 26695] sp P41259 SYC_HELPY CysteinyI-tRNA synthetase (Cysteine-tRNA ligase) (CysRS)	Fusobacterium nucleatum subsp. nucleatum ATCC 25586, section 8 of 197 of the complete genome	91	6.00E-10 6.1.1.16
8713, 8714	54302166	30	7.00E-36	Photobacterium profundum SS9	hypothetical protein PBPRB0486 [Photobacterium profundum SS9] emb CAG22339.1 hypothetical protein [Photobacterium profundum]			2.7.3.-
8715, 8716	48853522	42	2.00E-35	Cytophaga hutchinsonii	COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii]			3.1.-

8717, 8718	34556461	68	1.00E-107	Wolinella succinogenes DSM 1740	DNA GYRASE SUBUNIT B [Wolinella succinogenes DSM 1740] emb CAE09176.1 DNA GYRASE SUBUNIT B [Wolinella succinogenes]	Helicobacter hepaticus ATCC 51449 section 4 of 6 of the complete genome	82	1.00E-17	5.99.1.3
8719, 8720	56461066	31	5.00E-23	Idiomarina lithiensis L2TR	tRNA nucleotidyltransferase [Idiomarina lithiensis L2TR] gb AAV82798.1 tRNA nucleotidyltransferase [Idiomarina lithiensis L2TR]				2.7.7.19
8725, 8726	37912882	39	4.00E-32	uncultured marine proteobacterium ANT32C12	predicted methylase [uncultured marine proteobacterium ANT32C12]				
8727, 8728	5578860	45	1.00E-56	Streptomyces coelicolor A3(2)	putative endo alpha-1,4 polygalactosaminidase [Streptomyces coelicolor A3(2)] pir T35294 probable endo alpha-1,4 polygalactosaminidase - Streptomyces coelicolor ref NP_626431.1 putative endo alpha-1,4 polygalactosaminidase [Streptomyces coelicolor A3(2)]				
8729, 8730	48858604	31	2.00E-18	Clostridium thermocellum ATCC 27405	COG3580: Uncharacterized protein conserved in bacteria [Clostridium thermocellum ATCC 27405] hypothetical protein BSJ40760 [Bacillus subtilis subsp. subtilis str. 168] emb CAB16113.1 yyaP [Bacillus subtilis subsp. subtilis str. 168] pir S66001 conserved hypothetical protein yyaP - Bacillus subtilis sp P37508 YYAP_BACSU Hypothetical protein yyaP db BAA05207.1 unknown [Bacillus subtilis]				3.4.24.-
8731, 8732	16081128	38	5.00E-31	Chloroflexus aurantiacus	COG0407: Uroporphyrinogen-III decarboxylase [Chloroflexus aurantiacus]				4.1.1.37
8733, 8734	34397745	33	1.00E-15	Porphyromonas gingivalis W83	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase [Porphyromonas gingivalis W83] ref NP_905907.1 guanosine-3',5'-bis(diphosphate) 3'- pyrophosphohydrolase [Porphyromonas gingivalis W83] hypothetical protein CPE1684 [Clostridium perfringens str. 13] db BAB81390.1 conserved hypothetical protein [Clostridium perfringens str. 13]				2.7.6.5
8735, 8736	18310666	34	3.00E-17	Clostridium perfringens str. 13					
8737, 8738	34556647	40	1.00E-38	Wolinella succinogenes DSM 1740	hypothetical protein WS0204 [Wolinella succinogenes DSM 1740] emb CAE09362.1 hypothetical protein [Wolinella succinogenes] conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_112612.1 hypothetical protein MCA0072 [Methylococcus capsulatus str. Bath]				2.7.1.13 0
8739, 8740	53756478	40	5.00E-22	Methylococcus capsulatus str. Bath					

8741, 8742	39996430	63	5.00E-32	Geobacter sulfurreducens PCA	hypothetical protein GSU1328 [Geobacter sulfurreducens PCA] gb AAR34704.1 conserved hypothetical protein [Geobacter sulfurreducens PCA]			
8745, 8746	AAW2084 6	27	6.00E-11		Desc:H. pylori secreted or periplasmic protein, 12ae1140orf3. Org:Helicobacter pylori			
8747, 8748	34557578	43	4.00E-63	Wolinella succinogenes DSM 1740	CIAB PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10293.1 CIAB PROTEIN [Wolinella succinogenes]			
8749, 8750	45656989	50	2.00E-68	Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130	methylmalonyl-CoA mutase [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130] gb AAS69712.1 methylmalonyl-CoA mutase [Leptospira interrogans serovar Copenhageni str. Fio Cruz L1-130]			
875, 876	46324266	34	4.00E-18	Burkholderia cepacia R1808	hypothetical protein Bucepa03000401 [Burkholderia cepacia R1808]			
8753, 8754	34557543	33	7.00E-43	Wolinella succinogenes DSM 1740	PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10258.1 PUTATIVE PERIPLASMIC PROTEIN [Wolinella succinogenes] emb CAD5552.1 NapL protein [Wolinella succinogenes] dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46] dbj BAD50186.1 dolichol-phosphate mannosyltransferase [Bacteroides fragilis YCH46]			2.4.1.83
8757, 8758	53731539	53	8.00E-40	Methanococcus burtonii DSM 6242	hypothetical protein Mbur03001017 [Methanococcus burtonii DSM 6242]			
8759, 8760	53730423	39	2.00E-22	Dechloromonas aromatica RCB	COG0642: Signal transduction histidine kinase [Dechloromonas aromatica RCB]			2.7.3.-
8761, 8762	48846020	27	1.00E-09	Geobacter metallireducens GS-15	COG0642: Signal transduction histidine kinase [Geobacter metallireducens GS-15]			
8763, 8764	42528141	49	3.00E-77	Treponema denticola ATCC 35405	Fic family protein [Treponema denticola ATCC 35405] gb AAS13158.1 Fic family protein [Treponema denticola ATCC 35405]			
8765, 8766	34556616	35	7.00E-38	Wolinella succinogenes DSM 1740	CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes]		90	2.00E-10

8767, 8768	57238514	43	3.00E-20	Campylobacter jejuni RM1221	DNA-binding response regulator [Campylobacter jejuni RM1221] gbIAAW36097.1] DNA-binding response regulator [Campylobacter jejuni RM1221]			2.7.-
877, 878	2352096	45	4.00E-15	Fervidobacterium islandicum	orf, similar to serine/threonine protein phosphatase [Fervidobacterium islandicum]			3.1.3.16
8771, 8772	32261568	32	4.00E-17	Helicobacter hepaticus ATCC 51449	two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] ref NP_859552.1 two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449]			2.7.3.-
8775, 8776	39995927	44	6.00E-25	Geobacter sulfurreducens PCA	hypothetical protein GSU0821 [Geobacter sulfurreducens PCA] gbIAAR34151.1] conserved hypothetical protein [Geobacter sulfurreducens PCA]			
8777, 8778	48854259	46	3.00E-65	Cytophaga hutchinsonii	COG3550: Uncharacterized protein related to capsule biosynthesis enzymes [Cytophaga hutchinsonii]			
8779, 8780	32477010	60	6.00E-51	Rhodopirellula baltica SH 1	hypothetical protein RB11494 [Rhodopirellula baltica SH 1] emb CAD79157.1] conserved hypothetical protein [Pirellula sp.]			
8781, 8782	46140776	36	2.00E-36	Dechloromonas aromatica RCB	COG1028: Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) [Dechloromonas aromatica RCB]			1.-
8785, 8786	34397071	29	5.00E-19	Porphyromonas gingivalis W83	TPR domain protein [Porphyromonas gingivalis W83] ref NP_905236.1 TPR domain protein [Porphyromonas gingivalis W83]			
8787, 8788	57240778	53	2.00E-73	Campylobacter lari RM2100	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Campylobacter lari RM2100] gb EAL55171.1 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Campylobacter lari RM2100]			2.7.7.60
8789, 8790	57241023	42	5.00E-17	Campylobacter lari RM2100	conserved hypothetical protein TIGR00278, putative [Campylobacter lari RM2100] gb EAL54719.1] conserved hypothetical protein TIGR00278, putative [Campylobacter lari RM2100]			
879, 880	29349252	54	2.00E-86	Bacteroides thetaiotaomicron VPI-5482	ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482] gb AAO78949.1] ATP-dependent DNA helicase recQ [Bacteroides thetaiotaomicron VPI-5482]			3.6.1.-
8791, 8792	6967683	48	3.00E-25	Campylobacter jejuni subsp. jejuni NCTC 11168	hypothetical protein Cj0190c [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281400.1 hypothetical protein Cj0190c [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81437 hypothetical protein Cj0190c [Imported] - Campylobacter jejuni (strain NCTC 11168)			
8793, 8794	34558255	28	1.00E-21	Wolinella succinogenes DSM 1740	hypothetical protein WS1967 [Wolinella succinogenes DSM 1740] emb CAE10970.1] hypothetical protein [Wolinella succinogenes]			
8797, 8798	57240790	38	2.00E-14	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari RM2100] gb EAL55183.1] conserved hypothetical protein [Campylobacter lari RM2100]			
8799, 8800	51573391	19	9.00E-11	Borrelia garinii PBI	hypothetical protein BG0579 [Borrelia garinii PBI] ref YP_073008.1 hypothetical protein BG0579 [Borrelia garinii PBI]			

8801, 8802	48478360	30	1.00E-11	Picrophilus torridus DSM 9790	thiamin-phosphate pyrophosphorylase [Picrophilus torridus DSM 9790] gb AAAT43873.1 thiamin-phosphate pyrophosphorylase [Picrophilus torridus DSM 9790]			2.5.1.3
8803, 8804	34397900	28	1.00E-09	Porphyromonas gingivalis W83	hypothetical protein PG1988 [Porphyromonas gingivalis W83] ref NP_906062.1 hypothetical protein PG1988 [Porphyromonas gingivalis W83]			
8805, 8806	57238621	38	2.00E-22	Campylobacter jejuni RM1221	DNA-binding response regulator, putative [Campylobacter jejuni RM1221] gb AAW36204.1 DNA-binding response regulator, putative [Campylobacter jejuni RM1221]			
8807, 8808	15612433	51	2.00E-44	Helicobacter pylori J99	LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN [Helicobacter pylori J99] gb AAD06957.1 LIPOPOLYSACCHARIDE CORE BIOSYNTHESIS PROTEIN [Helicobacter pylori J99] sp Q9ZJE4 COAD_HELPJ Phosphopantetheine adenylyltransferase (Pantetheine-phosphate adenylyltransferase) (PPAT) (Dephospho-CoA pyrophosphorylase) pir C71814 lipopolysaccharide core biosynthesis protein - Helicobacter pylori (strain J99)			2.7.7.3
8809, 8810	34557029	53	3.00E-44	Wolfinella succinogenes DSM 1740	INTEGRAL MEMBRANE PROTEIN WITH KINASE ACTIVITY [Wolfinella succinogenes DSM 1740] emb CAE09744.1 INTEGRAL MEMBRANE PROTEIN WITH KINASE ACTIVITY [Wolfinella succinogenes]			2.7.4.9
881, 882	29349478	35	4.00E-22	Bacteroides thetaiotaomicron VPI-5482	RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482] gb AAO79175.1 RNA polymerase ECF-type sigma factor [Bacteroides thetaiotaomicron VPI-5482]			
8811, 8812	34557014	37	5.00E-47	Wolfinella succinogenes DSM 1740	hypothetical protein WS0597 [Wolfinella succinogenes DSM 1740] emb CAE09729.1 conserved hypothetical protein [Wolfinella succinogenes]			
8813, 8814	34396203	43	6.00E-48	Porphyromonas gingivalis W83	L-threonine-O-3-phosphate decarboxylase, putative [Porphyromonas gingivalis W83] ref NP_904371.1 L-threonine-O-3-phosphate decarboxylase, putative [Porphyromonas gingivalis W83]			2.6.1.9
8815, 8816	48854595	30	5.00E-10	Cytophaga hutchinsonii	hypothetical protein Chut02002797 [Cytophaga hutchinsonii]			
8817, 8818	57168226	31	6.00E-23	Campylobacter coli RM2228	CMP-N-acetylneuraminic acid synthetase (neuA) [Campylobacter coli RM2228] gb EAL57269.1 CMP-N-acetylneuraminic acid synthetase (neuA) [Campylobacter coli RM2228] emb CAE73738.1 acylneuraminat cytidyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_282457.1 acylneuraminat cytidyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir D81274 N-acetylneuraminat cytidyltransferase (EC 2.7.7.43) C 1311 [imported] - Campylobacter jejuni (strain NCTC 11168)			2.7.7.43
8819, 8820	29346635	60	1.00E-100	Bacteroides thetaiotaomicron VPI-5482	GDP-fucose synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76332.1 GDP-fucose synthetase [Bacteroides thetaiotaomicron VPI-5482]			5.1.3.-

8821, 8822	29347648	42	9.00E-49	Bacteroides thetaiotaomicron VPI-5482	putative biotin-(acetyl-CoA carboxylase) synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77345.1 putative biotin-(acetyl-CoA carboxylase) synthetase [Bacteroides thetaiotaomicron VPI-5482]	6.3.4.15
8823, 8824	34556663	44	2.00E-26	Wolinella succinogenes DSM 1740	ANTHRANILATE ISOMERASE [Wolinella succinogenes DSM 1740] emb CAE09378.1 ANTHRANILATE ISOMERASE [Wolinella succinogenes] DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10122.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes]	5.3.1.24
8825, 8826	34557407	38	1.00E-41	Wolinella succinogenes DSM 1740	hypothetical protein WS1025 [Wolinella succinogenes DSM 1740] emb CAE10126.1 hypothetical protein [Wolinella succinogenes] integrase-recombinase protein [Methanothermobacter thermoautotrophicus str. Delta H] gb AAB85391.1 integrase-recombinase protein [Methanothermobacter thermoautotrophicus str. Delta H] pir D69219 integrase-recombinase protein - Methanobacterium thermoautotrophicum (strain Delta H)	2.7.3.-
8827, 8828	34557411	22	2.00E-18	Wolinella succinogenes DSM 1740	COG0357: Predicted S-adenosylmethionine-dependent methyltransferase involved in bacterial cell division [Desulfotobacterium hafnense DCB-2] HD-GYP domain containing protein [Clostridium acetobutylicum ATCC 824] gb AAK81572.1 HD-GYP domain containing protein [Clostridium acetobutylicum ATCC 824] pir A97348 HD-GYP domain containing protein [imported] - Clostridium acetobutylicum COG3401: Fibronectin type 3 domain-containing protein [Cytophaga hutchinsonii] sensory box/GGDEF family protein [Geobacter sulfurreducens PCA] gb AAR35392.1 sensory box/GGDEF family protein [Geobacter sulfurreducens PCA]	2.7.3.-
8831, 8832	15678913	41	2.00E-36	Methanothermobac ter thermoautotrophicus str. Delta H	hypothetical protein LB146 [Leptospira interrogans serovar Lai str. 56601] gb AAN51705.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601]	2.7.2.4
8833, 8834	23121135	36	1.00E-32	Desulfotobacterium hafnense DCB-2		
8835, 8836	15996883	31	1.00E-19	Clostridium acetobutylicum ATCC 824		
8837, 8838	48853982	25	2.00E-13	Cytophaga hutchinsonii		
8839, 8840	39997114	51	1.00E-50	Geobacter sulfurreducens PCA		
8841, 8842	34557317	28	5.00E-12	Wolinella succinogenes DSM 1740		
8843, 8844	55822355	34	4.00E-39	Streptococcus thermophilus CNRZ1066		
8845, 8846	24217207	50	2.00E-40	Leptospira interrogans serovar Lai str. 56601		

8847, 8848	57242267	37	3.00E-29	Campylobacter upsaliensis RM3195	MutS2 family protein , putative [Campylobacter upsaliensis RM3195] gb EAL53729.1 MutS2 family protein , putative [Campylobacter upsaliensis RM3195]				
8849, 8850	34557846	41	2.00E-19	Wolinella succinogenes DSM 1740	hypothetical protein WS1513 [Wolinella succinogenes DSM 1740] emb CAE10561.1 conserved hypothetical protein [Wolinella succinogenes] cytochrome c biogenesis protein (ycf5) [Campylobacter lari RM2100] gb EAL55842.1 cytochrome c biogenesis protein (ycf5) [Campylobacter lari RM2100]				
8851, 8852	57240528	32	6.00E-36	Campylobacter lari RM2100	hypothetical protein GSU2532 [Geobacter sulfurreducens PCA] gb AAR35905.1 conserved hypothetical protein [Geobacter sulfurreducens PCA]				
8853, 8854	39997627	25	2.00E-08	Geobacter sulfurreducens PCA				2.7.3.-	
8855, 8856	23126560	47	1.00E-25	Nostoc punctiforme PCC 73102	COG3437: Response regulator containing a CheY-like receiver domain and an HD-GYP domain [Nostoc punctiforme PCC 73102] ATP sulfurylase GTP-binding subunit/APS kinase [Pseudomonas aeruginosa PAO1] ref ZP_00137930.2 COG2895: GTPases - Sulfate adenylylate transferase subunit 1 [Pseudomonas aeruginosa UCBPP-PA14] gb AAC46387.1 ATP sulfurylase GTP-binding subunit/APS kinase [Pseudomonas aeruginosa] pir [D83091 ATP sulfurylase GTP-binding subunit/APS kinase PA4442 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_253132.1 ATP sulfurylase GTP-binding subunit/APS kinase [Pseudomonas aeruginosa PAO1] sp O50274 CYSN_PSEAE CysN/cysC bifunctional enzyme [includes: Sulfate adenylyltransferase subunit 1 (Sulfate adenylylate transferase) (SAT) (ATP-sulfurylase large subunit); Adenylyl- sulfate kinase (APS kinase) (ATP adenosine-5'-phosphosulfate 3'- phosphotransferase)] conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_860475.1 hypothetical protein HH0944 [Helicobacter hepaticus ATCC 51449]			2.7.7.4	
8857, 8858	9950676	60	2.00E-21	Pseudomonas aeruginosa PAO1					3.4.13.9
8861, 8862	32262494	67	1.00E-51	Helicobacter hepaticus ATCC 51449					
8863, 8864	33861261	31	3.00E-14	Prochlorococcus marinus subsp. pastoris str. CCMP1986	putative potassium channel, VIC family [Prochlorococcus marinus subsp. pastoris str. CCMP1986] emb CAE19163.1 putative potassium channel, VIC family [Prochlorococcus marinus subsp. pastoris str. CCMP1986]				
8867, 8868	23129547	36	3.00E-43	Nostoc punctiforme PCC 73102	COG0732: Restriction endonuclease S subunits [Nostoc punctiforme PCC 73102]				3.1.21.3
887, 888	48854835	77	3.00E-48	Cytophaga hutchinsonii	COG0302: GTP cyclohydrolase I [Cytophaga hutchinsonii]				3.5.4.16

8871, 8872	34557247	63	4.00E-62	Wolfinella succinogenes DSM 1740	TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolfinella succinogenes DSM 1740] emb CAE0962.1 TWO-COMPONENT HYBRID SENSOR AND REGULATOR [Wolfinella succinogenes]	Wolfinella succinogenes, complete genome; segment 3/7	85	2.00E-07	2.7.3.-
8873, 8874	57238223	62	3.00E-56	Campylobacter jejuni RM1221	(d)Nucleoside polyphosphate hydrolase [Campylobacter jejuni RM1221] gb AAW35806.1 (d)Nucleoside polyphosphate hydrolase [Campylobacter jejuni RM1221]				3.6.1.-
8875, 8876	57238224	45	2.00E-33	Campylobacter jejuni RM1221	oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter jejuni RM1221] gb AAW35807.1 oxygen-independent coproporphyrinogen III oxidase, putative [Campylobacter jejuni RM1221] emb CAB75216.1 putative oxidoreductase [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281763.1 putative oxidoreductase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir C81405 probable oxidoreductase Cj0580c [imported] - Campylobacter jejuni (strain NCTC 11168)				1.-.-.-
8879, 8880	39995112	46	6.00E-33	Geobacter sulfurreducens PCA	DNA polymerase III, beta subunit [Geobacter sulfurreducens PCA] gb AAR33336.1 DNA polymerase III, beta subunit [Geobacter sulfurreducens PCA]				2.7.7.7
8881, 8882	46141215	70	3.00E-94	Psychrobacter sp. 273-4	COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Psychrobacter sp. 273-4]				3.1.21.3
8885, 8886	15616067	44	1.00E-24	Bacillus halodurans C-125	ABC transporter (ATP-binding protein) [Bacillus halodurans C-125] db BAB07224.1 ABC transporter (ATP-binding protein) [Bacillus halodurans C-125] pir JAB4088 ABC transporter (ATP-binding protein) BH3505 [imported] - Bacillus halodurans (strain C-125)				1.8.-.-
8887, 8888	20089086	44	4.00E-10	Methanosarcina acetivorans C2A	hypothetical protein MA0188 [Methanosarcina acetivorans C2A] gb AAM03641.1 hypothetical protein (multi-domain) [Methanosarcina acetivorans str. C2A]				
8889, 8890	28210443	33	2.00E-32	Clostridium tetani E88	aminotransferase cobD [Clostridium tetani E88] gb AAO35324.1 aminotransferase cobD [Clostridium tetani E88]				2.6.1.9
889, 890	48854835	76	2.00E-63	Cytophaga hutchinsonii	COG0302: GTP cyclohydrolase I [Cytophaga hutchinsonii]				3.5.4.16
8891, 8892	42528086	38	4.00E-30	Treponema denticola ATCC 35405	DNA polymerase III, gamma and tau subunits, putative [Treponema denticola ATCC 35405] gb AAS13103.1 DNA polymerase III, gamma and tau subunits, putative [Treponema denticola ATCC 35405]				2.7.7.7
8893, 8894	27366536	31	2.00E-33	Vibrio vulnificus CMCP6	FOG: CheY-like receiver [Vibrio vulnificus CMCP6] gb AAO07053.1 FOG: CheY-like receiver [Vibrio vulnificus CMCP6]				2.7.3.-
8895, 8896	27367375	49	8.00E-60	Vibrio vulnificus CMCP6	FOG: CheY-like receiver [Vibrio vulnificus CMCP6] gb AAO07892.1 FOG: CheY-like receiver [Vibrio vulnificus CMCP6]				2.7.3.-
8897, 8898	54024734	39	8.00E-37	Nocardia farcinica IFM 10152	putative restriction-modification system endonuclease [Nocardia farcinica IFM 10152] db BAD57612.1 putative restriction-modification system endonuclease [Nocardia farcinica IFM 10152]				3.1.21.3

89, 90	15614312	44	2.00E-29	Bacillus halodurans C-125	DNA-3-methyladenine glycosidase [Bacillus halodurans C-125] dbj BAB05468.1 DNA-3-methyladenine glycosidase [Bacillus halodurans C-125] pir E83868 DNA-3-methyladenine glycosidase BH1749 [imported] - Bacillus halodurans [strain C-125]	3.2.2.21
8901, 8902	34558460	55	4.00E-84	Wolinella succinogenes DSM 1740	hypothetical protein WS2184 [Wolinella succinogenes DSM 1740] emb CAE11175.1 CONSERVED HYPOTHETICAL PROTEIN [Wolinella succinogenes]	
8903, 8904	39936981	52	1.00E-68	Rhodopseudomonas palustris CGA009	possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009] emb CAE29361.1 possible ADP-heptose synthase [Rhodopseudomonas palustris CGA009]	2.7.-
8905, 8906	34558655	34	6.00E-44	Wolinella succinogenes DSM 1740	HYBRID SENSORY HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09370.1 HYBRID SENSORY HISTIDINE KINASE [Wolinella succinogenes]	2.7.3.-
8907, 8908	48856125	54	1.00E-43	Cytophaga hutchinsonii	COG1858: Cytochrome c peroxidase [Cytophaga hutchinsonii]	
891, 892	48733625	46	1.00E-60	Pseudomonas fluorescens PfO-1	COG3173: Predicted aminoglycoside phosphotransferase [Pseudomonas fluorescens PfO-1]	
8911, 8912	42524534	48	1.00E-54	Bdellovibrio bacteriovorus HD100	long-chain fatty-acid-CoA ligase [Bdellovibrio bacteriovorus HD100] emb CAE0907.1 long-chain fatty-acid-CoA ligase [Bdellovibrio bacteriovorus HD100]	6.2.1.3
8915, 8916	31324519	43	6.00E-19	Campylobacter coli	PtmF [Campylobacter coli]	
8917, 8918	48860157	31	3.00E-07	Clostridium thermocellum ATCC 27405	COG2896: Molybdenum cofactor biosynthesis enzyme [Clostridium thermocellum ATCC 27405]	
8919, 8920	32263209	36	1.00E-41	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861188.1 hypothetical protein HH1657 [Helicobacter hepaticus ATCC 51449]	2.7.3.-
8923, 8924	34558149	31	2.00E-26	Wolinella succinogenes DSM 1740	SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes DSM 1740] emb CAE10864.1 SIGNAL TRANSDUCTION RESPONSE REGULATOR-CheY like receiver and GGDEF domain [Wolinella succinogenes]	
8925, 8926	34557202	65	8.00E-70	Wolinella succinogenes DSM 1740	ATP PHOSPHORIBOSYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE09917.1 ATP PHOSPHORIBOSYLTRANSFERASE [Wolinella succinogenes] sp Q7M9N0 HIS1_WOLSU ATP phosphoribosyltransferase [ATP-PRase] (ATP-PR)	2.4.2.17
8927, 8928	15605806	48	2.00E-29	Aquifex aeolicus VF5	hypothetical protein aq_265 [Aquifex aeolicus VF5] gb AAC06589.1 hypothetical protein [Aquifex aeolicus VF5] pir C70324 conserved hypothetical protein aq_265 - Aquifex aeolicus	2.7.3.-

8929, 8930	57505466	50	1.00E-39	Campylobacter upsaliensis RM3195	aminoacyl-histidine dipeptidase [Campylobacter upsaliensis RM3195] gb EAL53077.1 aminoacyl-histidine dipeptidase [Campylobacter upsaliensis RM3195]			3.4.13.3	
8931, 8932	37222114	33	2.00E-29	uncultured bacterium	Uvs065 [uncultured bacterium]				
8933, 8934	40062476	36	8.00E-52	uncultured bacterium 105	hypothetical protein EBAC750-01A01.2 [uncultured bacterium 105]			2.7.9.2	
8935, 8936	28210272	40	2.00E-19	Clostridium tetani E88	hypothetical protein CTC00532 [Clostridium tetani E88] gb AAO35153.1 conserved protein [Clostridium tetani E88]				
8937, 8938	57169018	75	4.00E-19	Campylobacter coli RM2228	Thymidylate synthase complementing protein superfamily [Campylobacter coli RM2228] gb EAL56253.1 Thymidylate synthase complementing protein superfamily [Campylobacter coli RM2228]				
8939, 8940	16331975	55	1.00E-75	Synechocystis sp. PCC 6803	pyruvate oxidoreductase [Synechocystis sp. PCC 6803] dbj BAA10774.1 pyruvate oxidoreductase [Synechocystis sp. PCC 6803] pir S77082 pyruvate (flavodoxin) dehydrogenase (EC 1.2.99.-) nifJ - Synechocystis sp. (strain PCC 6803) sp P52965 NIFJ_SYNY3 Putative pyruvate-flavodoxin oxidoreductase		1.2.7.1		
8941, 8942	46135305	39	3.00E-24	Anabaena variabilis ATCC 29413	COG0395: ABC-type sugar transport system, permease component [Anabaena variabilis ATCC 29413]				
8945, 8946	46142567	44	1.00E-26	Methanococcoides burtonii DSM 6242	COG0270: Site-specific DNA methylase [Methanococcoides burtonii DSM 6242]			2.1.1.73	
8947, 8948	34558177	23	2.00E-11	Wolinella succinogenes DSM 1740	hypothetical protein WS1882 [Wolinella succinogenes DSM 1740] emb CAE10892.1 hypothetical protein [Wolinella succinogenes]				
8949, 8950	34557666	25	4.00E-11	Wolinella succinogenes DSM 1740	hypothetical protein WS1305 [Wolinella succinogenes DSM 1740] emb CAE10381.1 hypothetical protein [Wolinella succinogenes]				
895, 896	48855611	23	7.00E-10	Cytophaga hutchinsonii	COG3696: Putative silver efflux pump [Cytophaga hutchinsonii]				
8953, 8954					Desulfotalea psychrophila LSV54 chromosome	##	9.00E-07		
8957, 8958	34557246	29	3.00E-34	Wolinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE09961.1 SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]			2.7.3.-	
8961, 8962	51891757	49	5.00E-57	Symbiobacterium thermophilum IAM 14863	long-chain fatty-acid-CoA ligase [Symbiobacterium thermophilum IAM 14863] dbj BAD39604.1 long-chain fatty-acid-CoA ligase [Symbiobacterium thermophilum IAM 14863]			6.2.1.3	

8963, 8964	32473996	42	7.00E-22	Rhodopirellula baltica SH 1	hypothetical protein RB5963 [Rhodopirellula baltica SH 1] emb CAD74532.1 hypothetical protein [Pirellula sp.]				
8967, 8968	34556798	61	8.00E-71	Wolinella succinogenes DSM 1740	DNA GYRASE SUBUNIT A [Wolinella succinogenes DSM 1740] emb CAE09513.1 DNA GYRASE SUBUNIT A [Wolinella succinogenes]	Campylobacter jejuni strain S3BR1 DNA gyrase subunit A (gyrA) gene, partial cds	80	2.00E-15	5.99.1.3
8969, 8970	29346638	51	7.00E-93	Bacteroides thetaiotaomicron VPI-5482	fructose-1,6-bisphosphatase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76335.1 fructose-1,6-bisphosphatase [Bacteroides thetaiotaomicron VPI-5482]	Clostridium tetani E88, section 3 of 10 of the complete genome	93	2.00E-13	3.1.3.11
897, 898	15606535	24	2.00E-09	Aquifex aedificus VF5	hypothetical protein aq_1332 [Aquifex aedificus VF5] gb AAC07320.1 hypothetical protein [Aquifex aedificus VF5] pir D70415 conserved				
8971, 8972	24380120	37	1.00E-14	Streptococcus mutans UA159	putative aspartokinase [Streptococcus mutans UA159] gb AAN59381.1 putative aspartokinase [Streptococcus mutans UA159]			2.7.2.4	
8973, 8974	23023654	28	4.00E-09	Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293	COG0527: Aspartokinases [Leuconostoc mesenteroides subsp. mesenteroides ATCC 8293]			2.7.2.4	
8975, 8976	32262428	60	9.00E-36	Helicobacter hepaticus ATCC 51449	ATP-dependent zinc metalloproteinase [Helicobacter hepaticus ATCC 51449] ref NP_860410.1 ATP-dependent zinc metalloproteinase [Helicobacter hepaticus ATCC 51449]			3.4.24.-	
8977, 8978	34557847	33	6.00E-20	Wolinella succinogenes DSM 1740	ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes DSM 1740] emb CAE10562.1 ATPase EC 3.4.24.-ATP-dependent Zn proteases [Wolinella succinogenes]			3.4.24.-	
8979, 8980	27365382	30	4.00E-07	Vibrio vulnificus CMCP6	Predicted ATP-binding protein involved in virulence [Vibrio vulnificus CMCP6] gb AAO10437.1 Predicted ATP-binding protein involved in virulence [Vibrio vulnificus CMCP6]				
8981, 8982	53713068	32	4.00E-13	Bacteroides fragilis YCH46	hypothetical protein BF1779 [Bacteroides fragilis YCH46] dbj BAD48526.1				
8983, 8984	34558497	55	3.00E-42	Wolinella succinogenes DSM 1740	PUTATIVE INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE11212.1 PUTATIVE INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes]			3.4.24.-	
8987, 8988	34558447	47	2.00E-52	Wolinella succinogenes DSM 1740	PUTATIVE CATION-TRANSPORTING ATPASE [Wolinella succinogenes DSM 1740] emb CAE11162.1 PUTATIVE CATION-TRANSPORTING ATPASE [Wolinella succinogenes]			3.6.1.-	
8989, 8990	30721677	26	6.00E-07	Plasmodium falciparum	phosphoprotein 300 [Plasmodium falciparum]				

899, 900	27376391	33	3.00E-17	110	Bradyrhizobium japonicum USDA	putative isopenicillin N epimerase [Bradyrhizobium japonicum USDA 110] dbj BAC46545.1 bir1280 [Bradyrhizobium japonicum USDA 110]				
8991, 8992	18310283	43	5.00E-54	13	Clostridium perfringens str. 13	2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Clostridium perfringens str. 13] dbj BAB81007.1 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Clostridium perfringens str. 13] sp Q8XKU2 GPMI_CLOPE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (Phosphoglyceromutase) (BPG-independent PGAM) (IPGM)				5.4.2.1
8993, 8994	57241727	47	2.00E-29		Campylobacter lari RM2100	Iron(III) ABC transporter, ATP-binding protein [Campylobacter lari RM2100] gb EAL54397.1 iron(III) ABC transporter, ATP-binding protein [Campylobacter lari RM2100]				1.8.-
8995, 8996	46140416	43	1.00E-23		Dechloromonas aromatica RCB	COG3842: ABC-type spermidine/putrescine transport systems, ATPase components [Dechloromonas aromatica RCB]				1.8.-
8997, 8998	48853662	26	1.00E-21		Cytophaga hutchinsonii	COG1538: Outer membrane protein [Cytophaga hutchinsonii]				
9003, 9004	30249660	31	1.00E-25		Nitrosomonas europaea ATCC 19718	hypothetical protein NE1698 [Nitrosomonas europaea ATCC 19718] emb CAD85609.1 conserved hypothetical protein [Nitrosomonas europaea ATCC 19718]				
9007, 9008	30248800	32	9.00E-21		Nitrosomonas europaea ATCC 19718	possible capK protein [Nitrosomonas europaea ATCC 19718] emb CAD84707.1 possible capK protein [Nitrosomonas europaea ATCC 19718]				6.2.1.30
9009, 9010	29345890	31	4.00E-38		Bacteroides thetaiotaomicron VPI-5482	glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75587.1 glycosyltransferase [Bacteroides thetaiotaomicron VPI-5482]				2.7.8.6
901, 902	27376391	34	6.00E-08		Bradyrhizobium japonicum USDA 110	putative isopenicillin N epimerase [Bradyrhizobium japonicum USDA 110] dbj BAC46545.1 bir1280 [Bradyrhizobium japonicum USDA 110]				
9011, 9012	ABG9157	48	1.00E-76			Desc:Purine/pyrimidine triphosphate type nucleotidyltransferase #156. Org:Aquifex aeolicus				2.7.7.13
9013, 9014	ABG9157	33	2.00E-49			Desc:Purine/pyrimidine triphosphate type nucleotidyltransferase #156. Org:Aquifex aeolicus				2.7.7.13
9019, 9020	39997715	29	2.00E-23		Geobacter sulfurreducens PCA	stage II sporulation-related protein [Geobacter sulfurreducens PCA] gb AAR35993.1 stage II sporulation-related protein [Geobacter sulfurreducens PCA]				
9021, 9022	48853894	31	3.00E-27		Cytophaga hutchinsonii	COG0457: FOG: TPR repeat [Cytophaga hutchinsonii]				
9023, 9024	29347759	40	2.00E-36		Bacteroides thetaiotaomicron VPI-5482	transposase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77456.1 transposase [Bacteroides thetaiotaomicron VPI-5482]				

9025, 9026	23129857	33	1.00E-30	Nostoc punctiforme PCC 73102	COG3920: Signal transduction histidine kinase [Nostoc punctiforme PCC 73102]	Methanosarcina acetivorans str. C2A, section 317 of 534 of the complete genome	91	6.00E-07	2.7.3.-
9027, 9028	ABP6529 5	49	6.00E-17		Desc:Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:39. Org:Bifidobacterium longum				
9029, 9030	34556616	42	5.00E-67	Wolinella succinogenes DSM 1740	CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes DSM 1740] emb CAE09331.1 CATION EFFLUX (ACRB/ACRD/ACRF FAMILY) [Wolinella succinogenes]				
903, 904	53714524	29	4.00E-11	Bacteroides fragilis YCH46	hypothetical protein BF3237 [Bacteroides fragilis YCH46] dbj BAD49982.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
9033, 9034	34557339	58	3.00E-33	Wolinella succinogenes DSM 1740	SENSORY TRANSDUCTION REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10054.1 SENSORY TRANSDUCTION REGULATOR [Wolinella succinogenes]				
9035, 9036	51245785	54	1.00E-36	Desulfotalea psychrophila LSV54	probable phosphoserine aminotransferase [Desulfotalea psychrophila LSV54] emb CAG36662.1 probable phosphoserine aminotransferase				2.6.1.52
9037, 9038	34558042	48	1.00E-63	Wolinella succinogenes DSM 1740	DIHYDROPTEROATE SYNTHASE [Wolinella succinogenes DSM 1740] emb CAE10757.1 DIHYDROPTEROATE SYNTHASE [Wolinella succinogenes]				2.5.1.15
9039, 9040	53711616	21	5.00E-18	Bacteroides fragilis YCH46	hypothetical protein BF0325 [Bacteroides fragilis YCH46] dbj BAD47074.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
9043, 9044	42628871	38	8.00E-30	Haemophilus influenzae R2846	CQG0147: Anthranilate/para-aminobenzoate synthases component I [Haemophilus influenzae R2846]				4.1.3.-
9045, 9046	34557248	37	1.00E-40	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes DSM 1740] emb CAE09963.1 PUTATIVE TWO-COMPONENT REGULATOR [Wolinella succinogenes]				2.7.3.-
9047, 9048	15605731	36	1.00E-12	Aquifex aeolicus VF5	AP4A hydrolase [Aquifex aeolicus VF5] gb AAC06510.1 AP4A hydrolase [Aquifex aeolicus VF5] pir JAT0315 AP4A hydrolase - Aquifex aeolicus				3.6.1.-
9049, 9050	34556741	29	4.00E-09	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09456.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]				
905, 906	46201521	25	3.00E-12	Magnetospirillum magnetotacticum MS-1	COG3287: Uncharacterized conserved protein [Magnetospirillum magnetotacticum MS-1]				

9051, 9052	19704556	27	1.00E-21	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	hypothetical protein FN1221 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL95417.1 Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]				
9053, 9054	54302555	55	3.00E-70	Photobacterium profundum SS9	hypothetical protein PBPR80876 [Photobacterium profundum SS9] emb CAG22748.1 hypothetical protein [Photobacterium profundum]				
9055, 9056	53691429	33	2.00E-17	Desulfovibrio desulfuricans G20	COG1022: Long-chain acyl-CoA synthetases (AMP-forming) [Desulfovibrio desulfuricans G20]				6.2.1.3
9057, 9058	51854402	31	7.00E-23	Oryza sativa (japonica cultivar- group)	putative serine protease [Oryza sativa (japonica cultivar-group)] gb AA177386.1 putative serine protease [Oryza sativa (japonica cultivar- group)]				
9059, 9060	45520556	41	3.00E-67	Methylobacillus flagellatus KT	COG0835: Chemotaxis signal transduction protein [Methylobacillus flagellatus KT]				
9061, 9062	53729945	24	3.00E-07	Dechloromonas aromatica RCB	COG0835: Chemotaxis signal transduction protein [Dechloromonas aromatica RCB]				
9063, 9064	34557963	39	4.00E-27	Wolinella succinogenes DSM 1740	FLAVOPROTEIN [Wolinella succinogenes DSM 1740] emb CAE10678.1 FLAVOPROTEIN [Wolinella succinogenes]				
9065, 9066	57169052	32	6.00E-19	Campylobacter coli RM2228	general secretory pathway protein F [Campylobacter coli RM2228] gb EAL56201.1 general secretory pathway protein F [Campylobacter coli RM2228]				
9067, 9068	28209891	50	9.00E-18	Clostridium tetani E88	NAD(FAD)-utilizing dehydrogenase [Clostridium tetani E88] gb AAO34772.1 NAD(FAD)-utilizing dehydrogenase [Clostridium tetani E88]				
9069, 9070	50929519	47	5.00E-27	Oryza sativa (japonica cultivar- group)	OSJNBa0043A12.24 [Oryza sativa (japonica cultivar-group)] emb CAE02819.1 OSJNBa0043A12.24 [Oryza sativa (japonica cultivar- group)]				2.7.1.10 0
907, 908	57339644	49	8.00E-50	synthetic construct Wolinella	hypothetical protein FTT0520 [synthetic construct]				
9073, 9074	34558184	38	3.00E-14	succinogenes DSM 1740	hypothetical protein WS1889 [Wolinella succinogenes DSM 1740] emb CAE10899.1 hypothetical protein [Wolinella succinogenes]				
9083, 9084	34558196	60	4.00E-26	Wolinella succinogenes DSM 1740	DNA PRIMASE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wolinella succinogenes]				2.7.7.-
9085, 9086	51245189	35	7.00E-13	Desulfotalea psychrophila LSV54	hypothetical protein DP1337 [Desulfotalea psychrophila LSV54] emb CAG36086.1 unknown protein [Desulfotalea psychrophila LSV54]				

9089, 9090	11499619	29	4.00E-21	Archaeoglobus fulgidus DSM 4304 uncultured	translation initiation factor eIF-2B, subunit delta (eif2BD) [Archaeoglobus fulgidus DSM 4304] gb AAB89217.1 translation initiation factor eIF-2B, subunit delta (eif2BD) [Archaeoglobus fulgidus DSM 4304] pir D69504 translation initiation factor eIF-2B, subunit delta (eif2BD) homolog - Archaeoglobus fulgidus sp O28242 E2B2_ARCFU Putative translation initiation factor eIF-2B subunit 2 (eIF-2B GDP-GTP exchange factor)				
909, 910	52550513	36	2.00E-08	archaeon GZfos9D8	conserved hypothetical protein [uncultured archaeon GZfos9D8] Leucyl/phenylalanyl-tRNA--protein transferase [Nitrosomonas europaea ATCC 19718] emb CAD86131.1 Leucyl/phenylalanyl-tRNA--protein transferase [Nitrosomonas europaea ATCC 19718] sp Q82ST5 LFTF_NITEU Leucyl/phenylalanyl-tRNA--protein transferase (L/F-transferase) (Leucyltransferase) (Phenylalanyltransferase)				2.3.2.6
9091, 9092	30250151	50	9.00E-54	Nitrosomonas europaea ATCC 19718	hypothetical protein Chut02001547 [Cytophaga hutchinsonii]				
9093, 9094	48855221	39	3.00E-07	Cytophaga hutchinsonii	COG0642: Signal transduction histidine kinase [Magnetospirillum magnetotacticum MS-1]				2.7.3.-
9097, 9098	46202456	35	3.00E-29	Magnetospirillum magnetotacticum MS-1	fructose-1,6-bisphosphatase [Campylobacter lari RM2100] gb EAL54888.1 fructose-1,6-bisphosphatase [Campylobacter lari RM2100] two-component system response regulator protein [Bacteroides thetaiotaomicron VPI-5482] gb AAO79671.1 two-component system response regulator protein [Bacteroides thetaiotaomicron VPI-5482] Signal transduction histidine kinase [Vibrio vulnificus CMCP6] gb AAO07333.1 Signal transduction histidine kinase [Vibrio vulnificus CMCP6]				3.1.3.11
9099, 9100	57241192	37	2.00E-30	Campylobacter lari RM2100	hypothetical protein BF0193 [Bacteroides fragilis YCH46] dbj BAD46942.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
91, 92	29349974	37	2.00E-30	Bacteroides thetaiotaomicron VPI-5482	hypothetical protein BF3578 [Bacteroides fragilis YCH46] dbj BAD50321.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
9101, 9102	27366816	44	1.00E-67	Vibrio vulnificus CMCP6	Autolysin sensor kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94426.1 Autolysin sensor kinase [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] COG3279: Response regulator of the LysR/AIGR family [Microbulbifer degradans 2-40]				2.7.3.-
9103, 9104	53711484	30	6.00E-12	Bacteroides fragilis YCH46					3.1.1.61
9105, 9106	53714863	47	1.00E-47	Bacteroides fragilis YCH46					
9109, 9110	19703565	41	5.00E-17	Fusobacterium nucleatum subsp. nucleatum ATCC 25586					
9111, 9112	48862014	45	3.00E-22	Microbulbifer degradans 2-40					

9113, 9114	23508673	28	2.00E-07	Plasmodium falci-parum 3D7	MAEBL, putative [Plasmodium falci-parum 3D7] gb AAL10509.1 erythrocyte binding protein 1 [Plasmodium falci-parum] gb AAN36066.1 MAEBL, putative [Plasmodium falci-parum 3D7] gb AAM90625.1 chimeric erythrocyte-binding protein MAEBL [Plasmodium falci-parum]			
9115, 9116	54028700	22	4.00E-08	Polaromonas sp. J5666	COG5001: Predicted signal transduction protein containing a membrane domain, an EAL and a GGDEF domain [Polaromonas sp. J5666]			
9123, 9124	34558286	56	2.00E-72	Wolinella succinogenes DSM 1740	FLAGELLAR BASAL-BODY M-RING PROTEIN FLIF [Wolinella succinogenes DSM 1740] emb CAE11001.1 FLAGELLAR BASAL-BODY M- RING PROTEIN FLIF [Wolinella succinogenes]			
9125, 9126	48836065	38	9.00E-13	Thermobifida fusca	COG1609: Transcriptional regulators [Thermobifida fusca]			
9127, 9128	34558082	51	9.00E-29	Wolinella succinogenes DSM 1740	LIPOPROTEIN [Wolinella succinogenes DSM 1740] emb CAE10797.1 LIPOPROTEIN [Wolinella succinogenes]			
9129, 9130	15896496	36	4.00E-40	Clostridium acetobutylicum ATCC 824	Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] gb AAK81185.1 Sensory transduction protein containing HD_GYP domain [Clostridium acetobutylicum ATCC 824] pir F97299 sensory transduction protein containing HD_GYP domain [Imported] - Clostridium acetobutylicum			
913, 914	15678598	45	2.00E-26	Methanothermobac- ter thermautotrophicus str. Delta H	hypothetical protein MTH570 [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85076.1 unknown [Methanothermobacter thermautotrophicus str. Delta H] pir E69175 hypothetical protein MTH570 - Methanothermobacterium thermautotrophicum (strain Delta H)			
9133, 9134	52007674	33	5.00E-16	Thiobacillus denitrificans ATCC 25259	COG1959: Predicted transcriptional regulator [Thiobacillus denitrificans ATCC 25259]			
9135, 9136	29347043	54	5.00E-39	Bacteroides thetaiotaomicron VPI-5482	mannose-1-phosphate guanylyltransferase [Bacteroides thetaiotaomicron VPI- 5482] gb AAO76740.1 mannose-1-phosphate guanylyltransferase [Bacteroides thetaiotaomicron VPI-5482]			2.7.7.13
9137, 9138	23474120	35	3.00E-39	Desulfovibrio desulfuricans G20	COG1061: DNA or RNA helicases of superfamily II [Desulfovibrio desulfuricans G20]			
9139, 9140	23474120	36	5.00E-30	Desulfovibrio desulfuricans G20	COG1061: DNA or RNA helicases of superfamily II [Desulfovibrio desulfuricans G20]			
9141, 9142	37678505	73	1.00E-97	Vibrio vulnificus YJ016	putative LPS biosynthesis protein [Vibrio vulnificus YJ016] dbj BAC93085.1 putative LPS biosynthesis protein [Vibrio vulnificus YJ016]	Vibrio vulnificus YJ016 DNA, chromosome I, complete sequence	85	5.00E-10

9143, 9144	34558833	35	4.00E-48	Alvinella pompejana eplibionti 7G3	phenylalanyl-tRNA synthetase beta subunit [Alvinella pompejana eplibionti 7G3]			6.1.1.20
9145, 9146	34558357	51	7.00E-68	Wolinella succinogenes DSM 1740	conserved hypothetical protein-PUTATIVE Mg DEPENDENT DNase [Wolinella succinogenes DSM 1740] emb CAE11072.1 conserved hypothetical protein-PUTATIVE Mg DEPENDENT DNase [Wolinella succinogenes]			3.1.21.-
9147, 9148	34558357	54	4.00E-46	Wolinella succinogenes DSM 1740	conserved hypothetical protein-PUTATIVE Mg DEPENDENT DNase [Wolinella succinogenes DSM 1740] emb CAE11072.1 conserved hypothetical protein-PUTATIVE Mg DEPENDENT DNase [Wolinella succinogenes]			3.1.21.-
9149, 9150	23114483	37	3.00E-40	Desulfotobacterium hafniense DCB-2	COG2931: RTX toxins and related Ca2+-binding proteins [Desulfotobacterium hafniense DCB-2]			
915, 916	50086533	40	6.00E-10	Acinetobacter sp. ADP1	hypothetical protein ACIAD3581 [Acinetobacter sp. ADP1] emb CAG70221.1 conserved hypothetical protein [Acinetobacter sp. ADP1]			2.3.1.-
9151, 9152	34557851	32	2.00E-39	Wolinella succinogenes DSM 1740	hypothetical protein WS1518 [Wolinella succinogenes DSM 1740] emb CAE10566.1 conserved hypothetical protein [Wolinella succinogenes]			
9157, 9158	34396892	30	3.00E-13	Porphyromonas gingivalis W83	ISPg7, transposase [Porphyromonas gingivalis W83] ref NP_904759.1			
9159, 9160	46319318	48	5.00E-57	Burkholderia cepacia R1808	ISPG7, transposase [Porphyromonas gingivalis W83] COG0513: Superfamily II DNA and RNA helicases [Burkholderia cepacia R1808]			2.7.7.-
9161, 9162	34557573	33	2.00E-29	Wolinella succinogenes DSM 1740	SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes]			2.7.3.-
9163, 9164	23128221	34	5.00E-17	Nostoc punctiforme PCC 73102	COG4328: Uncharacterized protein conserved in bacteria [Nostoc punctiforme PCC 73102]			
9165, 9166	34557016	52	3.00E-23	Wolinella succinogenes DSM 1740	hypothetical protein WS0599 [Wolinella succinogenes DSM 1740] emb CAE09731.1 conserved hypothetical protein [Wolinella succinogenes]			
9167, 9168	13472325	31	3.00E-22	Mesorhizobium loti MAFF303099	endo-1,3-1,4-beta-glycanase [Mesorhizobium loti MAFF303099] dbj BAB49678.1 endo-1,3-1,4-beta-glycanase [Mesorhizobium loti MAFF303099]			3.2.1.-
9169, 9170	23103201	50	2.00E-53	Azotobacter vinelandii	COG2871: Na+-transporting NADH:ubiquinone oxidoreductase, subunit NqrF [Azotobacter vinelandii]			1.6.5.-
917, 918	21241362	50	1.00E-76	Xanthomonas axonopodis pv. citri str. 306	dipeptidyl peptidase IV [Xanthomonas axonopodis pv. citri str. 306] gb AAM35480.1 dipeptidyl peptidase IV [Xanthomonas axonopodis pv. citri str. 306]			

9173, 9174	34556562	80	2.00E-97	1740	Wolinella succinogenes DSM	PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes DSM 1740] emb CAE09277.1 PEPTIDE CHAIN RELEASE FACTOR 2 [Wolinella succinogenes]			
9177, 9178	15669248	31	4.00E-11	2661	Methanocaldococcus jannaschii DSM	capsular polysaccharide biosynthesis protein M [Methanocaldococcus jannaschii DSM 2661] gb AAB99063.1 capsular polysaccharide biosynthesis protein M [Methanocaldococcus jannaschii DSM 2661] pir B64432 capsular polysaccharide biosynthesis protein M homolog - Methanocaldococcus jannaschii sp Q58459 YA59_METJA Hypothetical glycosyl transferase MJ1059			2.4.1.-
9179, 9180	50591112	27	2.00E-09	89/1591	Streptococcus suis	COG0438: Glycosyltransferase [Streptococcus suis 89/1591]			2.-.-.-
9185, 9186	AAW9853	56	1.00E-76			Desc:H. pylori GHPO 1479 protein. Org:Helicobacter pylori	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 3/6	95	4.00E-08 1.8.-.-
9189, 9190	46130289	56	1.00E-32	7942	Synechococcus elongatus PCC	COG0517: FOG: CBS domain [Synechococcus elongatus PCC 7942]			2.7.3.-
919, 920	48853693	54	7.00E-38		Cytophaga hutchinsonii	COG1801: Uncharacterized conserved protein [Cytophaga hutchinsonii]			
9193, 9194	45683694	41	1.00E-31	BNC1	Mesorhizobium sp.	COG0438: Glycosyltransferase [Mesorhizobium sp. BNC1]			
9197, 9198	45508536	39	3.00E-20	ATCC 29413	Anabaena variabilis	COG0535: Predicted Fe-S oxidoreductases [Anabaena variabilis ATCC 29413] gb AA93025.1 NifX2			
9201, 9202	20807566	29	1.00E-17	MB4	Thermoanaerobacter tengcongensis	Diguanylate cyclase/phosphodiesterase domain 1 (GGDEF) [Thermoanaerobacter tengcongensis MB4] gb AAM2434.1 Diguanylate cyclase/phosphodiesterase domain 1 (GGDEF) [Thermoanaerobacter tengcongensis MB4]			2.7.3.-
9207, 9208	57168029	42	3.00E-24	RM2228	Campylobacter coli	ADP-heptose-1ps heptosyltransferase II (rfaf) [Campylobacter coli RM2228] gb EAL57072.1 ADP-heptose-1ps heptosyltransferase II (rfaf) [Campylobacter coli RM2228]			
9209, 9210	48633897	39	5.00E-09	MC-1	Magnetococcus sp.	COG0840: Methyl-accepting chemotaxis protein [Magnetococcus sp. MC-1]			
921, 922	21241377	50	2.00E-31		Xanthomonas axonopodis pv. citri str. 306	endonuclease [Xanthomonas axonopodis pv. citri str. 306] gb AAM35495.1			3.2.2.23
9211, 9212	48853603	46	2.00E-52		Cytophaga hutchinsonii	COG0809: S-adenosylmethionine tRNA-ribosyltransferase-isomerase (queuine synthetase) [Cytophaga hutchinsonii]			5.-.-.-

9213, 9214	9948626	51	1.00E-71	Pseudomonas aeruginosa PAO1	conserved hypothetical protein [Pseudomonas aeruginosa PAO1] pir B83326 conserved hypothetical protein PA2566 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_251256.1 hypothetical protein PA2566 [Pseudomonas aeruginosa PAO1]			1.6.99.3
9215, 9216	32261568	40	2.00E-45	Helicobacter hepaticus ATCC 51449	two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449] ref NP_859552.1 two-component sensor histidine kinase family protein [Helicobacter hepaticus ATCC 51449]			2.7.3.-
9217, 9218	57168343	33	5.00E-44	Campylobacter coli RM2228	conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56825.1 conserved hypothetical protein [Campylobacter coli RM2228]			
9219, 9220	53712708	36	2.00E-42	Bacteroides fragilis YCH46	hypothetical protein BF1415 [Bacteroides fragilis YCH46] dbj BAD48166.1 conserved hypothetical protein [Bacteroides fragilis YCH46] related to two-component system sensory/regulatory protein (Ntr family) [Desulfotalea psychrophila LSV54] emb CAG37842.1 related to two- component system sensory/regulatory protein (Ntr family) [Desulfotalea psychrophila LSV54]			2.7.3.-
9221, 9222	51246965	38	1.00E-37	Desulfotalea psychrophila LSV54	biotin synthetase [Clostridium perfringens str. 13] dbj BAB81250.1 biotin synthetase [Clostridium perfringens str. 13]			2.8.1.6
9225, 9226	18310526	44	4.00E-18	Clostridium perfringens str. 13	COG0536: Predicted GTPase [Cytophaga hutchinsonii] hypoxanthine-guanine phosphoribosyltransferase [Bacteroides thetataomicron VPI-5482] gb AAO79491.1 hypoxanthine-guanine phosphoribosyltransferase [Bacteroides thetataomicron VPI-5482]			2.4.2.8
9227, 9228	48853834	77	1.00E-102	Cytophaga hutchinsonii	COG0587: DNA polymerase III, alpha subunit [Mesorhizobium sp. BNC1]			2.7.7.7
9229, 9230	29349794	53	9.00E-50	Bacteroides thetataomicron VPI-5482	sensory box sensor histidine kinase/response regulator [Dehalococcoides ethenogenes 195] gb AAW39739.1 sensory box sensor histidine kinase/response regulator [Dehalococcoides ethenogenes 195] SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10288.1 SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes]			2.7.3.-
923, 924	45684496	37	1.00E-21	Mesorhizobium sp. BNC1	SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes DSM 1740] emb CAE10872.1 SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes]			2.7.3.-
9231, 9232	57234234	39	6.00E-24	Dehalococcoides ethenogenes 195	hypothetical protein lpp0207 [Legionella pneumophila str. Paris] emb CAH11354.1 hypothetical protein [Legionella pneumophila str. Paris]			2.7.3.-
9233, 9234	34557573	35	6.00E-13	Wolinella succinogenes DSM 1740				
9235, 9236	34558157	44	8.00E-16	Wolinella succinogenes DSM 1740				
9239, 9240	54296182	33	1.00E-27	Legionella pneumophila str. Paris				

9245, 9246	29608580	31	3.00E-18	Streptomyces avermitilis MA-4680	hypothetical protein [Streptomyces avermitilis MA-4680] ref NP_826099.1 hypothetical protein SAV4922 [Streptomyces avermitilis MA-4680]				
9247, 9248	34557912	40	5.00E-38	Wolinella succinogenes DSM 1740	hypothetical protein WS1588 [Wolinella succinogenes DSM 1740] emb CAE10627.1 conserved hypothetical protein [Wolinella succinogenes] two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482] gb AAO79283.1 two-component system sensor histidine kinase/response regulator, hybrid (one-component system) [Bacteroides thetaiotaomicron VPI-5482]				
925, 926	29349586	27	1.00E-11	Bacteroides thetaitaomicron VPI-5482					
9251, 9252	34557353	34	6.00E-35	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10068.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]				2.7.3.-
9253, 9254	34558157	29	6.00E-18	Wolinella succinogenes DSM 1740	SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes DSM 1740] emb CAE10872.1 SENSOR KINASE OF TWO-COMPONENT REGULATORY SYSTEM [Wolinella succinogenes]				2.7.3.-
9255, 9256	57506022	57	1.00E-29	Campylobacter upsaliensis RM3195	chemotaxis regulatory protein Cj1118c [Campylobacter upsaliensis RM3195] chemotaxis regulatory protein Cj1118c [Campylobacter upsaliensis RM3195]				2.7.3.-
9257, 9258	37913015	45	2.00E-37	uncultured marine alpha proteobacterium HOT2C01	predicted sugar fermentation stimulation protein [uncultured marine alpha proteobacterium HOT2C01]				
9261, 9262	29655162	32	3.00E-21	Coxiella burnetii RSA 493	hypothetical protein CBU1877 [Coxiella burnetii RSA 493] gb AAO91388.1 conserved domain protein [Coxiella burnetii RSA 493]				
9263, 9264	38637724	38	4.00E-11	Cupriavidus necator	putative integrase/recombinase [Cupriavidus necator] gb AAP85812.1 putative integrase/recombinase [Ralstonia eutropha]				
9265, 9266	34556591	49	2.00E-31	Wolinella succinogenes DSM 1740	PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolinella succinogenes DSM 1740] emb CAE09306.1 PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolinella succinogenes]				4.2.1.70
9267, 9268	34556593	33	8.00E-09	Wolinella succinogenes DSM 1740	hypothetical protein WS0145 [Wolinella succinogenes DSM 1740] emb CAE09308.1 conserved hypothetical protein [Wolinella succinogenes] sp Q7MST9 TRMB_WOLSU tRNA (guanine-N(7))-methyltransferase (tRNA(m7G46)-methyltransferase)				2.1.1.-
9269, 9270	34556592	33	8.00E-26	Wolinella succinogenes DSM 1740	PUTATIVE FIBRONECTIN DOMAIN-CONTAINING LIPOPROTEIN [Wolinella succinogenes DSM 1740] emb CAE09307.1 PUTATIVE FIBRONECTIN DOMAIN-CONTAINING LIPOPROTEIN [Wolinella succinogenes]				

927, 928	48862188	36	3.00E-09	Microbulbifer degradans 2-40	COG0745: Response regulators consisting of a CheY-like receiver domain and a winged-helix DNA-binding domain [Microbulbifer degradans 2-40]				
9273, 9274	19703530	26	4.00E-13	Fusobacterium nucleatum subsp. nucleatum ATCC 25586	hypothetical protein FN0185 [Fusobacterium nucleatum subsp. nucleatum ATCC 25586] gb AAL94391.1 Hypothetical protein [Fusobacterium nucleatum subsp. nucleatum ATCC 25586]				
9275, 9276	57168392	37	3.00E-23	Campylobacter coli RM2228	conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56874.1 conserved hypothetical protein [Campylobacter coli RM2228]				
9277, 9278	34556741	22	2.00E-10	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE09456.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]				
9279, 9280	15823603	35	9.00E-35	Sphaerotilus natans	putative RNA polymerase associated protein [Sphaerotilus natans]				2.7.7.-
9281, 9282	48860351	48	9.00E-52	Clostridium thermocellum ATCC 27405	COG2206: HD-GYP domain [Clostridium thermocellum ATCC 27405]				
9283, 9284	34558426	67	7.00E-80	Wolinella succinogenes DSM 1740	CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN [Wolinella succinogenes DSM 1740] emb CAE11141.1 CARBAMOYL-PHOSPHATE SYNTHASE LARGE CHAIN [Wolinella succinogenes]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 1/6	81	1.00E-23	6.3.5.5
9285, 9286	29348936	63	1.00E-85	Bacteroides thetaiotaomicron VPI-5482	alpha-1,2-mannosidase [Bacteroides thetaiotaomicron VPI-5482] gb AAC78633.1 alpha-1,2-mannosidase [Bacteroides thetaiotaomicron VPI- 5482]	Bacteroides thetaiotaomicron VPI-5482, section 18 of 21 of the complete genome	83	5.00E-07	
9287, 9288	53712180	31	2.00E-07	Bacteroides fragilis YCH46	hypothetical protein BF0887 [Bacteroides fragilis YCH46] dbj BAD47638.1 hypothetical protein [Bacteroides fragilis YCH46]				
9289, 9290	57167668	49	3.00E-59	Campylobacter coli RM2228	DNA repair protein RecN, putative [Campylobacter coli RM2228] gb EAL57454.1 DNA repair protein RecN, putative [Campylobacter coli RM2228]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 2/6	93	2.00E-09	
929, 930	48856028	46	1.00E-37	Cytophaga hutchinsonii	COG1057: Nicotinic acid mononucleotide adenyltransferase [Cytophaga hutchinsonii]				2.7.7.18
9291, 9292	57241121	41	9.00E-39	Campylobacter lari RM2100	DNA repair protein RecN, putative [Campylobacter lari RM2100] gb EAL54817.1 DNA repair protein RecN, putative [Campylobacter lari RM2100]				

9293, 9294	57505945 AAY7460	32	7.00E-07	Campylobacter upsaliensis RM3195	hypothetical protein CUPA0081 [Campylobacter upsaliensis gb EAL52535.1 hypothetical protein CUPA0081 [Campylobacter upsaliensis RM3195]				
9295, 9296	4	45	3.00E-78		Desc:Neisseria meningitidis ORF 164 protein sequence SEQ ID NO:682. Org:Neisseria meningitidis				6.2.1.3
9297, 9298	53758726	39	4.00E-30	Methylococcus capsulatus str. Bath	oxygen-independent coproporphyrinogen III oxidase family protein, putative [Methylococcus capsulatus str. Bath] ref YP_113360.1 oxygen-independent coproporphyrinogen III oxidase family protein, putative [Methylococcus capsulatus str. Bath]				
9299, 9300	34558271	72	2.00E-94	Wolinella succinogenes DSM 1740	DNA POLYMERASE III ALPHA SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10986.1 DNA POLYMERASE III ALPHA SUBUNIT [Wolinella succinogenes]				
93, 9303, 9304	45357832 56315748	39 34	1.00E-30 3.00E-26	Methanococcus maripaludis S2 Azoarcus sp. EBN1	hypothetical protein MMP0269 [Methanococcus maripaludis S2] emb CAF29825.1 conserved hypothetical protein [Methanococcus maripaludis S2] conserved hypothetical protein [Azoarcus sp. EBN1]				
9305, 9306	57240361	37	3.00E-12	Campylobacter lari RM2100	conserved hypothetical protein [Campylobacter lari gb EAL55475.1 conserved hypothetical protein [Campylobacter lari RM2100]				
9309, 9310	34763472	63	2.00E-75	Fusobacterium nucleatum subsp. vincentii ATCC 49256	Fe-S OXIDOREDUCTASE (1.8.-.-) [Fusobacterium nucleatum subsp. vincentii ATCC 49256] gb EAA23990.1 Fe-S OXIDOREDUCTASE (1.8.-.-) [Fusobacterium nucleatum subsp. vincentii ATCC 49256]				1.8.-.-
9311, 9312	34556560	35	2.00E-54	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]				
9313, 9314	9655294	32	7.00E-13	Vibrio cholerae O1 biovar eltor str. N16961	conserved hypothetical protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_230490.1 hypothetical protein VC0842 [Vibrio cholerae O1 biovar eltor str. N16961] gb AAK20799.1 unknown [Vibrio cholerae] gb AAK20769.1 unknown [Vibrio cholerae] pir G82273 conserved hypothetical protein VC0842 [imported] - Vibrio cholerae (strain N16961 serogroup O1)				
9315, 9316	53735933	41	6.00E-52	Crocospaera watsonii WH 8501	COG2202: FOG: PAS/PAC domain [Crocospaera watsonii WH 8501]				
9317, 9318	34557196	53	4.00E-44	Wolinella succinogenes DSM 1740	LIPID A DISACCHARIDE SYNTHASE [Wolinella succinogenes DSM 1740] emb CAE09911.1 LIPID A DISACCHARIDE SYNTHASE [Wolinella succinogenes]				2.4.1.18 2

9319, 9320	37679818	39	2.00E-12	Vibrio vulnificus YJ016	ATP-dependent DNA ligase [Vibrio vulnificus YJ016] dbj BAC94398.1 ATP-dependent DNA ligase [Vibrio vulnificus YJ016]			6.5.1.1
9321, 9322	57240881	37	3.00E-32	Campylobacter lari RM2100	molybdenum cofactor biosynthesis protein [Campylobacter lari RM2100] gb EAL55274.1 molybdenum cofactor biosynthesis protein [Campylobacter lari RM2100]			
9323, 9324	34396573	35	5.00E-07	Porphyromonas gingivalis W83	hypothetical protein PG0439 [Porphyromonas gingivalis W83] ref NP_904740.1 hypothetical protein PG0439 [Porphyromonas gingivalis W83]			
9325, 9326	28195134	48	2.00E-31	Agrobacterium tumefaciens	OphA [Agrobacterium tumefaciens]			
9327, 9328	27807025	50	1.00E-40	ubiquinone	NADH dehydrogenase flavoprotein 2 (24kD) [ubiquinone] [NADH-ubiquinone reductase 24 kDa mitochondrial] [Bos taurus] sp P04394 NUHM_BOVIN NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial precursor (Polypeptide I) pir B30113 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) 24K chain precursor - bovine gb AAA87358.1 NADH-ubiquinone reductase 24 kDa subunit [Bos taurus]			1.6.5.3
9329, 9330	27365565	38	1.00E-36	Vibrio vulnificus CMCP6	Transcriptional regulator [Vibrio vulnificus CMCP6] ref NP_934898.1 transcriptional regulator [Vibrio vulnificus YJ016] gb AAO10820.1 transcriptional regulator [Vibrio vulnificus CMCP6] gb AAK31574.1 transcriptional regulator [Vibrio vulnificus] dbj BAC94869.1 transcriptional regulator [Vibrio vulnificus YJ016]			2.7.3.-
9331, 9332	52548588	28	4.00E-16	uncultured archaeon GZfos17F1	FOG TPR repeat [uncultured archaeon GZfos17F1]			
9333, 9334	53714264	40	3.00E-37	Bacteroides fragilis YCH46	folypolyglutamate synthase [Bacteroides fragilis YCH46] dbj BAD49722.1 folypolyglutamate synthase [Bacteroides fragilis YCH46]			6.3.2.17
9335, 9336	21673114	27	1.00E-15	Chlorobium tepidum TLS	hypothetical protein CT0275 [Chlorobium tepidum TLS] gb AAM71521.1 hypothetical protein [Chlorobium tepidum TLS]			
9339, 9340	46140415	53	5.00E-41	Dechloromonas aromatica RCB	COG2360: Leu/Phe-tRNA-protein transferase [Dechloromonas aromatica RCB]			2.3.2.6
9341, 9342	52549555	34	3.00E-13	uncultured archaeon GZfos27G5	transposase [uncultured archaeon GZfos27G5]			
9343, 9344	34557172	35	1.00E-42	Wolinella succinogenes DSM 1740	SENSORY PROTEIN, CONTAINING EAL-DOMAIN [Wolinella succinogenes DSM 1740] emb CAE09887.1 SENSORY PROTEIN, CONTAINING EAL-DOMAIN [Wolinella succinogenes]			
9345, 9346	56707343	41	6.00E-19	Francisella tularensis subsp. tularensis Schu 4	Acetyltransferase [Francisella tularensis subsp. tularensis Schu 4] emb CAG44810.1 Acetyltransferase [Francisella tularensis subsp. tularensis]			2.3.1.12

9347, 9348	37519796	28	2.00E-11	Gloeobacter violaues PCC 7421	hypothetical protein glr0227 [Gloeobacter violaceus PCC 7421] dbj BAC88168.1 glr0227 [Gloeobacter violaceus PCC 7421]			
9349, 9350	15607034	38	9.00E-16	Aquifex aeolicus VF5	hypothetical protein aq_2067 [Aquifex aeolicus VF5] gb AAC07822.1 hypothetical protein [Aquifex aeolicus VF5] pir C70477 conserved hypothetical protein aq_2067 - Aquifex aeolicus			
935, 936	18977094	57	3.00E-56	Pyrococcus furius DSM 3638	alkyl hydroperoxide reductase subunit c [Pyrococcus furiosus DSM 3638] gb AAL80846.1 alkyl hydroperoxide reductase subunit c [Pyrococcus furius DSM 3638]	1.6.4.-		
9353, 9354	37527191	38	4.00E-23	Photobacterium luminescens subsp. laumondii TTO1	hypothetical protein plu3313 [Photobacterium luminescens subsp. laumondii TTO1] emb CAE15687.1 unnamed protein product [Photobacterium luminescens subsp. laumondii TTO1]	2.7.3.-		
9355, 9356	34558184	30	1.00E-24	Wolinella succinogenes DSM 1740	hypothetical protein WS1889 [Wolinella succinogenes DSM 1740] emb CAE10899.1 hypothetical protein [Wolinella succinogenes]			
9357, 9358	34556947	41	4.00E-19	Wolinella succinogenes DSM 1740	hypothetical protein WS0526 [Wolinella succinogenes DSM 1740] emb CAE09662.1 hypothetical protein [Wolinella succinogenes]			
9363, 9364	34557494	45	8.00E-27	Wolinella succinogenes DSM 1740	PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes DSM 1740] emb CAE10209.1 PUTATIVE UREA AMIDOLYASE [Wolinella succinogenes]	6.3.4.6		
9365, 9366	53713853	28	1.00E-09	Bacteroides fragilis YCH46	hypothetical protein BF2562 [Bacteroides fragilis YCH46] dbj BAD49311.1 hypothetical protein [Bacteroides fragilis YCH46]			
9367, 9368	34557273	45	1.00E-25	Wolinella succinogenes DSM 1740	hypothetical protein WS0881 [Wolinella succinogenes DSM 1740] emb CAE09988.1 hypothetical protein [Wolinella succinogenes]	2.7.1.14 8		
9369, 9370	32262467	41	3.00E-17	Helicobacter hepaticus ATCC 51449	hypothetical protein HH0918 [Helicobacter hepaticus ATCC 51449] ref NP_860449.1 hypothetical protein HH0918 [Helicobacter hepaticus ATCC 51449]			
937, 938	15669750	44	7.00E-56	Methanocaldococcus jannaschii DSM 2661	aspartyl-tRNA synthetase (aspS) [Methanocaldococcus jannaschii DSM 2661] gb AAB99575.1 aspartyl-tRNA synthetase (aspS) [Methanocaldococcus jannaschii DSM 2661] pir B64494 aspartate-tRNA ligase (EC 6.1.1.12) - Methanocaldococcus jannaschii sp Q58950 SYD_METJA Aspartyl-tRNA synthetase (Aspartate-tRNA ligase) (AspRS)	6.1.1.12		
9371, 9372	57506092	36	2.00E-22	Campylobacter upsallensis RM3195	site-specific recombinase, phage integrase family, putative [Campylobacter upsallensis RM3195] gb EAL52368.1 site-specific recombinase, phage integrase family, putative [Campylobacter upsallensis RM3195]			

9381, 9382	57505780	49	7.00E-44	Campylobacter upsaliensis RM3195	Phosphoglycolate phosphatase [Campylobacter upsaliensis RM3195] gb EAL52841.1 Phosphoglycolate phosphatase [Campylobacter upsaliensis RM3195]			3.1.3.18	
9383, 9384	34557641	54	3.00E-32	Wolinella succinogenes DSM 1740	MEMBRANE-BOUND LYTC MUREIN TRANSGLYCOSYLASE C [Wolinella succinogenes DSM 1740] emb CAE10356.1 MEMBRANE-BOUND LYTC MUREIN TRANSGLYCOSYLASE C [Wolinella succinogenes]			3.2.1.-	
9385, 9386	57237342	44	1.00E-18	Campylobacter jejuni RM1221	transcription elongation factor GreA [Campylobacter jejuni RM1221] gb AAW34925.1 transcription elongation factor GreA [Campylobacter jejuni RM1221] emb CAB72754.1 transcription elongation factor [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281480.1 transcription elongation factor [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81447 transcription elongation factor Cj0287c [imported] - Campylobacter jejuni (strain NCTC 11168) sp Q9PIK9 GRE_A_CAMJE Transcription elongation factor greA (Transcript cleavage factor greA)				
9387, 9388	9654693	44	6.00E-27	Vibrio cholerae O1 biovar eltor str. N16961	methyl-accepting chemotaxis protein [Vibrio cholerae O1 biovar eltor str. N16961] ref NP_229938.1 methyl-accepting chemotaxis protein [Vibrio cholerae O1 biovar eltor str. N16961] pir F82342 methyl-accepting chemotaxis protein VC0282 [imported] - Vibrio cholerae (strain N16961 serogroup O1)			2.7.3.-	
9389, 9390	16799970	53	1.00E-37	Listeria innocua Clip11262	hypothetical protein lin0897 [Listeria innocua Clip11262] emb CAC96129.1 lin0897 [Listeria innocua] pir A11544 conserved hypothetical protein lin0897 [Imported] - Listeria innocua (strain Clip11262)				
939, 940	46114100	34	9.00E-25	Exiguobacterium sp. 255-15	COG2357: Uncharacterized protein conserved in bacteria [Exiguobacterium sp. 255-15]				
9395, 9396	53711901	60	9.00E-93	Bacteroides fragilis YCH46	threonine synthase [Bacteroides fragilis YCH46] dbj BAD47359.1 threonine synthase [Bacteroides fragilis YCH46]			4.2.99.2	
9397, 9398	48853586	68	7.00E-73	Cytophaga hutchinsonii	COG0466: ATP-dependent Lon protease, bacterial type [Cytophaga hutchinsonii]	Buchnera aphidicola str. Sg (Schizaphis graminum) section 47 of 57 of the complete genome	86	7.00E-123	3.4.21.5
9399, 9400	53682950	27	2.00E-12	Desulfotobacterium hafnense DCB-2	COG1506: Dipeptidyl aminopeptidases/acylaminoacyl-peptidases [Desulfotobacterium hafnense DCB-2]				
9403, 9404	53712001	33	8.00E-37	Bacteroides fragilis YCH46	DNA polymerase III alpha subunit [Bacteroides fragilis YCH46] dbj BAD47459.1 DNA polymerase III alpha subunit [Bacteroides fragilis YCH46]				2.7.7.7

9407, 9408	33594842	59	1.00E-98	Bordetella parapertussis 12822	putative asparagine synthetase [Bordetella parapertussis 12822] emb CAE39864.1 putative asparagine synthetase [Bordetella parapertussis]			6.3.5.4
9409, 9410, 9411, 942	6968464	40	2.00E-30	Campylobacter jejuni subsp. jejuni NCTC 11168	possible purine/pyrimidine phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168] pir A81305 probable purine/pyrimidine phosphoribosyltransferase Cj1028c [imported] - Campylobacter jejuni (strain NCTC 11168) ref NP_282178.1 possible purine/pyrimidine phosphoribosyltransferase [Campylobacter jejuni subsp. jejuni NCTC 11168]			
941, 942	48864233	42	6.00E-20	Microbulbifer degradans 2-40	COG0845: Membrane-fusion protein [Microbulbifer degradans 2-40]			
9411, 9412	57241187	52	1.00E-73	Campylobacter lari RM2100	glutamyl-tRNA synthetase [Campylobacter lari RM2100] gb EAL54883.1 glutamyl-tRNA synthetase [Campylobacter lari RM2100]			6.1.1.17
9415, 9416	34558436	45	2.00E-57	Wolinella succinogenes DSM 1740	FERROCHELATASE LIKE PROTEIN, HemH [Wolinella succinogenes DSM 1740] emb CAE11151.1 FERROCHELATASE LIKE PROTEIN, HemH [Wolinella succinogenes] sp Q7M7P9 HEMZ_WOLSU Ferrochelatase (Protoheme ferro-lyase) (Heme synthetase)			4.99.1.1
9417, 9418	46142296	60	1.00E-106	Methanococcoides burtonii DSM 6242	COG4804: Uncharacterized conserved protein [Methanococcoides burtonii DSM 6242]			
9421, 9422	42523963	29	7.00E-17	Bdellovibrio bacteriovorus HD100	hypothetical protein Bc2538 [Bdellovibrio bacteriovorus HD100] emb CAE80336.1 hypothetical protein predicted by Glimmer/Critica [Bdellovibrio bacteriovorus HD100]			
9423, 9424	34556564	51	3.00E-75	Wolinella succinogenes DSM 1740	PUTATIVE OXIDOREDUCTASE [Wolinella succinogenes DSM 1740] emb CAE09279.1 PUTATIVE OXIDOREDUCTASE [Wolinella succinogenes]			1.-.-.-
9425, 9426	11500024	28	4.00E-19	Archaeoglobus fulgidus DSM 4304	spermidine/putrescine ABC transporter, periplasmic spermidine/putrescine- binding protein:(potD) [Archaeoglobus fulgidus DSM 4304]			
9427, 9428	18976874	33	9.00E-11	Pyrococcus furius DSM 3638	iron(III) dicitrate transport system permease protein fece [Pyrococcus furius DSM 3638] gb AAL80626.1 iron(III) dicitrate transport system permease protein fece [Pyrococcus furius DSM 3638]			
9429, 9430	15644626	43	4.00E-55	Thermotoga maritima MSB8	transketolase, N-terminal subunit [Thermotoga maritima MSB8]			2.2.1.1
943, 944	53713329	30	7.00E-30	Bacteroides fragilis YCH46	putative two-component system sensor histidine kinase [Bacteroides fragilis YCH46] dbj BAD48787.1 putative two-component system sensor histidine kinase [Bacteroides fragilis YCH46]			2.7.3.-
9431, 9432	34557407	43	1.00E-35	Wolinella succinogenes DSM 1740	DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes DSM 1740] emb CAE10122.1 DIGUANYLATE CYCLASE (FRAGMENT) [Wolinella succinogenes]			2.7.3.-

9433, 9434	34557728	34	7.00E-19	Wolinella succinogenes DSM 1740	CHEY AND CHEB GENES (CHEMOTAXIS PROTEIN) [Wolinella succinogenes DSM 1740] emb CAE10443.1 CHEY AND CHEB GENES (CHEMOTAXIS PROTEIN) [Wolinella succinogenes]			
9437, 9438	57169066	26	2.00E-23	Campylobacter coli RM2228	conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56215.1 conserved hypothetical protein [Campylobacter coli RM2228]			
9439, 9440	48860369	31	2.00E-19	Clostridium thermocellum ATCC 27405	COG4585: Signal transduction histidine kinase [Clostridium thermocellum ATCC 27405]			2.7.3.-
9443, 9444	34557809	68	2.00E-85	Wolinella succinogenes DSM 1740	ABC TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10524.1 ABC TRANSPORT SYSTEM ATP-BINDING PROTEIN [Wolinella succinogenes]	Campylobacter jejuni subsp. jejuni NCTC 11168 complete genome; segment 4/6	82	2.00E-09 1.8.-.-
9445, 9446	57285504	56	2.00E-30	Staphylococcus aureus subsp. aureus COL	type I restriction-modification system, S subunit, EcoA family, putative [Staphylococcus aureus subsp. aureus COL] ref NP_373643.1 probable restriction modification system specificity subunit [Staphylococcus aureus subsp. aureus N315] db BAB56594.1 probable restriction modification system specificity subunit [Staphylococcus aureus subsp. aureus Mu50] pir B89808 hypothetical protein hsdS [imported] - Staphylococcus aureus (strain N315) db BAB41621.1 probable restriction modification system specificity subunit [Staphylococcus aureus subsp. aureus N315] ref NP_370956.1 probable restriction modification system specificity subunit [Staphylococcus aureus subsp. aureus Mu50] ref YP_185367.1 type I restriction-modification system, S subunit, EcoA family, putative [Staphylococcus aureus subsp. aureus COL]	Desc:Staphylococ- cus aureus contig SEQ ID #546. Org:Staphylococcus aureus	87	5.00E-10 3.1.21.3
9447, 9448	48855054	50	3.00E-22	Cytophaga hutchinsonii	COG0491: Zn-dependent hydrolases, including glyoxylases [Cytophaga hutchinsonii]			3.1.2.6
945, 946	15678643	45	4.00E-53	Methanothermobac- ter thermautotrophicus str. Delta H	adenylosuccinate synthetase [Methanothermobacter thermautotrophicus str. Delta H] gb AAB85121.1 adenylosuccinate synthetase [Methanothermobacter thermautotrophicus str. Delta H] pir G69181 adenylosuccinate synthetase - Methanobacterium thermautotrophicum (strain Delta H) sp Q26712 PURA_METTH Adenylosuccinate synthetase (IMP-aspartate ligase) (AdSS) (AMPSase)			6.3.4.4
9453, 9454	34557754	45	1.00E-65	Wolinella succinogenes DSM 1740	TRANSCRIPTIONAL REGULATOR (NIFA FAMILY) [Wolinella succinogenes DSM 1740] emb CAE10489.1 TRANSCRIPTIONAL REGULATOR (NIFA FAMILY) [Wolinella succinogenes]			2.7.3.9

9455, 9456	46142296	74	3.00E-74	Methanococcoides burtonii DSM 6242	COG4804: Uncharacterized conserved protein [Methanococcoides burtonii] DSM 6242]				
9457, 9458	34557246	27	8.00E-34	Wolinella succinogenes DSM 1740	SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes DSM 1740] embjCAE09961.1] SENSORY TRANSDUCTION HISTIDINE KINASE [Wolinella succinogenes]			2.7.3.-	
9459, 9460	34557573	49	6.00E-75	Wolinella succinogenes DSM 1740	SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] embjCAE10288.1] SENSORY BOX/GGDEF FAMILY PROTEIN [Wolinella succinogenes]			2.7.3.-	
9461, 9462	57241121	43	9.00E-41	Campylobacter lari RM2100	DNA repair protein RecN, putative [Campylobacter lari RM2100] gbjEAL54817.1] DNA repair protein RecN, putative [Campylobacter lari RM2100]				
9463, 9464	57505936	27	2.00E-13	Campylobacter upsallensis RM3195	hypothetical protein CUPA0072 [Campylobacter upsallensis RM3195] gbjEAL52526.1] hypothetical protein CUPA0072 [Campylobacter upsallensis RM3195]			2.1.1.11 3	
9465, 9466	20089049	28	5.00E-15	Methanosarcina acetivorans C2A	hypothetical protein MA0151 [Methanosarcina acetivorans C2A] gbjAAM03604.1] predicted protein [Methanosarcina acetivorans str. C2A]				
9467, 9468	45524150	63	6.00E-81	Crocospaera watsonii WH 8501	COG0674: Pyruvate:ferredoxin oxidoreductase and related 2- oxoacid:ferredoxin oxidoreductases, alpha subunit [Crocospaera watsonii WH 8501]			1.2.7.1	
9469, 9470	53731591	48	5.00E-27	Methanococcoides burtonii DSM 6242	COG0784: FOG: CheY-like receiver [Methanococcoides burtonii DSM 6242] putative isoprenyl synthetase [Bacteroides thetaiotaomicron VPI-5482] gbjAAO77165.1] putative isoprenyl synthetase [Bacteroides thetaiotaomicron VPI-5482]			2.7.3.-	
9471, 9472	29347468	49	1.00E-50	Bacteroides thetaitaomicron VPI-5482	EXBDITOLR FAMILY TRANSPORT PROTEIN [Wolinella succinogenes DSM 1740] embjCAE09656.1] EXBDITOLR FAMILY TRANSPORT PROTEIN [Wolinella succinogenes]			2.5.1.1	
9473, 9474	15668190	37	2.00E-42	Methanocaldococ- cus jannaschii DSM 2661	Glu-tRNA amidotransferase (gatB) [Methanocaldococcus jannaschii DSM 2661] gbjAAB97995.1] Glu-tRNA amidotransferase (gatB) [Methanocaldococcus jannaschii DSM 2661] spjQ60325[GATE_METJA Glutamyl-tRNA(Gln) amidotransferase subunit E (Glu-ADT subunit E) pfrjC64302 hypothetical protein MJ0019 - Methanococcus jannaschii hypothetical protein BT4316 [Bacteroides thetaiotaomicron VPI-5482] gbjAAO79421.1] conserved hypothetical protein [Bacteroides thetaitaomicron VPI-5482]			6.3.5.-	
9475, 9476	29349724	31	8.00E-16	Bacteroides thetaitaomicron VPI-5482	prespore protein MF12 [Dictyostellium discoideum]				
9477, 9478	7595898	33	3.00E-07	Dictyostellium discoideum					

9479, 9480	15606976	32	8.00E-18	Aquifex aeolicus VF5	hypothetical protein aq_1980 [Aquifex aeolicus VF5] gb AAC07760.1 hypothetical protein [Aquifex aeolicus VF5] p A70470 conserved hypothetical protein aq_1980 - Aquifex aeolicus				
9481, 9482	45527937	31	7.00E-30	Crocospaera watsonii WH 8501	COG0471: Di- and tricarboxylate transporters [Crocospaera watsonii WH 8501]				
9485, 9486	1197006	50	8.00E-56	Bacteroides fragilis	unknown protein [Bacteroides fragilis] gb AAA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for insertion sequence element IS4351 (Transposon TN4551)				
9487, 9488	53756727	22	6.00E-16	Methylococcus capsulatus str. Bath	conserved hypothetical protein [Methylococcus capsulatus str. Bath] ref YP_115226.1 hypothetical protein MCA2832 [Methylococcus capsulatus str. Bath]				
9489, 9490	48845594	21	3.00E-12	Geobacter metallireducens GS	COG1538: Outer membrane protein [Geobacter metallireducens GS-15]				
949, 950	32041369	37	3.00E-40	Pseudomonas aeruginosa UCBPP-PA14	COG1864: DNA/RNA endonuclease G, NUC1 [Pseudomonas aeruginosa UCBPP-PA14]				
9491, 9492	53711426	34	3.00E-26	Bacteroides fragilis YCH46	hypothetical protein BF0135 [Bacteroides fragilis YCH46] dbj BAD46884.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
9493, 9494	18309802	32	6.00E-24	Clostridium perfringens str. 13	hypothetical protein CPE0820 [Clostridium perfringens str. 13] dbj BAB80526.1 conserved hypothetical protein [Clostridium perfringens str. 13]				
9495, 9496	34557163	37	2.00E-24	Wollinella succinogenes DSM 1740	PUTATIVE PHOSPHATE ABC TRANSPORTER [Wollinella succinogenes DSM 1740] emb CAE09878.1 PUTATIVE PHOSPHATE ABC TRANSPORTER [Wollinella succinogenes]				
9499, 9500	34557678	36	4.00E-46	Wollinella succinogenes DSM 1740	hypothetical protein WS1317 [Wollinella succinogenes DSM 1740] emb CAE10393.1 conserved hypothetical protein [Wollinella succinogenes]				
95, 96	53731382	62	9.00E-67	Methanococcus burtonii DSM 6242	COG0610: Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Methanococcus burtonii DSM 6242]				3.1.21.3
9503, 9504	34557782	43	5.00E-31	Wollinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes DSM 1740] emb CAE10497.1 PUTATIVE TWO-COMPONENT SENSOR [Wollinella succinogenes]				2.7.3.-
9509, 9510	34558486	31	2.00E-18	Wollinella succinogenes DSM 1740	POLYPEPTIDE DEFORMYLASE PDF FORMYL METHIONINE DEFORMYLASE [Wollinella succinogenes DSM 1740] emb CAE11201.1 POLYPEPTIDE DEFORMYLASE PDF FORMYL METHIONINE DEFORMYLASE [Wollinella succinogenes] sp Q7M7M2 DEF_WOLSU Peptide deformylase (PDF) (Polypeptide deformylase)				3.5.1.88

951, 952	30018489	60	5.00E-99	Bacillus cereus ATCC 14579	4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 14579] gb AAP07321.1 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus ATCC 14579]			1.13.11. 27
9511, 9512	57169064	34	2.00E-20	Campylobacter coli RM2228	conserved hypothetical protein [Campylobacter coli RM2228] gb EAL56213.1 conserved hypothetical protein [Campylobacter coli RM2228]			
9513, 9514	53714701	48	2.00E-51	Bacteroides fragilis YCH46	histidyl-tRNA synthetase [Bacteroides fragilis YCH46] dbj BAD50159.1 histidyl-tRNA synthetase [Bacteroides fragilis YCH46]			6.1.1.21
9515, 9516	29347250	70	1.00E-66	Bacteroides thetaiotaomicron VPI-5482	histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76947.1 histidyl-tRNA synthetase [Bacteroides thetaiotaomicron VPI- 5482] sp Q8A6N7 SYH_BACTN Histidyl-tRNA synthetase (Histidine--tRNA ligase) (HisRS)			6.1.1.21
9517, 9518	34558209	42	6.00E-44	Wolnella succinogenes DSM 1740	conserved hypothetical protein-SAM dependent methyltransferases [Wolnella succinogenes DSM 1740] emb CAE10924.1 conserved hypothetical protein-SAM dependent methyltransferases [Wolnella succinogenes]			2.1.1.52
9521, 9522	57236932	43	6.00E-46	Campylobacter jejuni RM1221	cytochrome c551 peroxidase [Campylobacter jejuni RM1221] gb AAW34515.1 cytochrome c551 peroxidase [Campylobacter jejuni RM1221]			1.11.1.5
9523, 9524	46187441	25	2.00E-13	Pseudomonas syringae pv. syringae B728a	COG2274: ABC-type bacteriocin/antibiotic exporters, contain an N-terminal double-glycine peptidase domain [Pseudomonas syringae pv. syringae B728a]			
9525, 9526	46142516	54	9.00E-67	Methanococcoides burtonii DSM 6242	COG0399: Predicted pyridoxal phosphate-dependent enzyme apparently involved in regulation of cell wall biogenesis [Methanococcoides burtonii DSM 6242]			
9527, 9528	34557050	49	4.00E-25	Wolnella succinogenes DSM 1740	FERREDOXIN DOMAIN INTEGRAL MEMBRANE [Wolnella succinogenes DSM 1740] emb CAE09765.1 FERREDOXIN DOMAIN INTEGRAL MEMBRANE [Wolnella succinogenes]			
9529, 9530	48833354	28	1.00E-19	Magnetococcus sp. MC-1	COG1309: Transcriptional regulator [Magnetococcus sp. MC-1]			
9531, 9532	52006058	23	1.00E-08	Thiobacillus denitrificans ATCC 25259	COG2128: Uncharacterized conserved protein [Thiobacillus denitrificans ATCC 25259]			
9533, 9534	34557353	34	3.00E-38	Wolnella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolnella succinogenes DSM 1740] emb CAE10068.1 GGDEF FAMILY PROTEIN [Wolnella succinogenes]			
9535, 9536	53714372	26	5.00E-10	Bacteroides fragilis YCH46	hypothetical protein BF5085 [Bacteroides fragilis YCH46] dbj BAD49830.1 hypothetical protein [Bacteroides fragilis YCH46]			

9537, 9538	56421836	44	1.00E-48	Geobacillus kaustophilus HTA426	transposase [Geobacillus kaustophilus HTA426] ref YP_148757.1 transposase [Geobacillus kaustophilus HTA426] ref YP_146188.1 transposase [Geobacillus kaustophilus HTA426] dbj BAD77586.1 transposase [Geobacillus kaustophilus HTA426] dbj BAD77189.1 transposase [Geobacillus kaustophilus HTA426] dbj BAD74620.1 transposase [Geobacillus kaustophilus HTA426]				
9539, 9540	45658394	33	4.00E-12	Leptospira interrogans serovar Copenhageni str. Flocruz L1-130	hypothetical protein LIC12553 [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130] ref NP_711308.1 hypothetical protein LA1128 [Leptospira interrogans serovar Lai str. 56601] gb AAAN48327.1 unknown protein [Leptospira interrogans serovar lai str. 56601] gb AAS71117.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. Flocruz L1-130]				
9541, 9542	53713469	37	1.00E-17	Bacteroides fragilis YCH46	putative helicase [Bacteroides fragilis YCH46] dbj BAD48927.1 putative helicase [Bacteroides fragilis YCH46]				3.6.1.-
9543, 9544	27367788	56	4.00E-48	Vibrio vulnificus CMCP6	3,4-dihydroxy-2-butanone 4-phosphate synthase [Vibrio vulnificus CMCP6] ref NP_936316.1 3,4-dihydroxy-2-butanone 4-phosphate synthase [Vibrio vulnificus YJ016] gb AAO08305.1 3,4-dihydroxy-2-butanone 4-phosphate synthase [Vibrio vulnificus CMCP6] sp Q7MFR0 RIBB_VIBVY 3,4-dihydroxy- 2-butanone 4-phosphate synthase (DHBP synthase) sp Q8D485 RIBB_VIBVU 3,4-dihydroxy-2-butanone 4-phosphate synthase (DHBP synthase) dbj BAC96286.1 3,4-dihydroxy-2-butanone 4-phosphate synthase [Vibrio vulnificus YJ016]				3.5.4.25
9547, 9548	23015349	53	3.00E-68	Magnetospirillum magnetotacticum MS-1	COG1032: Fe-S oxidoreductase [Magnetospirillum magnetotacticum MS-1]				1.97.1.4
9549, 9550	34556398	51	4.00E-52	Wolinella succinogenes DSM 1740	PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolinella succinogenes DSM 1740] emb CAE11113.1 PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wolinella succinogenes]				4.2.1.70
955, 956	32476719	46	7.00E-64	Rhodopirella baltica SH 1	putative oxidoreductase [Rhodopirella baltica SH 1] emb CAD77091.1 putative oxidoreductase [Pirella sp.]				1.-.-.-
9553, 9554	34556517	48	7.00E-19	Wolinella succinogenes DSM 1740	hypothetical protein WS0063 [Wolinella succinogenes DSM 1740] emb CAE09232.1 conserved hypothetical protein [Wolinella succinogenes]				
9555, 9556	57167724	43	4.00E-31	Campylobacter coli RM2228	16S rRNA processing protein RimM, putative [Campylobacter coli RM2228] gb EAL57510.1 16S rRNA processing protein RimM, putative [Campylobacter coli RM2228]				
9557, 9558	53713881	50	1.00E-47	Bacteroides fragilis YCH46	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase [Bacteroides fragilis YCH46] dbj BAD49339.1 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase [Bacteroides fragilis YCH46]				2.7.1.14 8

9559, 9560	57240278	28	7.00E-20	Campylobacter lari RM2100	probable transcription regulator Cj0571 [Campylobacter lari RM2100] gb EAL55392.1 probable transcription regulator Cj0571 [Campylobacter lari RM2100]			
9565, 9566	20806611	25	7.00E-15	Thermoanaerobact er tengcongensis MB4	Transcriptional regulator [Thermoanaerobacter tengcongensis MB4] gb AAM23386.1 Transcriptional regulator [Thermoanaerobacter tengcongensis MB4]			
9567, 9568	48854159	36	7.00E-28	Cytophaga hutchinsonii	COG0596: Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily) [Cytophaga hutchinsonii] deoxyguanosinetriphosphate triphosphohydrolase [Pseudomonas aeruginosa PAO1] pir H83505 deoxyguanosinetriphosphate triphosphohydrolase PA1124 [imported] - Pseudomonas aeruginosa (strain PAO1) ref NP_249815.1 deoxyguanosinetriphosphate triphosphohydrolase [Pseudomonas aeruginosa PAO1] sp Q914L1 DGTP_PSEAE Probable deoxyguanosinetriphosphate triphosphohydrolase (dGTPase) (dGTP triphosphohydrolase)		3.1.1.24	
9569, 9570	9947043	53	3.00E-45	Pseudomonas aeruginosa PAO1 Wolnella	PHOSPHOENOLPYRUVATE SYNTHASE [Wolnella succinogenes DSM 1740] emb CAE09937.1 PHOSPHOENOLPYRUVATE SYNTHASE [Wolnella succinogenes] COG0652: Peptidyl-prolyl cis-trans isomerase (rotamase) - cyclophilin family [Burkholderia cepacia R1808]			3.1.5.1
9571, 9572	34557222	61	2.00E-83	succinogenes DSM 1740	GDP-mannose pyrophosphorylase homolog [Actinobacillus actinomycetemcomitans] ExsB protein [Chlorobium tepidum TLS] gb AAM71774.1 ExsB protein [Chlorobium tepidum TLS]			2.7.9.2
9573, 9574	46321918	61	4.00E-47	Burkholderia cepacia R1808 Actinobacillus	ABC transporter [Bacillus licheniformis ATCC 14580] gb AAU21793.1 ABC transporter [Bacillus licheniformis ATCC 14580] ref YP_089831.1 YbaE [Bacillus licheniformis ATCC 14580] gb AAU39138.1 YbaE [Bacillus licheniformis DSM 13]			5.2.1.8
9575, 9576	7592813	49	2.00E-77	actinomycetemcom itans	hypothetical protein ECA1089 [Erwinia carotovora subsp. atroseptica SCRI1043] emb CAG74000.1 hypothetical protein [Erwinia carotovora subsp. atroseptica SCRI1043]			2.7.7.22
9577, 9578	21673367	59	7.00E-49	Chlorobium tepidum TLS	hypothetical protein WS0453 [Wolnella succinogenes DSM 1740] emb CAE09595.1 hypothetical protein [Wolnella succinogenes] PREDICTED TRANSCRIPTIONAL REGULATOR [Wolnella succinogenes DSM 1740] emb CAE10254.1 PREDICTED TRANSCRIPTIONAL REGULATOR [Wolnella succinogenes]			1.8.-.-
9579, 9580	52078640	49	3.00E-64	Bacillus licheniformis ATCC 14580				
9581, 9582	50120029	21	3.00E-07	Erwinia carotovora subsp. atroseptica SCRI1043				
9583, 9584	34556880	27	1.00E-10	Wolnella succinogenes DSM 1740				
9585, 9586	34557539	45	2.00E-24	Wolnella succinogenes DSM 1740				

9587, 9588	34556543	62	2.00E-71	Wolinella succinogenes DSM 1740	PUTATIVE PHOSPHOHYDROLASE [Wolinella succinogenes DSM 1740] emb CAE09258.1 PUTATIVE PHOSPHOHYDROLASE [Wolinella succinogenes] sp Q7MAQ8 HIS2_WOLSU Histidine biosynthesis bifunctional protein hisIE [includes: Phosphoribosyl-AMP cyclohydrolase (PRA-CH); Phosphoribosyl-ATP pyrophosphatase (PRA-PH)]			3.5.4.19
959, 960	48854559	50	3.00E-38	Cytophaga hutchinsonii	COG1162: Predicted GTPases [Cytophaga hutchinsonii]			
9591, 9592	47569586	25	2.00E-17	Bacillus cereus G9241	sporulation kinase [Bacillus cereus G9241] gb EAL12142.1 sporulation kinase [Bacillus cereus G9241]			2.7.3.-
9593, 9594	34557851	39	2.00E-49	Wolinella succinogenes DSM 1740	hypothetical protein WS1518 [Wolinella succinogenes DSM 1740] emb CAE10566.1 conserved hypothetical protein [Wolinella succinogenes]			
9595, 9596	32262690	44	6.00E-46	Helicobacter hepaticus ATCC 51449	transaldolase [Helicobacter hepaticus ATCC 51449] ref NP_860671.1 transaldolase [Helicobacter hepaticus ATCC 51449]			2.2.1.2
9597, 9598	1197006	54	1.00E-60	Bacteroides fragilis Wolinella succinogenes DSM 1740	unknown protein [Bacteroides fragilis] gb AA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for insertion sequence element IS4351 (Transposon TN4551)	Vibrio vulnificus CMCP6 chromosome I section 9 of 11 of the complete sequence	85 2.00E-09	
9601, 9602	34556843	39	1.00E-41	Wolinella succinogenes DSM 1740	hypothetical protein WS0414 [Wolinella succinogenes DSM 1740] emb CAE09558.1 conserved hypothetical protein [Wolinella succinogenes]			2.7.3.-
9603, 9604	48833864	47	7.00E-30	Magnetococcus sp. MC-1	COG3706: Response regulator containing a CheY-like receiver domain and a GGDEF domain [Magnetococcus sp. MC-1]			2.7.3.-
9607, 9608	23501737	66	8.00E-37	Brucella suis 1330	ribulose-phosphate 3-epimerase [Brucella suis 1330] gb AAN29779.1 ribulose-phosphate 3-epimerase [Brucella suis 1330]			5.1.3.1
9611, 9612	23127382	26	6.00E-12	Nostoc punctiforme PCC 73102	COG0419: ATPase involved in DNA repair [Nostoc punctiforme PCC 73102]			3.1.11.-
9615, 9616	48844618	42	3.00E-55	Geobacter metallireducens GS-15	COG2902: NAD-specific glutamate dehydrogenase [Geobacter metallireducens GS-15]			1.4.1.2
9621, 9622	34557571	58	5.00E-85	Wolinella succinogenes DSM 1740	GLUTAMATE SYNTHASE, LARGE SUBUNIT [Wolinella succinogenes DSM 1740] emb CAE10286.1 GLUTAMATE SYNTHASE, LARGE SUBUNIT [Wolinella succinogenes]			1.4.1.13
9623, 9624	57238620	47	6.00E-38	Campylobacter jejuni RM1221	ispD/ispF bifunctional enzyme [Campylobacter jejuni RM1221] gb AAW36203.1 ispD/ispF bifunctional enzyme [Campylobacter jejuni RM1221]			2.7.7.60

9625, 9626	57240551	61	1.00E-80	Campylobacter lari RM2100	conserved hypothetical integral membrane protein [Campylobacter lari RM2100] gb EAL55665.1 conserved hypothetical integral membrane protein [Campylobacter lari RM2100]			
9627, 9628	57242456	27	8.00E-13	Campylobacter upsaliensis RM3195	probable periplasmic protein Cj0530 [Campylobacter upsaliensis RM3195] gb EAL53524.1 probable periplasmic protein Cj0530 [Campylobacter upsaliensis RM3195]			
9629, 9630	34558270	37	2.00E-14	Wolinella succinogenes DSM 1740	hypothetical protein WS1982 [Wolinella succinogenes DSM 1740] emb CAE10985.1 hypothetical protein [Wolinella succinogenes] transcriptional regulator YtrA [Bacillus licheniformis ATCC 14580] gb AAU24683.1 transcriptional regulator YtrA [Bacillus licheniformis ATCC 14580] ref YP_092738.1 YtrA [Bacillus licheniformis ATCC 14580] gb AAU42045.1 YtrA [Bacillus licheniformis DSM 13] hypothetical protein PBPR0876 [Photobacterium profundum SS9] emb CAG22748.1 hypothetical protein [Photobacterium profundum]			
9631, 9632	52081530	46	1.00E-14	Bacillus licheniformis ATCC 14580				
9633, 9634	54302555	43	8.00E-35	Photobacterium profundum SS9	hypothetical protein wblA [imported] - Vibrio cholerae dbj BAA33632.1 probable beta-D-galactoside 2-alpha-L-fucosyl transferase [Vibrio cholerae] hypothetical protein TTE2678 [Thermoanaerobacter tengcongensis MB4] gb AAM25797.1 hypothetical protein TTE2678 [Thermoanaerobacter tengcongensis MB4]	2.4, 1.69		
9635, 9636	11282475	39	9.00E-56	Thermoanaerobact er tengcongensis MB4	ABC transporter, ATP-binding protein [Methanosarcina acetivorans C2A] gb AAM07031.1 ABC transporter, ATP-binding protein [Methanosarcina acetivorans str. C2A]			
9637, 9638	20809022	24	2.00E-08	Methanosarcina acetivorans C2A	pxo1-13 [Bacillus anthracis] gb AAD32317.1 pxo1-13 [Bacillus anthracis] pir E55092 hypothetical protein pxo1-13 - Bacillus anthracis virulence plasmid pXO1	1.8, --		
9639, 9640	20092476	42	5.00E-31	Bacillus anthracis Wolinella succinogenes DSM 1740	SULFATE ADENYLTRANSFERASE [Wolinella succinogenes DSM 1740] emb CAE10944.1 SULFATE ADENYLTRANSFERASE [Wolinella succinogenes]			2.7, 7.4
9641, 9642	10956260	29	1.00E-17	Acinetobacter sp. ADP1	cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAG67958.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] emb CAA86930.1 cobyrinic acid synthase [Acinetobacter sp. ADP1] sp Q43989 COBQ_ACIAD Cobyrinic acid synthase			3, ---
9645, 9646	34558229	46	8.00E-46	Wolinella succinogenes DSM 1740	MOLYBDENUM-PTERIN-BINDING PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10827.1 MOLYBDENUM-PTERIN-BINDING PROTEIN [Wolinella succinogenes]			
9647, 9648	50084270	53	8.00E-68	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	site-specific recombinase, phage integrase family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS96234.1 site-specific recombinase, phage integrase family [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			
9649, 9650	34558112	47	8.00E-20	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough				
	46580167	22	2.00E-08	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough				

965, 966	39998205	63	4.00E-69	Geobacter sulfurreducens PCA	long-chain-fatty-acid-CoA ligase, putative [Geobacter sulfurreducens PCA] gb AAR34429.1 long-chain-fatty-acid-CoA ligase, putative [Geobacter sulfurreducens PCA]			6.2.1.3
9651, 9652	48831352	31	2.00E-17	Magnetococcus sp. MC-1	COG0642: Signal transduction histidine kinase [Magnetococcus sp. MC-1]			
9653, 9654	42524060	47	1.00E-38	Bdellovibrio bacteriovorus HD100	adenylate cyclase [Bdellovibrio bacteriovorus HD100] emb CAE80433.1 adenylate cyclase [Bdellovibrio bacteriovorus HD100]			4.6.1.1
9655, 9656	48853682	31	2.00E-09	Cytophaga hutchinsonii	COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Cytophaga hutchinsonii]			2.3.1.51
9657, 9658	46118958	48	6.00E-41	Crocospaera watsonii WH 8501	COG2081: Predicted flavoproteins [Crocospaera watsonii WH 8501]			
9659, 9660	46578435	38	2.00E-60	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	methyl-accepting chemotaxis protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS94502.1 methyl-accepting chemotaxis protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			2.7.3.-
9661, 9662	47779389	52	2.00E-63	uncultured gamma proteobacterium eBACHOT4E07	predicted HsdM [uncultured gamma proteobacterium eBACHOT4E07]			2.1.1.72
9663, 9664	34558345	43	3.00E-24	Wolinella succinogenes DSM 1740	PANTOTHENATE METABOLISM FLAVOPROTEIN [Wolinella succinogenes DSM 1740] emb CAE11060.1 PANTOTHENATE METABOLISM FLAVOPROTEIN [Wolinella succinogenes]			6.3.2.5
9665, 9666	46579872	28	1.00E-27	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	glutamyl-tRNA reductase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gb AAS95939.1 glutamyl-tRNA reductase [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			1.2.1.-
9667, 9668	56964394	31	6.00E-15	Bacillus clausii KSM-K16	uroporphyrinogen III cosynthase [Bacillus clausii KSM-K16] dbj BAD65164.1			4.2.1.75
9669, 9670	34557978	38	2.00E-57	Wolinella succinogenes DSM 1740	PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10693.1 PENICILLIN-BINDING PROTEIN / CELL DIVISION PROTEIN [Wolinella succinogenes]			2.3.2.-
967, 968	23128197	45	3.00E-75	Nostoc punctiforme PCC 73102	COG1505: Serine proteases of the peptidase family S9A [Nostoc punctiforme PCC 73102]			3.4.21.2 6
9671, 9672	32263303	55	2.00E-25	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_861282.1 hypothetical protein HH1751 [Helicobacter hepaticus ATCC 51449]			3.1.-.-

9673, 9674	29345875	56	1.00E-35	Bacteroides thetaiotaomicron VPI-5482	dTDP-4-dehydrohamnose reductase [Bacteroides thetaiotaomicron VPI-5482] gb AAO75572.1 dTDP-4-dehydrohamnose reductase [Bacteroides thetaiotaomicron VPI-5482]			1.1.1.13 3
9675, 9676	45250013	66	2.00E-47	Aneurinibacillus thermoaerophilus	dTDP-glucose 4,6-dehydratase [Aneurinibacillus thermoaerophilus]			4.2.1.46
9677, 9678	56461438	63	6.00E-72	Idiomarina loihlensis L2TR	Glutamate dehydrogenase [Idiomarina loihlensis L2TR] gb AAV83170.1 Glutamate dehydrogenase [Idiomarina loihlensis L2TR]		87 5.00E-07	1.4.1.4
9679, 9680	57242734	45	8.00E-48	Campylobacter upsaliensis RM3195	response regulator, putative [Campylobacter upsaliensis RM3195] gb EAL53447.1 response regulator, putative [Campylobacter upsaliensis RM3195]		93 2.00E-09	2.7.3.-
9681, 9682	57240513	41	3.00E-33	Campylobacter lari RM2100	signal-transducing protein, histidine kinase, putative [Campylobacter lari RM2100] gb EAL55627.1 signal-transducing protein, histidine kinase, putative [Campylobacter lari RM2100]			2.7.3.-
9683, 9684	16326479	44	2.00E-18	Rhizobium leguminosarum bv. trifolii	ImpC [Rhizobium leguminosarum bv. trifolii]			
9685, 9686	34557419	35	1.00E-22	Wolinella succinogenes DSM 1740	PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes DSM 1740] emb CAE10134.1 PUTATIVE TWO-COMPONENT SENSOR [Wolinella succinogenes]			2.7.3.-
9687, 9688	34556574	25	1.00E-10	Wolinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wolinella succinogenes DSM 1740] emb CAE09289.1 GGDEF FAMILY PROTEIN [Wolinella succinogenes]			
9689, 9690	29346464	26	3.00E-17	Bacteroides thetaiotaomicron VPI-5482	ATP-dependent helicase [Bacteroides thetaiotaomicron VPI-5482] gb AAO76161.1 ATP-dependent helicase [Bacteroides thetaiotaomicron VPI-5482]			
969, 970	48893318	33	3.00E-38	Trichodesmium erythraeum IMS101	COG0474: Cation transport ATPase [Trichodesmium erythraeum IMS101]			3.6.3.-
9691, 9692	34557601	40	2.00E-20	Wolinella succinogenes DSM 1740	hypothetical protein WS1236 [Wolinella succinogenes DSM 1740] emb CAE10316.1 hypothetical protein [Wolinella succinogenes]			2.7.7.7
9693, 9694	18254491	33	4.00E-09	Pectobacterium chrysanthemi	invertase [Pectobacterium chrysanthemi]			
9695, 9696	34557638	65	3.00E-97	Wolinella succinogenes DSM 1740	QUINOLINATE SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE10353.1 QUINOLINATE SYNTHETASE [Wolinella succinogenes]			

9697, 9698	57240463	56	7.00E-61	Campylobacter lari RM2100	aspartate carbamoyltransferase [Campylobacter lari RM2100] gb EAL55577.1 aspartate carbamoyltransferase [Campylobacter lari RM2100]			2.1.3.2
9699, 9700	34558267	54	5.00E-76	Wollinella succinogenes DSM 1740	PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wollinella succinogenes DSM 1740] emb CAE10982.1 PUTATIVE RIBOSOMAL PSEUDOURIDINE SYNTHASE [Wollinella succinogenes]			4.2.1.70
9705, 9706	50745174	33	3.00E-18	Gallus gallus	PREDICTED: similar to L-gulonon-gamma-lactone oxidase precursor [Gallus gallus]			1.1.3.8
9707, 9708	54311293	37	1.00E-21	Xenopus laevis	Unknown (protein for MGC:86416) [Xenopus laevis]			1.1.3.8
9709, 9710	57241815	34	1.00E-18	Campylobacter lari RM2100	signal-transducing protein, histidine kinase [Campylobacter lari RM2100] gb EAL54233.1 signal-transducing protein, histidine kinase [Campylobacter lari RM2100]			2.7.3.-
971, 972	48853467	59	1.00E-45	Cytophaga hutchinsonii	COG1473: Metal-dependent amidase/aminoacylase/carboxypeptidase [Cytophaga hutchinsonii]			3.5.1.14
9711, 9712	6978030	44	3.00E-51	Desulfovibrio gigas	putative Soj [Desulfovibrio gigas]			
9713, 9714	57240664	25	7.00E-12	Campylobacter lari RM2100	probable periplasmic protein Cj1621 [Campylobacter lari RM2100] gb EAL55057.1 probable periplasmic protein Cj1621 [Campylobacter lari RM2100]			
9715, 9716	34558196	57	7.00E-46	Wollinella succinogenes DSM 1740	DNA PRIMASE PROTEIN [Wollinella succinogenes DSM 1740] emb CAE10911.1 DNA PRIMASE PROTEIN [Wollinella succinogenes]	Wollinella succinogenes, complete genome; segment 6/7	91 3.00E-07	2.7.7.-
9719, 9720	21398586	32	1.00E-31	Bacillus anthracis str. A2012	EAL, Domain of unknown function 2 [Bacillus anthracis str. A2012] type I site-specific deoxyribonuclease, HsdR family [Pseudomonas syringae pv. tomato str. DC3000] ref NP_789870.1 type I site-specific			2.7.3.-
9721, 9722	28850485	38	2.00E-40	Pseudomonas syringae pv. tomato str. DC3000	deoxyribonuclease, HsdR family [Pseudomonas syringae pv. tomato str. DC3000]			3.1.21.3
9723, 9724	48858979	43	5.00E-18	Clostridium thermocellum ATCC 27405	hypothetical protein Chte02001700 [Clostridium thermocellum ATCC 27405]			
9725, 9726	15896339	32	8.00E-17	Clostridium acetobutylicum ATCC 824	NtrC family transcriptional regulator, ATPase domain fused to two PAS domains [Clostridium acetobutylicum ATCC 824] gb AAK81028.1 NtrC family transcriptional regulator, ATPase domain fused to two PAS domains [Clostridium acetobutylicum ATCC 824] pir A97280 ntrC family transcription regulator, ATPase domain fused to two PAS domains CAC3088 [imported] - Clostridium acetobutylicum			
9727, 9728	48864065	47	1.00E-29	Microbulbifer degradans 2-40	COG0328: Ribonuclease HI [Microbulbifer degradans 2-40]			3.1.26.4

9729, 9730	34556614	57	1.00E-69	Wolinella succinogenes DSM 1740	CARBOXYNORSPERMIDINE DECARBOXYLASE (NSPC) [Wolinella succinogenes DSM 1740] emb CAE09329.1 CARBOXYNORSPERMIDINE DECARBOXYLASE (NSPC) [Wolinella succinogenes]			4.1.1.-
973, 974	23125101	35	1.00E-12	Nostoc punctiforme PCC 73102	COG0454: Histone acetyltransferase HPA2 and related acetyltransferases [Nostoc punctiforme PCC 73102]			
9731, 9732	34556768	70	1.00E-103	Wolinella succinogenes DSM 1740	DIAMINOPELMATE DECARBOXYLASE DAP DECARBOXYLASE [Wolinella succinogenes DSM 1740] emb CAE09483.1 DIAMINOPELMATE DECARBOXYLASE DAP DECARBOXYLASE [Wolinella succinogenes] putative carbonate dehydratase, cynT [Parachlamydia sp. UWE25] emb CAF23782.1 putative carbonate dehydratase, cynT [Parachlamydia sp. UWE25]			4.1.1.20
9733, 9734	46446692	42	6.00E-39	Parachlamydia sp. UWE25				4.2.1.1
9735, 9736	34557590	28	2.00E-10	Wolinella succinogenes DSM 1740	PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10305.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes]			
9737, 9738	57506236	62	3.00E-67	Campylobacter upsaliensis RM3195	malate:quinone oxidoreductase, putative [Campylobacter upsaliensis RM3195] gb EAL52259.1 malate:quinone oxidoreductase, putative [Campylobacter upsaliensis RM3195]	Campylobacter [ejuni subsp. [ejuni] NCTC 11168 complete genome; segment 2/6	85 2.00E-10	1.1.99.1
9739, 9740	34557590	30	7.00E-17	Wolinella succinogenes DSM 1740	PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes DSM 1740] emb CAE10305.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolinella succinogenes]			
9743, 9744	48856925	27	2.00E-19	Cytophaga hutchinsonii	COG1309: Transcriptional regulator [Cytophaga hutchinsonii]			
9745, 9746	33637041	67	1.00E-95	Geobacillus stearothermophilus	glucose-1-phosphate thymidyltransferase [Geobacillus stearothermophilus] SPERMIDINE SYNTHASE SPEE [Wolinella succinogenes DSM 1740] emb CAE11142.1 SPERMIDINE SYNTHASE SPEE [Wolinella succinogenes] sp Q7M7Q6 SPEE_WOLSU Spermidine synthase (Putrescine aminopropyltransferase) (SPDSY)			2.7.7.24
9749, 9750	34558427	23	3.00E-12	Wolinella succinogenes DSM 1740				
9751, 9752	48839535	28	2.00E-24	Methanosarcina barkeri str. fusaro	COG2202: FOG: PAS/PAC domain [Methanosarcina barkeri str. fusaro] HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100] emb CAE80147.1 HD-GYP hydrolase domain containing protein [Bdellovibrio bacteriovorus HD100]			2.7.3.-
9757, 9758	42523774	27	1.00E-13	Bdellovibrio bacteriovorus HD100				
9765, 9766	48855616	30	9.00E-09	Cytophaga hutchinsonii	COG4775: Outer membrane protein/protective antigen OMA87 [Cytophaga hutchinsonii]			

9769, 9770	51892702	54	3.00E-77	Symbiobacterium thermophilum IAM 14863	putative 4-hydroxybenzoate decarboxylase [Symbiobacterium thermophilum IAM 14863] dbj BAD40549.1 putative 4-hydroxybenzoate decarboxylase [Symbiobacterium thermophilum IAM 14863]			4.1.1.-
977, 978	23098370	55	3.00E-37	Oceanobacillus ihayensis HTE831	hypothetical protein OB0915 [Oceanobacillus ihayensis HTE831] dbj BAC12871.1 hypothetical conserved protein [Oceanobacillus ihayensis HTE831]			
9771, 9772	2984569	35	2.00E-20	Aquifex aeolicus VF5	putative protein [Aquifex aeolicus VF5] ref NP_046416.1 hypothetical protein aq_aa25 [Aquifex aeolicus VF5] sp O66416 YZ25_AQUAE Hypothetical protein AA25			
9773, 9774	48856863	44	1.00E-48	Cytophaga hutchinsonii	COG1073: Hydrolases of the alpha/beta superfamily [Cytophaga hutchinsonii]			3.1.1.5
9775, 9776	56961907	40	1.00E-34	Bacillus clausii KSM-K16	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase [Bacillus clausii KSM-K16] dbj BAD62668.1 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase [Bacillus clausii KSM-K16]			2.7.7.60
9777, 9778	34555655	38	2.00E-16	Wolnella succinogenes DSM 1740	PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolnella succinogenes DSM 1740] emb CAE09280.1 PUTATIVE TRANSCRIPTIONAL REGULATOR [Wolnella succinogenes] emb CAD23185.1 putative transcriptional regulator protein [Wolnella succinogenes]			
9779, 9780	34555981	30	3.00E-19	Wolnella succinogenes DSM 1740	hypothetical protein WS0562 [Wolnella succinogenes DSM 1740] emb CAE09696.1 conserved hypothetical protein [Wolnella succinogenes] hypothetical protein CJE1655 [Campylobacter jejuni RM1221]			
9783, 9784	57238505	37	2.00E-16	Campylobacter jejuni RM1221	gbl AAW36088.1 conserved hypothetical protein [Campylobacter jejuni RM1221]			
9785, 9786	34397173	32	5.00E-18	Porphyromonas gingivalis W83	ribonucleotide reductase [Porphyromonas gingivalis W83] ref NP_905338.1 ribonucleotide reductase [Porphyromonas gingivalis W83]			1.17.4.1
9789, 9790	48846630	50	2.00E-75	Geobacter metallireducens GS-15	COG1086: Predicted nucleoside-diphosphate sugar epimerases [Geobacter metallireducens GS-15]			4.2.1.-
979, 980	23098370	58	2.00E-32	Oceanobacillus ihayensis HTE831	hypothetical protein OB0915 [Oceanobacillus ihayensis HTE831] dbj BAC12871.1 hypothetical conserved protein [Oceanobacillus ihayensis HTE831]			
9793, 9794	56962744	53	6.00E-73	Bacillus clausii KSM-K16	chaperone protein HtpG [Bacillus clausii KSM-K16] dbj BAD63509.1 chaperone protein HtpG [Bacillus clausii KSM-K16]			
9795, 9796	28211154	56	3.00E-58	Clostridium tetani E88	putative histidine decarboxylase [Clostridium tetani E88] gb AAO36035.1 putative histidine decarboxylase [Clostridium tetani E88]			4.1.1.15

9797, 9798	18311483	29	3.00E-17	Clostridium perfringens str. 13	leucine aminopeptidase [Clostridium perfringens str. 13] dbj BAB82207.1 leucine aminopeptidase [Clostridium perfringens str. 13] sp Q8XHI3 AMPA_CLOPE Probable cytosol aminopeptidase (Leucine aminopeptidase) (LAP) (Leucyl aminopeptidase)				3.4.11.1
9799, 9800	32261675	45	2.00E-59	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449] ref NP_959659.1 hypothetical protein HH0128 [Helicobacter hepaticus ATCC 51449]	Alvinella pompejana epibiont 6C6 fosmid clone 6C6, complete sequence	87	2.00E-09	6.3.2.15
9801, 9802	48782408	35	2.00E-35	Burkholderia fungorum LB400	COG0207: Thymidylate synthase [Burkholderia fungorum LB400]				2.1.1.45
9805, 9806	48863829	33	1.00E-21	Microbulbifer degradans 2-40	COG3769: Predicted hydrolase (HAD superfamily) [Microbulbifer degradans 2-40]				
9807, 9808	39995248	22	6.00E-08	Geobacter sulfurreducens PCA	hypothetical protein GSU0137 [Geobacter sulfurreducens PCA] gb AAR33472.1 hypothetical protein GSU0137 [Geobacter sulfurreducens PCA]				
981, 982	53714045	50	1.00E-55	Bacteroides fragilis YCH46	putative transcriptional regulator for phosphate uptake [Bacteroides fragilis YCH46] dbj BAD49503.1 putative transcriptional regulator for phosphate uptake [Bacteroides fragilis YCH46]				
9811, 9812	56542586	36	2.00E-10	Zymomonas mobilis subsp. mobilis ZM4	conserved hypothetical protein [Zymomonas mobilis subsp. mobilis ZM4] ref YP_161851.1 hypothetical protein ZMO0116 [Zymomonas mobilis subsp. mobilis ZM4]				
9817, 9818	51243917	44	4.00E-26	Desulfotalea psychrophila L.Sv54	related to pyruvate formate-lyase activating enzyme [Desulfotalea psychrophila L.Sv54] emb CAG34794.1 related to pyruvate formate-lyase activating enzyme [Desulfotalea psychrophila L.Sv54]				1.97.1.4
9821, 9822	48854003	27	8.00E-12	Cytophaga hutchinsonii	hypothetical protein Chut02003091 [Cytophaga hutchinsonii]				
9823, 9824	51891413	31	2.00E-16	Symbiobacterium thermophilum IAM 14863	transposase [Symbiobacterium thermophilum IAM 14863] dbj BAD39260.1 transposase [Symbiobacterium thermophilum IAM 14863]				
9825, 9826	57167713	49	3.00E-33	Campylobacter coli RM2228	probable proteinase Cj0701 [Campylobacter coli RM2228] gb EAL57499.1 probable proteinase Cj0701 [Campylobacter coli RM2228]				3.4.--
9827, 9828	51594858	35	8.00E-18	Yersinia pseudotuberculosis IP 32953	hypothetical protein YPTB0506 [Yersinia pseudotuberculosis IP 32953] emb CAH19746.1 conserved hypothetical protein [Yersinia pseudotuberculosis IP 32953]				
9829, 9830	23128114	37	7.00E-25	Nostoc punctiforme PCC 73102	hypothetical protein Npun02002480 [Nostoc punctiforme PCC 73102]				

983, 984	48854219	74	4.00E-70	Cytophaga hutchinsonii	COG1117: ABC-type phosphate transport system, ATPase component [Cytophaga hutchinsonii]	Mycobacterium smegmatis Inorganic phosphate transporter operon, complete sequence, PhoU (phoU) gene, complete cds; and unknown genes	90	2.00E-08	1.8.-
9831, 9832	48766646	39	3.00E-30	Rhodospirillum rubrum	COG2902: NAD-specific glutamate dehydrogenase [Rhodospirillum rubrum]				1.4.1.2
9833, 9834	1197006	55	3.00E-43	Bacteroides fragilis	unknown protein [Bacteroides fragilis] gb AA27430.1 ORF-1 [Bacteroides fragilis] sp P37247 TRA4_BACFR Transposase for insertion sequence element IS4351 (Transposon TN4551)	Vibrio vulnificus CMCP6 chromosome I section 9 of 11 of the complete sequence	85	1.00E-09	
9835, 9836	48853319	29	3.00E-09	Cytophaga hutchinsonii	hypothetical protein Chut2003935 [Cytophaga hutchinsonii]				
9837, 9838	48855703	33	1.00E-09	Cytophaga hutchinsonii	COG2972: Predicted signal transduction protein with a C-terminal ATPase domain [Cytophaga hutchinsonii]				2.7.3.-
9845, 9846	48855010	56	7.00E-29	Cytophaga hutchinsonii	COG1363: Cellulase M and related proteins [Cytophaga hutchinsonii]				3.2.1.4
9847, 9848	48855010	62	8.00E-84	Cytophaga hutchinsonii	COG1363: Cellulase M and related proteins [Cytophaga hutchinsonii]				3.2.1.4
9849, 9850	34558823	53	3.00E-76	Alvinella pompejana epibiont 7G3	MutS2 family protein [Alvinella pompejana epibiont 7G3]				
9851, 9852	53613159	43	7.00E-16	Azotobacter vinelandii	COG0454: Histone acetyltransferase HIPA2 and related acetyltransferases [Azotobacter vinelandii]				
9853, 9854	34557032	31	5.00E-17	Wolinella succinogenes DSM 1740	hypothetical protein WS0616 [Wolinella succinogenes DSM 1740] emb CAE09747.1 conserved hypothetical protein [Wolinella succinogenes]				
9857, 9858	47459024	39	2.00E-11	Mycoplasma mobile 163K	protoporphyrinogen oxidase [Mycoplasma mobile 163K] gb AAT27675.1 protoporphyrinogen oxidase [Mycoplasma mobile 163K] methionyl-tRNA synthetase [Thermococcus kodakaraensis] ref YP_183462.1 methionyl-tRNA synthetase [Thermococcus kodakaraensis]				2.1.1.-
9859, 9860	57159308	54	1.00E-76	Thermococcus kodakaraensis					6.1.1.10

9861, 9862	28210338	57	1.00E-89	Clostridium tetani E88	fructose-1,6-bisphosphatase [Clostridium tetani E88] fructose-1,6-bisphosphatase [Clostridium tetani E88]			3.1.3.11
9863, 9864	46578435	38	2.00E-55	Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough	methyl-accepting chemotaxis protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough] gblAAS94502.1 methyl-accepting chemotaxis protein, putative [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]			2.7.3.-
9867, 9868	20808761	31	3.00E-13	Thermoanaerobacter tengcongensis MB4	SAM-dependent methyltransferases [Thermoanaerobacter tengcongensis MB4] gblAAM25536.1 SAM-dependent methyltransferases [Thermoanaerobacter tengcongensis MB4]			2.1.1.-
9873, 9874	15678362	42	2.00E-37	Methanothermobacter thermautotrophicus str. Delta H	perosamine synthetase [Methanothermobacter thermautotrophicus str. Delta H] gblAAB84840.1 perosamine synthetase [Methanothermobacter thermautotrophicus str. Delta H] pir H69142 perosamine synthetase - Methanobacterium thermoautotrophicum (strain Delta H)	Methanobacterium thermoautotrophicum from bases 264585 to 276866 (section 24 of 148) of the complete genome	91 4.00E-10	
9875, 9876	48855342	58	2.00E-72	Cytophaga hutchinsonii	COG0612: Predicted Zn-dependent peptidases [Cytophaga hutchinsonii]			3.4.-
9877, 9878	52144139	38	6.00E-21	Bacillus cereus ZK	cardiolipin synthetase [Bacillus cereus ZK] gblAAU19158.1 cardiolipin synthetase [Bacillus cereus ZK]			2.7.8.-
9879, 9880	24214122	34	9.00E-36	Leptospira interrogans serovar Lai str. 56601	Serine/threonine protein kinases [Leptospira interrogans serovar Lai str. 56601] gblAAN48621.1 Serine/threonine protein kinases [Leptospira interrogans serovar lai str. 56601]			
9881, 9882								3.4.11.-
9883, 9884	48861156	26	3.00E-18	Microbulbifer degradans 2-40	hypothetical protein Mdeg02003535 [Microbulbifer degradans 2-40]			
9887, 9888	34557204	45	4.00E-56	Wolinella succinogenes DSM 1740	hypothetical protein WS0806 [Wolinella succinogenes DSM 1740] emb CAE09919.1 conserved hypothetical protein [Wolinella succinogenes]			
9889, 9890	53691858	50	7.00E-72	Desulfovibrio desulfuricans G20	hypothetical protein Ddes02000066 [Desulfovibrio desulfuricans G20]			
989, 990	53761461	49	8.00E-49	Ralstonia eutropha JMP134	COG5526: Uncharacterized conserved protein [Ralstonia eutropha JMP134]			
9893, 9894	34557685	34	4.00E-40	Wolinella succinogenes DSM 1740	HYPOTHETICAL INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10400.1 HYPOTHETICAL INTEGRAL MEMBRANE PROTEIN [Wolinella succinogenes]			

9897, 9898	40062562	38	8.00E-07	uncultured bacterium 159		FG-GAP repeat protein [uncultured bacterium 159]	Coxiella burnetii strain RSA 493, section 1 of 7 of the complete genome	4.00E-11	
9899, 9900	34556661	48	5.00E-54	Wolinella succinogenes DSM 1740		PUTATIVE FRUCTOSE-1,6-BISPHOSPHATASE [Wolinella succinogenes DSM 1740] emb CAE09376.1 PUTATIVE FRUCTOSE-1,6- BISPHOSPHATASE [Wolinella succinogenes]		3.1.3.11	
99, 100	4902890	29	3.00E-16	Streptococcus pneumoniae		galactosyl transferase [Streptococcus pneumoniae]		2.4.1.-	
9901, 9902	48859134	29	8.00E-18	Clostridium thermocellum ATCC 27405		COG0507: ATP-dependent exoDNAse (exonuclease V), alpha subunit - helicase superfamily I member [Clostridium thermocellum ATCC 27405]		3.1.11.5	
9903, 9904	23474422	29	4.00E-17	Desulfovibrio desulfuricans G20		COG0840: Methyl-accepting chemotaxis protein [Desulfovibrio desulfuricans G20]			
9905, 9906	48858423	41	4.00E-31	Clostridium thermocellum ATCC 27405		COG2206: HD-GYP domain [Clostridium thermocellum ATCC 27405]			
9909, 9910	29347707	56	5.00E-76	Bacteroides thetaiotaomicron VPI-5482		putative reverse transcriptase [Bacteroides thetaiotaomicron VPI-5482] gb AAO77404.1 putative reverse transcriptase [Bacteroides thetaiotaomicron VPI-5482]		2.7.7.49	
991, 992	53713337	63	4.00E-50	Bacteroides fragilis YCH46		putative GTP-binding protein [Bacteroides fragilis YCH46] db BAD48795.1 putative GTP-binding protein [Bacteroides fragilis YCH46]			
9913, 9914	34555818	26	7.00E-07	Wolinella succinogenes DSM 1740		HISTIDINE KINASE SENSOR PROTEIN [Wolinella succinogenes DSM 1740] emb CAE10833.1 HISTIDINE KINASE SENSOR PROTEIN [Wolinella succinogenes]			
9917, 9918	34556786	43	2.00E-58	Wolinella succinogenes DSM 1740		PUTATIVE PROCESSING PROTEASE [Wolinella succinogenes DSM 1740] emb CAE09501.1 PUTATIVE PROCESSING PROTEASE [Wolinella succinogenes]		3.4.-.-	
9919, 9920	34556712	46	4.00E-36	Wolinella succinogenes DSM 1740		GLUTAMYL-TRNA SYNTHETASE [Wolinella succinogenes DSM 1740] emb CAE09427.1 GLUTAMYL-TRNA SYNTHETASE [Wolinella succinogenes]		6.1.1.17	
9921, 9922	48895902	35	2.00E-15	Trichodesmium erythraeum IMS101		COG2755: Lysophospholipase L1 and related esterases [Trichodesmium erythraeum IMS101]			
9925, 9926	53713488	38	9.00E-43	Bacteroides fragilis YCH46		two-component system sensor histidine kinase [Bacteroides fragilis YCH46] db BAD48946.1 two-component system sensor histidine kinase [Bacteroides fragilis YCH46]		2.7.3.-	
9927, 9928	48853682	33	1.00E-26	Cytophaga hutchinsonii		COG0204: 1-acyl-sn-glycerol-3-phosphate acyltransferase [Cytophaga hutchinsonii]		2.3.1.51	

9929,	23506369	31	6.00E-10	Francisella tularensis subsp. novicida	galactose epimerase [Francisella tularensis subsp. novicida]				5.1.3.2
9930,				novicida					
9933,	48855702	43	4.00E-40	Cytophaga hutchinsonii	COG3279: Response regulator of the LysR/AlgR family [Cytophaga hutchinsonii]				2.7.-.-
9934									
9935,				Wolinella succinogenes DSM 1740	NADH-UBIQUINONE OXIDOREDUCTASE, NQO3 SUBUNIT NQO3 [Wolinella succinogenes DSM 1740] emb CAE09618.1 NADH-UBIQUINONE OXIDOREDUCTASE, NQO3 SUBUNIT NQO3 [Wolinella succinogenes]				1.6.5.3
9936	34556903	49	1.00E-59	Bacteroides thetaiotaomicron VPI-5482	topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482]				
9937,				Bacteroides thetaiotaomicron	gb AAO78685.1 topoisomerase IV subunit A [Bacteroides thetaiotaomicron VPI-5482]				5.99.1.-
9938	29348988	53	1.00E-90	Bacteroides thetaiotaomicron	putative isoprenyl synthetase [Bacteroides thetaiotaomicron VPI-5482]				
9939,				Bacteroides thetaiotaomicron	gb AAO77165.1 putative isoprenyl synthetase [Bacteroides thetaiotaomicron VPI-5482]				2.5.1.1
9940	29347468	47	2.00E-25	VPI-5482					
9941,				Geobacillus kaustophilus HTA426	type I restriction modification system M subunit (site-specific DNA-methyltransferase subunit) [Geobacillus kaustophilus HTA426]				
9942	56418878	59	2.00E-86	Wolinella succinogenes DSM 1740	db BAD74628.1 type I restriction modification system M subunit (site-specific DNA-methyltransferase subunit) [Geobacillus kaustophilus HTA426]				2.1.1.72
9943,				Wolinella succinogenes DSM 1740	SIGNAL-TRANSDUCING PROTEIN, HISTIDINE KINASE [Wolinella succinogenes DSM 1740] emb CAE10522.1 SIGNAL-TRANSDUCING PROTEIN, HISTIDINE KINASE [Wolinella succinogenes]				
9944	34557807	31	1.00E-14	Helicobacter hepaticus ATCC 51449	conserved hypothetical protein [Helicobacter hepaticus ATCC 51449]				2.7.3.-
9945,				Helicobacter hepaticus ATCC 51449	ref NP_861188.1 hypothetical protein HH1657 [Helicobacter hepaticus ATCC 51449]				
9946	32263209	37	9.00E-20	Wolinella succinogenes DSM 1740	UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE GLMU [Wolinella succinogenes DSM 1740] emb CAE11088.1 UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE GLMU [Wolinella succinogenes]				2.7.3.-
9947,				Wolinella succinogenes DSM 1740					
9948	34558373	66	9.00E-79	Bacteroides fragilis YCH46	putative GTPase [Bacteroides fragilis YCH46]				
9949,	53711977	50	6.00E-78	Leptospira interrogans serovar Copenhageni str. F100	hypothetical protein LIC13227 [Leptospira interrogans serovar Copenhageni str. F100] ref NP_714224.1 hypothetical protein LA4044 [Leptospira interrogans serovar Lai str. 56601] gb AA51242.1 conserved hypothetical protein [Leptospira interrogans serovar lai str. 56601] gb AA57172.1 conserved hypothetical protein [Leptospira interrogans serovar Copenhageni str. F100]				3.6.1.-
9950									
995,									
996	45659049	44	4.00E-25	Floccuz L1-130	serovar Copenhageni str. Floccuz L1-130				

9951, 9952	15669198	23	2.00E-11	2661	Methanocaldococcus jannaschii DSM	phosphate transport system regulatory protein (phoU) [Methanocaldococcus jannaschii DSM 2661] gb AAB9901.1.1 phosphate transport system regulatory protein (phoU) [Methanocaldococcus jannaschii DSM 2661] pir H64425 phosphate transport system regulatory protein homolog - [Methanocaldococcus jannaschii sp Q58415 PHOU_METJA Phosphate transport system protein phoU homolog				
9953, 9954	48893217	45	3.00E-16		Trichodesmium erythraeum IMS101	COG3914: Predicted O-linked N-acetylglucosamine transferase, SPINDLY family [Trichodesmium erythraeum IMS101]				
9963, 9964	ABP7392 2	45	7.00E-53			Desc:Candida albicans essential protein SEQ ID NO 7759. Org:Candida albicans			4.2.1.36	
9965, 9966	34557622	64	1.00E-106	1740	Wollinella succinogenes DSM	PREPROTEIN TRANSLOCASE SECA SUBUNIT [Wollinella succinogenes DSM 1740] emb CAE10337.1 PREPROTEIN TRANSLOCASE SECA SUBUNIT [Wollinella succinogenes]	Wollinella succinogenes, complete genome; segment 4/7	86	5.00E-11	
9967, 9968	34556981	30	4.00E-24	1740	Wollinella succinogenes DSM	hypothetical protein WS0562 [Wollinella succinogenes DSM 1740] emb CAE09696.1 conserved hypothetical protein [Wollinella succinogenes]				
9969, 9970	21673298	42	2.00E-43		Chlorobium tepidum TLS	ubiquinone/menaquinone biosynthesis methyltransferase [Chlorobium tepidum TLS] gb AAM71705.1 ubiquinone/menaquinone biosynthesis methyltransferase [Chlorobium tepidum TLS] sp Q8KF69 UBIE_CHLTE Menaquinone biosynthesis methyltransferase ubiE			2.1.1.-	
997, 998	21242456	41	2.00E-25		Xanthomonas axonopodis pv. citri str. 306	general stress protein [Xanthomonas axonopodis pv. citri str. 306] gb AAM36574.1 general stress protein [Xanthomonas axonopodis pv. citri str. 306]				
9971, 9972	23473540	36	1.00E-31		Desulfovibrio desulfuricans G20	COG0463: Glycoyltransferases involved in cell wall biogenesis [Desulfovibrio desulfuricans G20]			2.4.1.83	
9973, 9974	30250106	33	8.00E-10	19718	Nitrosomonas europaea ATCC	SAM (and some other nucleotide) binding motif [Nitrosomonas europaea ATCC 19718] emb CAD86083.1 SAM (and some other nucleotide) binding motif [Nitrosomonas europaea ATCC 19718]				
9975, 9976	53712362	42	3.00E-20		Bacteroides fragilis YCH46	hypothetical protein BF1070 [Bacteroides fragilis YCH46] dbj BAD47820.1 conserved hypothetical protein [Bacteroides fragilis YCH46]				
9977, 9978	54301960	45	2.00E-11		Photobacterium profundum SS9	hypothetical protein PBPR80280 [Photobacterium profundum SS9] emb CAG22153.1 hypothetical protein [Photobacterium profundum]				
9979, 9980	53712694	36	5.00E-09		Bacteroides fragilis YCH46	putative ferric aerobactin receptor [Bacteroides fragilis YCH46] dbj BAD48152.1 putative ferric aerobactin receptor [Bacteroides fragilis YCH46]				

9983, 9984	34557269	60	3.00E-85	Wollinella succinogenes DSM 1740	ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes DSM 1740] emb CAE09984.1 ATP-DEPENDENT DNA HELICASE EC 3.6.1. [Wollinella succinogenes]			3.6.1.-
9985, 9986	57237984	52	5.00E-61	Campylobacter jejuni RM1221	tRNA pseudouridine synthase B [Campylobacter jejuni RM1221] gb AAW35567.1 tRNA pseudouridine synthase B [Campylobacter jejuni RM1221]			4.2.1.70
9987, 9988	57242490	56	7.00E-72	Campylobacter upsaliensis RM3195	Mg chelatase-related protein [Campylobacter upsaliensis RM3195] gb EAL53558.1 Mg chelatase-related protein [Campylobacter upsaliensis RM3195]			
9989, 9990	6967683	51	1.00E-32	Campylobacter jejuni subsp. jejuni NCTC 11168	hypothetical protein Cj0190c [Campylobacter jejuni subsp. jejuni NCTC 11168] ref NP_281400.1 hypothetical protein Cj0190c [Campylobacter jejuni subsp. jejuni NCTC 11168] pir E81437 hypothetical protein Cj0190c [imported] - Campylobacter jejuni (strain NCTC 11168)			
999, 1000	48853385	46	1.00E-18	Cytophaga hutchinsonii	hypothetical protein Chut02003884 [Cytophaga hutchinsonii]			
9991, 9992	23130537	39	3.00E-37	Nostoc punctiforme PCC 73102	COG0778: Nitroreductase [Nostoc punctiforme PCC 73102]			
9993, 9994	34556638	60	1.00E-26	Wollinella succinogenes DSM 1740	ABC TRANSPORTER, ATP-BINDING PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09353.1 ABC TRANSPORTER, ATP-BINDING PROTEIN [Wollinella succinogenes]			1.8.-
9995, 9996	34556560	44	4.00E-60	Wollinella succinogenes DSM 1740	GGDEF FAMILY PROTEIN [Wollinella succinogenes DSM 1740] emb CAE09275.1 GGDEF FAMILY PROTEIN [Wollinella succinogenes]			

WHAT IS CLAIMED IS:

1. An isolated or recombinant nucleic acid comprising

(a) a nucleic acid sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues,

wherein the nucleic acid encodes at least one polypeptide having an enzymatic activity, or encodes a polypeptide or peptide capable of generating an antibody that binds specifically to a polypeptide having a sequence comprising any of the even numbered SEQ ID NO:s in the sequence listing, including from SEQ ID NO:2 through SEQ ID NO:26,898;

(b) a nucleic acid sequence that hybridizes under stringent conditions to a nucleic acid comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897,

wherein the nucleic acid encodes a polypeptide having an activity as set forth in Table 3, or encodes a polypeptide or peptide capable of generating an antibody that binds specifically to a polypeptide having a sequence comprising any of the even numbered SEQ ID NO:s in the sequence listing, including from SEQ ID NO:2 through SEQ ID NO:26,898,

and the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes,

and optionally the nucleic acid is at least about 20, 30, 40, 50, 60, 75, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more residues in length or the full length of the gene or transcript; and

(c) a nucleic acid sequence complementary to (a) or (b).

2. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is at least about 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897.

3. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identity is over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues, or the full length of a gene or a transcript.

4. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence comprises a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897.

5. The isolated or recombinant nucleic acid of claim 1, wherein the nucleic acid sequence encodes a polypeptide having a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897.

6. The isolated or recombinant nucleic acid of claim 1, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection.

7. The isolated or recombinant nucleic acid of claim 6, wherein the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

8. The isolated or recombinant nucleic acid of claim 1, wherein at least one enzymatic activity is one of the enzymatic activities described in Table 1, Table 2 or Table 3.

9. The isolated or recombinant nucleic acid of claim 1, wherein the protein is a structural or binding protein.

10. The isolated or recombinant nucleic acid of claim 8, wherein the enzymatic activity comprises aldolase, alpha-galactosidase, amidase, secondary amidase, amylase, catalase, dehalogenase, endoglucanase, epoxide hydrolase, or esterase activity.

11. The isolated or recombinant nucleic acid of claim 8, wherein the enzymatic activity comprises an activity in the carotenoid pathway.

12. The isolated or recombinant nucleic acid of claim 8, wherein the enzymatic activity comprises hydrolase, glucosidase, glycosidase, intein, isomerase, laccase, lipase, or monooxygenase activity.

13. The isolated or recombinant nucleic acid of claim 8, wherein the enzymatic activity comprises nitroreductase, nitrilase, P450 enzyme, pectate lyase, phosphatase, phospholipase, phytase, polymerase or xylanase activity.

14. The isolated or recombinant nucleic acid of claim 1, wherein the enzyme or protein is thermostable or thermotolerant.

15. The isolated or recombinant nucleic acid of claim 14, wherein the polypeptide retains enzyme activity under conditions comprising a temperature range of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C, or, the polypeptide retains enzyme activity after exposure to a temperature in the range from greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C.

16. An isolated or recombinant nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein, wherein the nucleic acid comprises a sequence that hybridizes under stringent conditions to a nucleic acid comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, and the nucleic acid encodes a polypeptide having enzyme activity or encodes a protein.

17. The isolated or recombinant nucleic acid of claim 16, wherein the nucleic acid is at least about 50, 75, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more residues in length or the full length of the gene or transcript.

18. The isolated or recombinant nucleic acid of claim 16, wherein the stringent conditions include a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes.

19. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein, wherein the probe comprises at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 150, 200, 250, 300, 350, 400, 450, 500 or more consecutive bases of a sequence comprising SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID

listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, wherein the probe identifies the nucleic acid by binding or hybridization.

20. The nucleic acid probe of claim 19, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

21. A nucleic acid probe for identifying a nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein, wherein the probe comprises a nucleic acid comprising at least about 10 consecutive residues of a nucleic acid sequence having at least 50% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by visual inspection.

22. The nucleic acid probe of claim 21, wherein the probe comprises an oligonucleotide comprising at least about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, about 60 to 100, or about 50 to 150 consecutive bases.

23. An amplification primer pair for amplifying a nucleic acid encoding a polypeptide having an enzymatic activity or encoding a protein, wherein the primer pair is capable of amplifying a nucleic acid comprising a sequence as set forth in claim 1 or claim 16, or a subsequence thereof.

24. The amplification primer pair of claim 23, wherein a member of the amplification primer pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of the sequence, or, about 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40 or more consecutive bases of the sequence.

25. An amplification primer pair, wherein the amplification primer pair comprises a first member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 42, 33, 34, 35 or more residues of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, and a second member having a sequence as set forth by about the first (the 5') 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 42, 33, 34, 35 or more residues of the complementary strand of the first member.

26. An enzyme-encoding or protein-encoding nucleic acid generated by amplification of a polynucleotide using an amplification primer pair as set forth in claim 23 or claim 25.

27. The enzyme-encoding or protein-encoding nucleic acid of claim 26, wherein the amplification is by polymerase chain reaction (PCR).

28. The enzyme-encoding or protein-encoding nucleic acid of claim 26, wherein the nucleic acid generated by amplification of a gene library.

29. The enzyme-encoding or protein-encoding nucleic acid of claim 28, wherein the gene library is an environmental library.

30. An isolated or recombinant polypeptide having an enzymatic activity or encoding a protein encoded by a nucleic acid as set forth in claim 26.

31. A method of amplifying a nucleic acid encoding a polypeptide having an enzymatic activity or encoding a protein comprising amplification of a template nucleic acid with an amplification primer pair capable of amplifying a nucleic acid sequence as set forth in claim 1 or claim 16, or a subsequence thereof.

32. An expression cassette comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 16.

33. A vector comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 16.

34. A cloning vehicle comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 16, wherein the cloning vehicle comprises a viral vector, a plasmid, a phage, a phagemid, a cosmid, a fosmid, a bacteriophage or an artificial chromosome.

35. The cloning vehicle of claim 34, wherein the viral vector comprises an adenovirus vector, a retroviral vector or an adeno-associated viral vector.

36. A bacterial artificial chromosome (BAC), a bacteriophage P1-derived vector (PAC), a yeast artificial chromosome (YAC) or a mammalian artificial chromosome (MAC) comprising a sequence as set forth in claim 1 or claim 16.

37. A transformed cell comprising a nucleic acid comprising a sequence as set forth in claim 1 or claim 16.

38. A transformed cell comprising an expression cassette as set forth in claim 32.

39. The transformed cell of claim 38, wherein the cell is a bacterial cell, a mammalian cell, a fungal cell, a yeast cell, an insect cell or a plant cell.

40. A transgenic non-human animal comprising a sequence as set forth in claim 1 or claim 16.

41. The transgenic non-human animal of claim 40, wherein the animal is a mouse, a goat, a rabbit, a sheep, a pig, a cow or a rat.

42. A transgenic plant comprising a sequence as set forth in claim 1 or claim 16.

43. The transgenic plant of claim 42, wherein the plant is a corn plant, a sorghum plant, a potato plant, a tomato plant, a wheat plant, an oilseed plant, a rapeseed plant, a soybean plant, a rice plant, a barley plant, a grass, or a tobacco plant.

44. A transgenic seed comprising a sequence as set forth in claim 1 or claim 16.

45. The transgenic seed of claim 44, wherein the seed is a corn seed, a wheat kernel, an oilseed, a rapeseed, a soybean seed, a palm kernel, a sunflower seed, a sesame seed, a rice, a barley, a peanut or a tobacco plant seed.

46. An antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 16, or a subsequence thereof.

47. The antisense oligonucleotide of claim 46, wherein the antisense oligonucleotide is between about 10 to 50, about 20 to 60, about 30 to 70, about 40 to 80, or about 60 to 100 bases in length.

48. A method of inhibiting the translation of an enzyme-encoding or protein-encoding message in a cell comprising administering to the cell or expressing in the cell an antisense oligonucleotide comprising a nucleic acid sequence complementary to or capable of hybridizing under stringent conditions to a sequence as set forth in claim 1 or claim 16.

49. A double-stranded inhibitory RNA (RNAi) molecule comprising a subsequence of a sequence as set forth in claim 1 or claim 16, wherein optionally the RNAi is an siRNA or an miRNA molecule.

50. The double-stranded inhibitory RNA (RNAi) molecule of claim 49, wherein the RNAi is about 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or more duplex nucleotides in length, wherein optionally the RNAi is an siRNA or an miRNA molecule.

51. A method of inhibiting the expression of an enzyme or a protein in a cell comprising administering to the cell or expressing in the cell a double-stranded inhibitory RNA (iRNA), wherein the RNA comprises a subsequence of a sequence as set forth in claim 1 or claim 16, wherein optionally the RNAi is an siRNA or an miRNA molecule.

52. An isolated or recombinant polypeptide (i) having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more or complete sequence identity to SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898, over a region of at least about 20, 30, 40, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700 or more residues, wherein optionally the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection, or, (ii) encoded by a nucleic acid having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more sequence identity to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, over a region of at least about 20, 30, 40, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700 or more residues, or encoded by a nucleic acid capable of hybridizing under stringent conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897.

53. The isolated or recombinant polypeptide of claim 52, wherein the sequence identity is over a region of at least about 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or is 100% sequence identity.

54. The isolated or recombinant polypeptide of claim 52, wherein the sequence identity is over a region of at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050 or more residues, or the full length of an enzyme.

55. The isolated or recombinant polypeptide of claim 52, wherein the polypeptide has a sequence as set forth in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898.

56. The isolated or recombinant polypeptide of claim 52, wherein the polypeptide has an enzymatic activity or encodes a protein.

57. The isolated or recombinant polypeptide of claim 56, wherein the enzymatic activity comprises aldolase, alpha-galactosidase, amidase, secondary amidase, amylase, catalase, dehalogenase, endoglucanase, epoxide hydrolase, or esterase activity.

58. The isolated or recombinant polypeptide of claim 56, wherein the enzymatic activity comprises an activity in the carotenoid pathway.

59. The isolated or recombinant polypeptide of claim 56, wherein the enzymatic activity comprises hydrolase, glucosidase, glycosidase, intein, isomerase, laccase, lipase, or monooxygenase activity.

60. The isolated or recombinant polypeptide of claim 56, wherein the enzymatic activity comprises nitroreductase, nitrilase, P450 enzyme, pectate lyase, phosphatase, phospholipase, phytase, polymerase or xylanase activity.

61. The isolated or recombinant polypeptide of claim 56, wherein the enzyme or the protein is thermostable or thermotolerant.

62. The isolated or recombinant polypeptide of claim 61, wherein the polypeptide retains enzymatic activity under conditions comprising a temperature range of between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 95°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or, the polypeptide retains enzymatic activity after exposure to a temperature in the range from between about 1°C to about 5°C, between about 5°C to about 15°C, between about 15°C to about 25°C, between about 25°C to about 37°C, between about 37°C to about 95°C, between about 55°C to about 85°C, between about 70°C to about 75°C, or between about 90°C to about 95°C, or more.

63. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 52 and lacking a signal sequence or a prepro sequence.

64. An isolated or recombinant polypeptide comprising a polypeptide as set forth in claim 52 and having a heterologous signal sequence or a heterologous prepro sequence.

65. The isolated or recombinant polypeptide of claim 56, wherein the enzymatic activity comprises a specific activity at about 37°C in the range from about 100 to about 1000 units per milligram of protein, from about 500 to about 750 units per milligram of protein, from about 500 to about 1200 units per milligram of protein, or from about 750 to about 1000 units per milligram of protein.

66. The isolated or recombinant polypeptide of claim 61, wherein thermotolerance comprises retention of at least half of the specific activity of the enzyme at 37°C after being heated to an elevated temperature.

67. The isolated or recombinant polypeptide of claim 61, wherein thermotolerance comprises retention of specific activity at 37°C in the range from about 500 to about 1200 units per milligram of protein after being heated to an elevated temperature.

68. The isolated or recombinant polypeptide of claim 52, wherein the polypeptide comprises at least one glycosylation site.

69. The isolated or recombinant polypeptide of claim 68, wherein the glycosylation is an N-linked glycosylation.

70. The isolated or recombinant polypeptide of claim 68, wherein the polypeptide is glycosylated after being expressed in a *P. pastoris* or a *S. pombe*.

71. The isolated or recombinant polypeptide of claim 56, wherein the polypeptide retains an enzymatic activity under conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0.

72. The isolated or recombinant polypeptide of claim 56, wherein the polypeptide retains an enzymatic activity under conditions comprising about pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5.

73. A protein preparation comprising a polypeptide as set forth in claim 52, wherein the protein preparation comprises a liquid, a solid or a gel.

74. A heterodimer comprising a polypeptide as set forth in claim 52 and a second domain.

75. The heterodimer of claim 74, wherein the second domain is a polypeptide and the heterodimer is a fusion protein.

76. The heterodimer of claim 74, wherein the second domain is an epitope or a tag.
77. A homodimer comprising a polypeptide as set forth in claim 52.
78. An immobilized polypeptide, wherein the polypeptide comprises a sequence as set forth in claim 52, or a subsequence thereof.
79. The immobilized polypeptide of claim 78, wherein the polypeptide is immobilized on a cell, a metal, a resin, a polymer, a ceramic, a glass, a microelectrode, a graphitic particle, a bead, a gel, a plate, an array or a capillary tube.
80. An array comprising an immobilized polypeptide as set forth in claim 52.
81. An array comprising an immobilized nucleic acid as set forth in claim 1 or claim 16.
82. An isolated or recombinant antibody that specifically binds to a polypeptide as set forth in claim 52.
83. The isolated or recombinant antibody of claim 82, wherein the antibody is a monoclonal or a polyclonal antibody.
84. A hybridoma comprising an antibody that specifically binds to a polypeptide as set forth in claim 52.
85. A method of isolating or identifying a polypeptide with an enzymatic activity or encoding a protein comprising the steps of:
- (a) providing an antibody as set forth in claim 82;
 - (b) providing a sample comprising polypeptides; and

(c) contacting the sample of step (b) with the antibody of step (a) under conditions wherein the antibody can specifically bind to the polypeptide, thereby isolating or identifying a polypeptide having enzymatic activity or encoding a protein.

86. A method of making an anti-enzyme or anti-protein antibody comprising administering to a non-human animal a nucleic acid as set forth in claim 1 or claim 16 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-enzyme or anti-protein antibody.

87. A method of making an anti-enzyme or anti-protein antibody comprising administering to a non-human animal a polypeptide as set forth in claim 52 or a subsequence thereof in an amount sufficient to generate a humoral immune response, thereby making an anti-enzyme or anti-protein antibody.

88. A method of producing a recombinant polypeptide comprising the steps of: (a) providing a nucleic acid operably linked to a promoter, wherein the nucleic acid comprises a sequence as set forth in claim 1 or claim 16; and (b) expressing the nucleic acid of step (a) under conditions that allow expression of the polypeptide, thereby producing a recombinant polypeptide.

89. The method of claim 88, further comprising transforming a host cell with the nucleic acid of step (a) followed by expressing the nucleic acid of step (a), thereby producing a recombinant polypeptide.

90. A method for identifying a polypeptide having an enzyme activity or encoding a protein comprising the following steps:

(a) providing a polypeptide as set forth in claim 52;

(b) providing an enzyme substrate; and

(c) contacting the polypeptide with the substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of a reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product detects a polypeptide having an enzyme activity or encoding a protein.

91. A method for identifying an enzyme or protein substrate comprising the following steps:

- (a) providing a polypeptide as set forth in claim 52;
- (b) providing a test substrate; and
- (c) contacting the polypeptide of step (a) with the test substrate of step (b) and detecting a decrease in the amount of substrate or an increase in the amount of reaction product, wherein a decrease in the amount of the substrate or an increase in the amount of a reaction product identifies the test substrate as an enzyme or protein substrate.

92. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

- (a) expressing a nucleic acid or a vector comprising the nucleic acid under conditions permissive for translation of the nucleic acid to a polypeptide, wherein the nucleic acid has a sequence as set forth in claim 1 or claim 16;
- (b) providing a test compound;
- (c) contacting the polypeptide with the test compound; and
- (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

93. A method of determining whether a test compound specifically binds to a polypeptide comprising the following steps:

- (a) providing a polypeptide as set forth in claim 52;
- (b) providing a test compound;
- (c) contacting the polypeptide with the test compound; and
- (d) determining whether the test compound of step (b) specifically binds to the polypeptide.

94. A method for identifying a modulator of an enzyme activity comprising the following steps:

- (a) providing a polypeptide as set forth in claim 56;
- (b) providing a test compound;
- (c) contacting the polypeptide of step (a) with the test compound of step (b) and measuring an activity of the enzyme, wherein a change in the enzyme activity

measured in the presence of the test compound compared to the activity in the absence of the test compound provides a determination that the test compound modulates the enzyme activity.

95. The method of claim 94, wherein the enzyme activity is measured by providing an enzyme substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product, or, an increase in the amount of the substrate or a decrease in the amount of a reaction product.

96. The method of claim 95, wherein a decrease in the amount of the substrate or an increase in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an activator of an enzyme activity.

97. The method of claim 95, wherein an increase in the amount of the substrate or a decrease in the amount of the reaction product with the test compound as compared to the amount of substrate or reaction product without the test compound identifies the test compound as an inhibitor of an enzyme activity.

98. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises sequence as set forth in claim 52, a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16.

99. The computer system of claim 98, further comprising a sequence comparison algorithm and a data storage device having at least one reference sequence stored thereon.

100. The computer system of claim 99, wherein the sequence comparison algorithm comprises a computer program that indicates polymorphisms.

101. The computer system of claim 98, further comprising an identifier that identifies one or more features in said sequence.

102. A computer readable medium having stored thereon a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 52; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16.

103. A method for identifying a feature in a sequence comprising the steps of: (a) reading the sequence using a computer program which identifies one or more features in a sequence, wherein the sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 52; a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16; and (b) identifying one or more features in the sequence with the computer program.

104. A method for comparing a first sequence to a second sequence comprising the steps of: (a) reading the first sequence and the second sequence through use of a computer program which compares sequences, wherein the first sequence comprises a polypeptide sequence or a nucleic acid sequence, wherein the polypeptide sequence comprises a polypeptide as set forth in claim 52 or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16; and (b) determining differences between the first sequence and the second sequence with the computer program.

105. The method of claim 104, wherein the step of determining differences between the first sequence and the second sequence further comprises the step of identifying polymorphisms.

106. The method of claim 104, further comprising an identifier that identifies one or more features in a sequence.

107. The method of claim 104, comprising reading the first sequence using a computer program and identifying one or more features in the sequence.

108. A method for isolating or recovering a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein from an environmental sample comprising the steps of:

(a) providing an amplification primer pair as set forth in claim 23 or claim 25;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to the amplification primer pair; and,

(c) combining the nucleic acid of step (b) with the amplification primer pair of step (a) and amplifying nucleic acid from the environmental sample, thereby isolating or recovering a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein from an environmental sample.

109. The method of claim 108, wherein each member of the amplification primer sequence pair comprises an oligonucleotide comprising at least about 10 to 50 consecutive bases of a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, or a subsequence thereof.

110. A method for isolating or recovering a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein from an environmental sample comprising the steps of:

(a) providing a polynucleotide probe comprising a sequence as set forth in claim 1 or claim 16, or a subsequence thereof;

(b) isolating a nucleic acid from the environmental sample or treating the environmental sample such that nucleic acid in the sample is accessible for hybridization to a polynucleotide probe of step (a);

(c) combining the isolated nucleic acid or the treated environmental sample of step (b) with the polynucleotide probe of step (a); and

(d) isolating a nucleic acid that specifically hybridizes with the polynucleotide probe of step (a), thereby isolating or recovering a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein from an environmental sample.

111. The method of claim 108 or claim 110, wherein the environmental sample comprises a water sample, a liquid sample, a soil sample, an air sample or a biological sample.

112. The method of claim 111, wherein the biological sample is derived from a bacterial cell, a protozoan cell, an insect cell, a yeast cell, a plant cell, a fungal cell or a mammalian cell.

113. A method of generating a variant of a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein comprising the steps of:

(a) providing a template nucleic acid comprising a sequence as set forth in claim 1 or claim 16; and

(b) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid.

114. The method of claim 113, further comprising expressing the variant nucleic acid to generate a variant enzyme or protein polypeptide.

115. The method of claim 113, wherein the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR) and a combination thereof.

116. The method of claim 113, wherein the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

117. The method of claim 113, wherein the method is iteratively repeated until an enzyme or protein having an altered or different activity or an altered or different stability from that of a polypeptide encoded by the template nucleic acid is produced.

118. The method of claim 117, wherein the variant enzyme or protein polypeptide is thermotolerant, and retains some activity after being exposed to an elevated temperature.

119. The method of claim 117, wherein the variant enzyme or protein polypeptide has increased glycosylation as compared to the enzyme or protein encoded by a template nucleic acid.

120. The method of claim 117, wherein the variant enzyme or protein polypeptide has an enzyme activity under a high temperature, wherein the enzyme encoded by the template nucleic acid is not active under the high temperature.

121. The method of claim 113, wherein the method is iteratively repeated until an enzyme or protein coding sequence having an altered codon usage from that of the template nucleic acid is produced.

122. The method of claim 113, wherein the method is iteratively repeated until an enzyme or protein gene having higher or lower level of message expression or stability from that of the template nucleic acid is produced.

123. A method for modifying codons in a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein comprising a sequence as set forth in claim 1 or claim 16; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented

in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

124. A method for modifying codons in a nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide with an enzyme activity or encoding a protein comprising a sequence as set forth in claim 1 or claim 16; and,

(b) identifying a codon in the nucleic acid of step (a) and replacing it with a different codon encoding the same amino acid as the replaced codon, thereby modifying codons in a nucleic acid encoding an enzyme or a protein.

125. A method for modifying codons in a nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein, to increase its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein, comprising a sequence as set forth in claim 1 or claim 16; and,

(b) identifying a non-preferred or a less preferred codon in the nucleic acid of step (a) and replacing it with a preferred or neutrally used codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in the host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to increase its expression in a host cell.

126. A method for modifying a codon in a nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein to decrease its expression in a host cell, the method comprising the following steps:

(a) providing a nucleic acid encoding a polypeptide having an enzyme activity or encoding a protein comprising a sequence as set forth in claim 1 or claim 16; and

(b) identifying at least one preferred codon in the nucleic acid of step (a) and replacing it with a non-preferred or less preferred codon encoding the same amino acid as the replaced codon, wherein a preferred codon is a codon over-represented in coding sequences in genes in a host cell and a non-preferred or less preferred codon is a codon under-represented in coding sequences in genes in the host cell, thereby modifying the nucleic acid to decrease its expression in a host cell.

127. The method of claim 125, wherein the host cell is a bacterial cell, a fungal cell, an insect cell, a yeast cell, a plant cell or a mammalian cell.

128. A method for producing a library of nucleic acids encoding a plurality of modified enzyme or protein active sites or substrate binding sites, wherein the modified active sites or substrate binding sites are derived from a first nucleic acid comprising a sequence encoding a first active site or a first substrate binding site the method comprising the following steps:

(a) providing a first nucleic acid encoding a first active site or first substrate binding site, wherein the first nucleic acid sequence comprises a sequence that hybridizes under stringent conditions to a sequence as set forth in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, and all nucleic acids disclosed in the SEQ ID listing, which include all odd numbered SEQ ID NO:s from SEQ ID NO:1 through SEQ ID NO:26,897, or a subsequence thereof, and the nucleic acid encodes an enzyme or protein active site or an enzyme or protein substrate binding site;

(b) providing a set of mutagenic oligonucleotides that encode naturally-occurring amino acid variants at a plurality of targeted codons in the first nucleic acid; and,

(c) using the set of mutagenic oligonucleotides to generate a set of active site-encoding or substrate binding site-encoding variant nucleic acids encoding a range of amino acid variations at each amino acid codon that was mutagenized, thereby producing a library of nucleic acids encoding a plurality of modified enzyme or protein active sites or substrate binding sites.

129. The method of claim 128, comprising mutagenizing the first nucleic acid of step (a) by a method comprising an optimized directed evolution system, Gene Site Saturation Mutagenesis (GSSM), or a synthetic ligation reassembly (SLR).

130. The method of claim 128, comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in vivo mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR) and a combination thereof.

131. The method of claim 128, comprising mutagenizing the first nucleic acid of step (a) or variants by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof.

132. A method for making a small molecule comprising the following steps:

- (a) providing a plurality of biosynthetic enzymes capable of synthesizing or modifying a small molecule, wherein one of the enzymes comprises an enzyme encoded by a nucleic acid comprising a sequence as set forth in claim 1 or claim 16;
- (b) providing a substrate for at least one of the enzymes of step (a); and
- (c) reacting the substrate of step (b) with the enzymes under conditions that facilitate a plurality of biocatalytic reactions to generate a small molecule by a series of biocatalytic reactions.

133. A method for modifying a small molecule comprising the following steps:

(a) providing an enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 52, or a polypeptide encoded by a nucleic acid comprising a nucleic acid sequence as set forth in claim 1 or claim 16;

(b) providing a small molecule; and

(c) reacting the enzyme of step (a) with the small molecule of step (b) under conditions that facilitate an enzymatic reaction catalyzed by the enzyme, thereby modifying a small molecule by an enzymatic reaction.

134. The method of claim 133, comprising a plurality of small molecule substrates for the enzyme of step (a), thereby generating a library of modified small molecules produced by at least one enzymatic reaction catalyzed by the enzyme.

135. The method of claim 133, further comprising a plurality of additional enzymes under conditions that facilitate a plurality of biocatalytic reactions by the enzymes to form a library of modified small molecules produced by the plurality of enzymatic reactions.

136. The method of claim 135, further comprising the step of testing the library to determine if a particular modified small molecule which exhibits a desired activity is present within the library.

137. The method of claim 136, wherein the step of testing the library further comprises the steps of systematically eliminating all but one of the biocatalytic reactions used to produce a portion of the plurality of the modified small molecules within the library by testing the portion of the modified small molecule for the presence or absence of the particular modified small molecule with a desired activity, and identifying at least one specific biocatalytic reaction that produces the particular modified small molecule of desired activity.

138. A method for determining a functional fragment of an enzyme comprising the steps of:

(a) providing an enzyme, wherein the enzyme comprises a polypeptide as set forth in claim 52, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16; and

(b) deleting a plurality of amino acid residues from the sequence of step (a) and testing the remaining subsequence for an enzyme activity, thereby determining a functional fragment of an enzyme.

139. The method of claim 138, wherein the enzyme activity is measured by providing an enzyme substrate and detecting a decrease in the amount of the substrate or an increase in the amount of a reaction product.

140. A method for whole cell engineering of new or modified phenotypes by using real-time metabolic flux analysis, the method comprising the following steps:

(a) making a modified cell by modifying the genetic composition of a cell, wherein the genetic composition is modified by addition to the cell of a nucleic acid comprising a sequence as set forth in claim 1 or claim 16;

(b) culturing the modified cell to generate a plurality of modified cells;

(c) measuring at least one metabolic parameter of the cell by monitoring the cell culture of step (b) in real time; and,

(d) analyzing the data of step (c) to determine if the measured parameter differs from a comparable measurement in an unmodified cell under similar conditions, thereby identifying an engineered phenotype in the cell using real-time metabolic flux analysis.

141. The method of claim 140, wherein the genetic composition of the cell is modified by a method comprising deletion of a sequence or modification of a sequence in the cell, or, knocking out the expression of a gene.

142. The method of claim 141, further comprising selecting a cell comprising a newly engineered phenotype.

143. The method of claim 142, further comprising culturing the selected cell, thereby generating a new cell strain comprising a newly engineered phenotype.

144. An isolated or recombinant signal sequence (signal peptide) consisting of a sequence as set forth in residues 1 to 14, 1 to 15, 1 to 16, 1 to 17, 1 to 18, 1

to 19, 1 to 20, 1 to 21, 1 to 22, 1 to 23, 1 to 24, 1 to 25, 1 to 26, 1 to 27, 1 to 28, 1 to 28, 1 to 30, 1 to 31, 1 to 32, 1 to 33, 1 to 34, 1 to 35, 1 to 36, 1 to 37, 1 to 38, 1 to 40, 1 to 41, 1 to 42, 1 to 43, 1 to 44, 1 to 45, 1 to 46, or 1 to 47, of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, and all polypeptides disclosed in the SEQ ID listing, which include all even numbered SEQ ID NO:s from SEQ ID NO:2 through SEQ ID NO:26,898.

145. A chimeric polypeptide comprising at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 144, and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

146. The chimeric polypeptide of claim 145, wherein the heterologous polypeptide or peptide is not an enzyme.

147. The chimeric polypeptide of claim 145, wherein the heterologous polypeptide or peptide is amino terminal to, carboxy terminal to or on both ends of the signal peptide (SP) or an enzyme catalytic domain (CD).

148. An isolated or recombinant nucleic acid encoding a chimeric polypeptide, wherein the chimeric polypeptide comprises at least a first domain comprising signal peptide (SP) having a sequence as set forth in claim 144, and at least a second domain comprising a heterologous polypeptide or peptide, wherein the heterologous polypeptide or peptide is not naturally associated with the signal peptide (SP).

149. A method of increasing thermotolerance or thermostability of a enzyme polypeptide, the method comprising glycosylating an enzyme, wherein the polypeptide comprises at least thirty contiguous amino acids of a polypeptide as set forth in claim 52, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16, thereby increasing thermotolerance or thermostability of the enzyme.

150. A method for overexpressing a recombinant enzyme in a cell comprising expressing a vector comprising a nucleic acid sequence as set forth in claim 1 or claim 16, wherein overexpression is effected by use of a high activity promoter, a dicistronic vector or by gene amplification of the vector.

151. A method of making a transgenic plant comprising the following steps:

(a) introducing a heterologous nucleic acid sequence into the cell, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 16, thereby producing a transformed plant cell;

(b) producing a transgenic plant from the transformed cell.

152. The method as set forth in claim 151, wherein the step (a) further comprises introducing the heterologous nucleic acid sequence by electroporation or microinjection of plant cell protoplasts.

153. The method as set forth in claim 152, wherein the step (a) comprises introducing the heterologous nucleic acid sequence directly to plant tissue by DNA particle bombardment or by using an *Agrobacterium tumefaciens* host.

154. A method of expressing a heterologous nucleic acid sequence in a plant cell comprising the following steps:

(a) transforming the plant cell with a heterologous nucleic acid sequence operably linked to a promoter, wherein the heterologous nucleic sequence comprises a sequence as set forth in claim 1 or claim 16;

(b) growing the plant under conditions wherein the heterologous nucleic acids sequence is expressed in the plant cell.

155. A method for decreasing the amount of a compound in a composition comprising the following steps:

(a) providing a polypeptide having an enzyme activity or encoding a protein as set forth in claim 52, or a polypeptide encoded by a nucleic acid as set forth in claim 1 or claim 16;

(b) providing a composition comprising the compound; and

(c) contacting the polypeptide of step (a) with the composition of step (b) under conditions wherein the enzyme hydrolyzes, breaks up or otherwise processes the compound in the composition.

156. The method as set forth in claim 155, wherein the composition comprises an animal food or feed.

157. A drink or beverage comprising at least one polypeptide as set forth in claim 52.

158. The drink or beverage of claim 157, wherein the drink or beverage is a food or feed supplement.

159. A food, a feed or a nutritional supplement comprising a polypeptide as set forth in claim 52.

160. A method for utilizing an enzyme or protein as a nutritional supplement in an animal diet, the method comprising:
preparing a nutritional supplement containing an enzyme or protein comprising at least thirty contiguous amino acids of a polypeptide as set forth in claim 52;
and
administering the nutritional supplement to the animal.

161. The method of claim 160, wherein the animal is a human.

162. The method of claim 160, wherein the animal is a ruminant or a monogastric animal.

163. The method of claim 160, wherein the enzyme or protein is prepared by expression of a polynucleotide encoding the enzyme or protein in an organism selected from the group consisting of a bacterium, a yeast, a plant, an insect, a fungus and an animal.

164. The method of claim 163, wherein the organism is selected from the group consisting of a *S. pombe*, *S. cerevisiae*, *Pichia pastoris*, *E. coli*, *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

165. An edible enzyme delivery matrix comprising a thermostable recombinant enzyme or protein having a sequence as set forth in claim 56.

166. A method for delivering an enzyme or protein supplement to an animal, the method comprising:

preparing an edible enzyme delivery matrix in the form of pellets comprising a granulate edible carrier and thermostable recombinant enzyme or protein having a sequence as set forth in claim 56, wherein the pellets readily disperse the enzyme or protein contained therein into aqueous media, and administering the edible enzyme delivery matrix to the animal.

167. The method of claim 166, wherein the granulate edible carrier comprises a carrier selected from the group consisting of a grain germ, a grain germ that is spent of oil, a hay, an alfalfa, a timothy, a soy hull, a sunflower seed meal and a wheat midd.

168. The method of claim 166, wherein the granulate edible carrier comprises grain germ that is spent of oil.

169. The method of claim 166, wherein the enzyme is glycosylated to provide thermostability at pelletizing conditions.

170. The method of claim 166, wherein the delivery matrix is formed by pelletizing a mixture comprising a grain germ and an enzyme or protein.

171. The method of claim 166, wherein the pelletizing conditions include application of steam.

172. The method of claim 166, wherein the pelletizing conditions comprise application of a temperature in excess of about 80°C for about 5 minutes and the

enzyme retains a specific activity of at least 350 to about 900 units per milligram of enzyme.

173. An isolated or recombinant nucleic acid comprising a sequence encoding a polypeptide having an enzyme activity and a signal sequence, wherein the nucleic acid comprises a sequence as set forth in claim 1.

174. The isolated or recombinant nucleic acid of claim 173, wherein the signal sequence is derived from another enzyme.

175. An isolated or recombinant nucleic acid comprising a sequence encoding a polypeptide having an enzyme activity or encoding a protein, wherein the sequence does not contain a signal sequence and the nucleic acid comprises a sequence as set forth in claim 1.

176. A pharmaceutical composition comprising a polypeptide as set forth in claim 52.

177. The pharmaceutical composition of claim 176 formulated as an edible delivery agent.

178. The pharmaceutical composition of claim 177, wherein the formulation comprises a tablet, a gel, a capsule or a gellab.

179. The pharmaceutical composition of claim 177, wherein the formulation comprises a lotion, a spray or a gel.

180. A method for delivering an enzyme or protein supplement to an animal, the method comprising:

- (a) providing a cell that recombinantly generates a polypeptide as set forth in claim 56, and
- (b) administering the cell or the recombinantly generated polypeptide to the animal.

181. The method as claim 180, wherein the cell is a plant cell, a bacterial cell, a yeast cell, an insect cell or an animal cell.

182. The method of claim 181, wherein the cell is selected from the group consisting of a *Schizosaccharomyces* sp., *Saccharomyces* sp., *Pichia* sp., *Escherichia* sp., *Streptomyces* sp., *Bacillus* sp. and *Lactobacillus* sp.

183. The method of claim 182, wherein the cell is *Saccharomyces pombe*.

184. The method of claim 182, wherein the cell is *Saccharomyces cerevisiae*.

185. The method of claim 182, wherein the cell is *Pichia pastoris*.

186. The method of claim 182, wherein the cell is *Escherichia coli*.

187. The method of claim 182, wherein the cell is *Bacillus cereus*.

188. A composition comprising an encapsulated formulation comprising at least one polypeptide as set forth in claim 56.

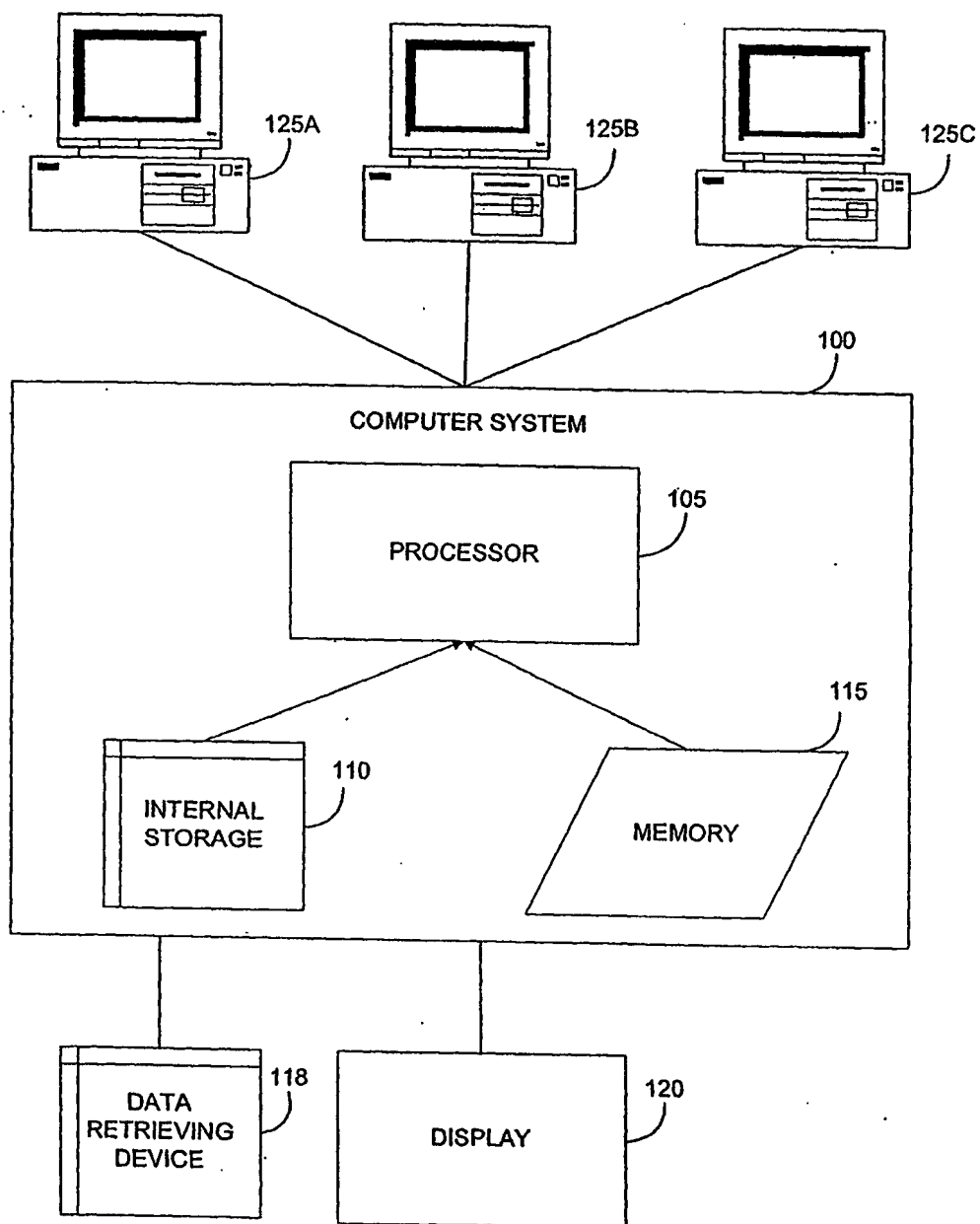


FIGURE 1

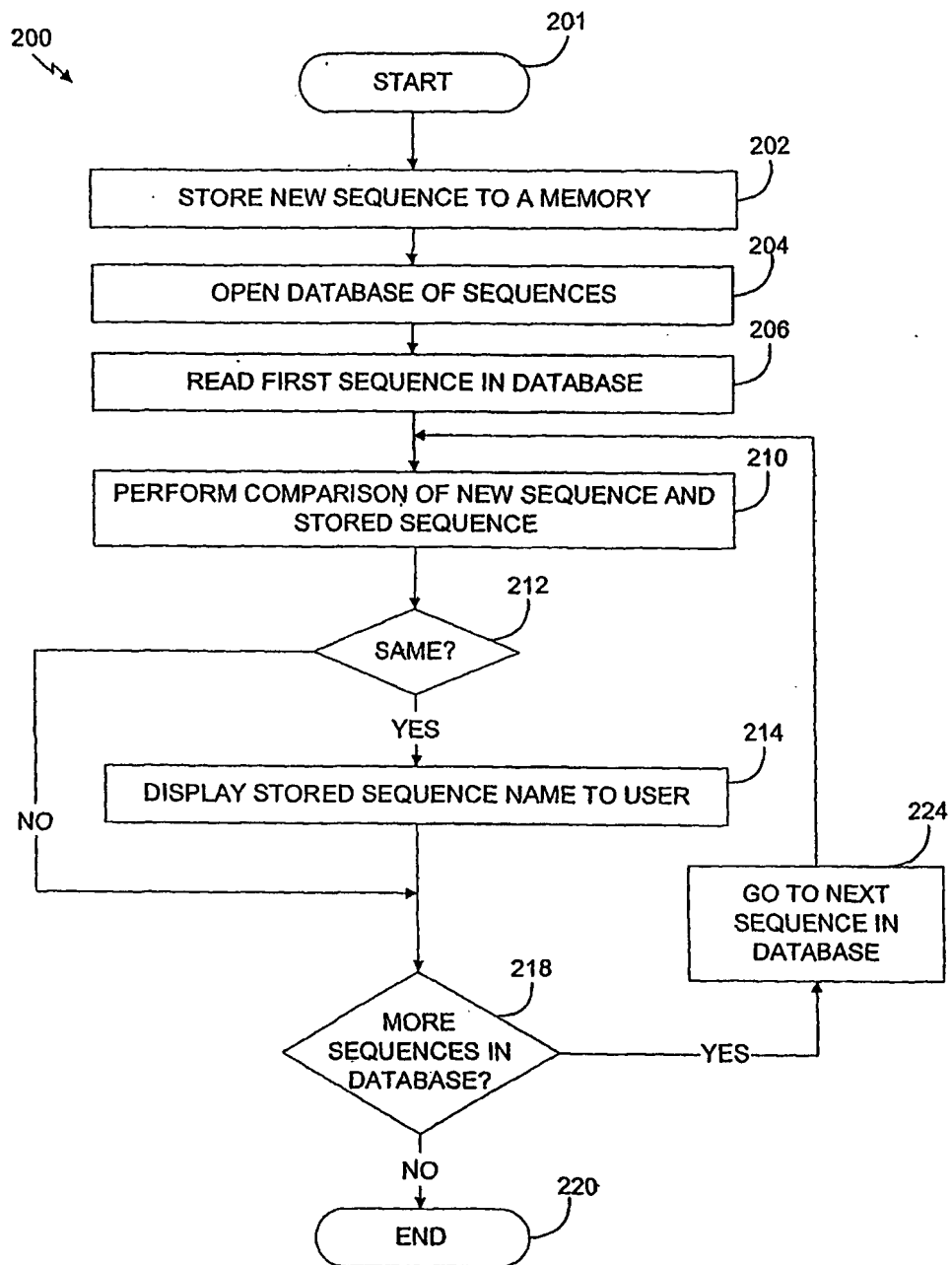


FIGURE 2

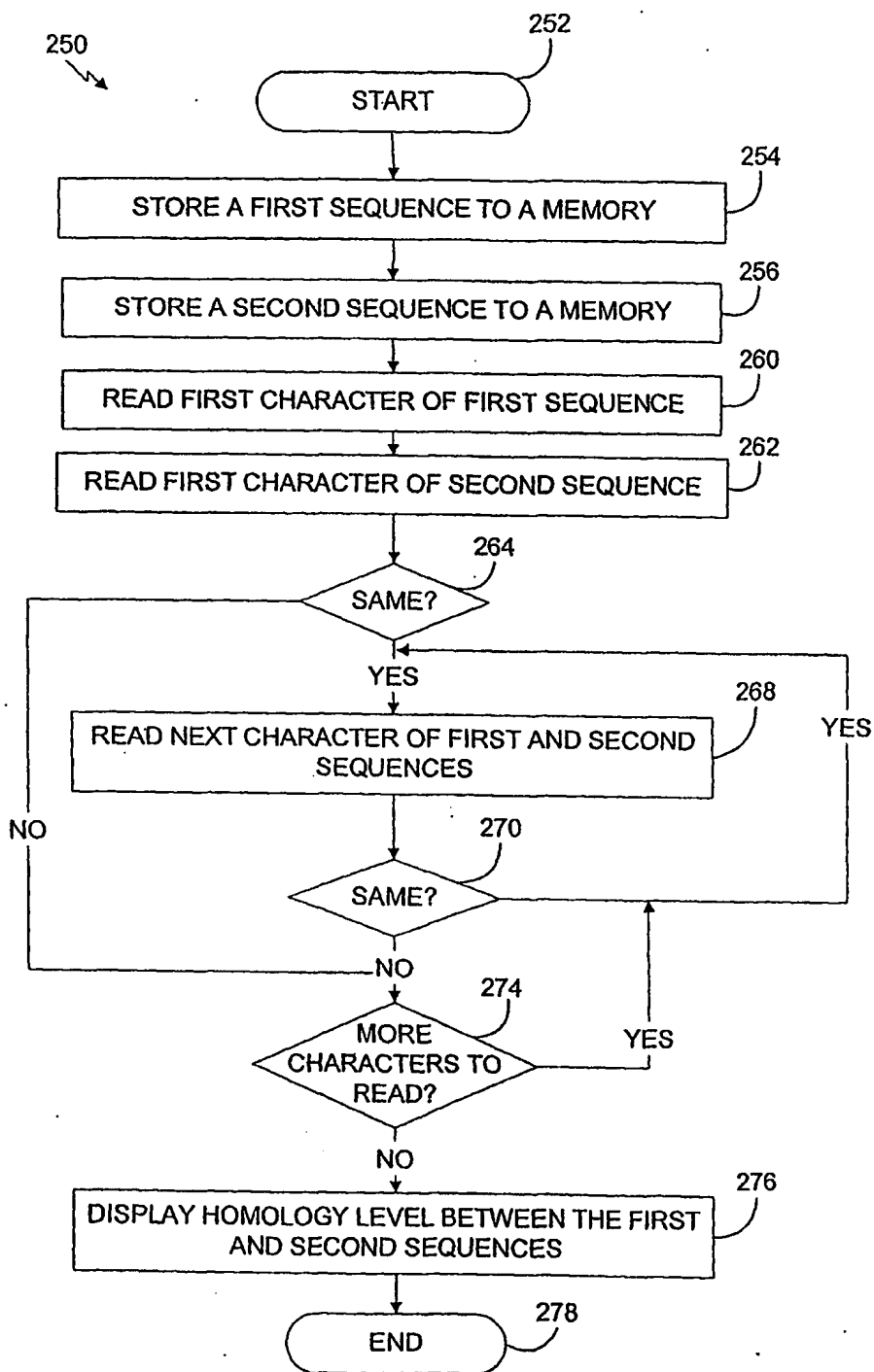


FIGURE 3

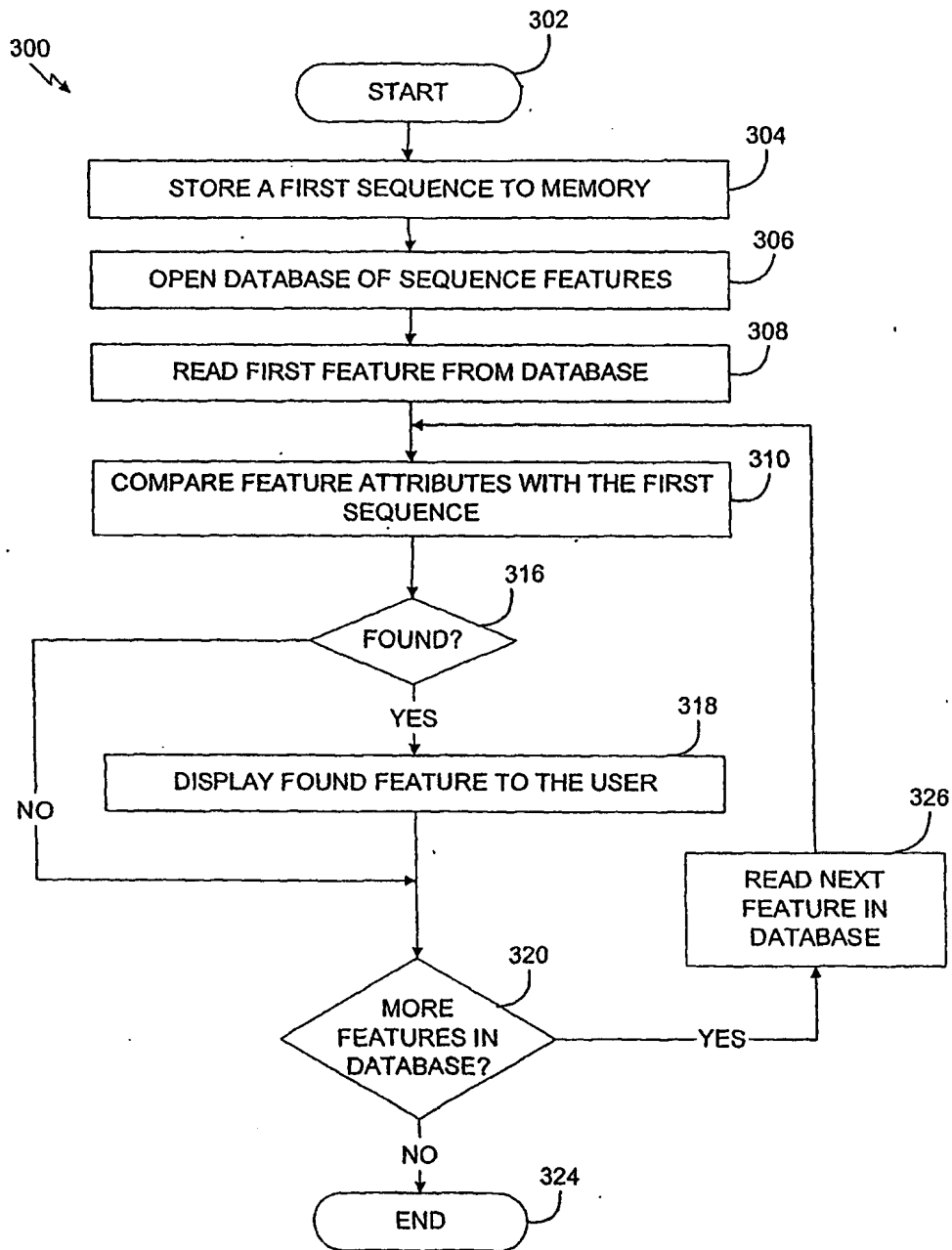


FIGURE 4